

LOCUS	AF165281	9497 bp	mRNA	linear	GenBank:U74563.1999
DEFINITION	Homo sapiens ATP cassette binding transporter 1 (ABCI) mRNA,				
	complete cds.				
ACCESSION	AF165281				
VERSION	AF165281.1	GI:5734100			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				

```

REFERENCE
AUTHORS      Eukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE        1 (bases 1 to 9497)

JOURNAL      Rust, S., Rostler, M., Funke, H., Reil, J., Amoura, Z., Piette, J. C.,
MEDLINE      Deleuze, J. F., Brewer, H. B., Duvrayer, N., Denefle, P. and Assmann, G.
PUBMED       Tangler disease is caused by mutations in the gene encoding
              ATP-binding cassette transporter 1
              Nat. Genet. 22 (4), 352-355 (1999)
              99364413
              10431238

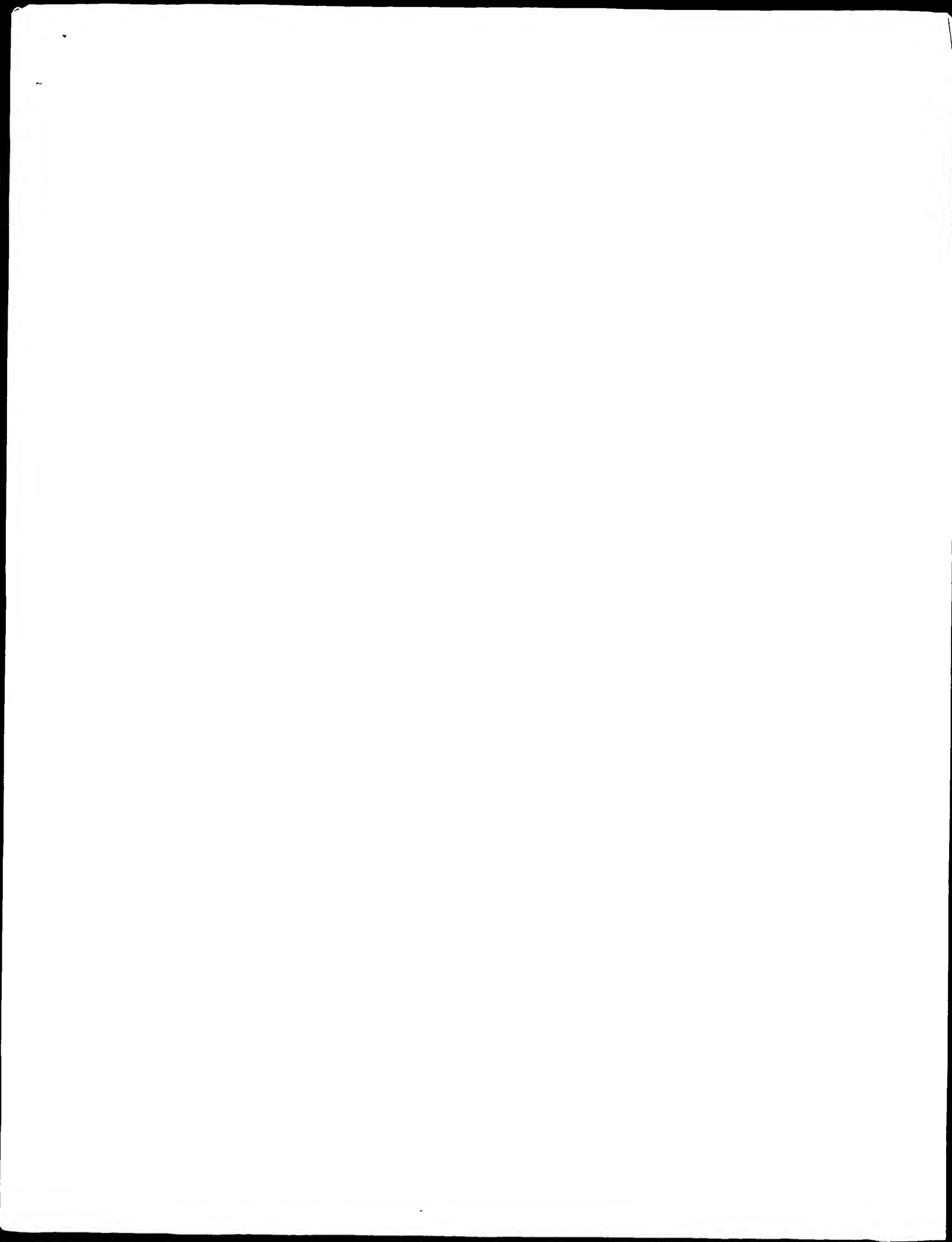
REFERENCE    2 (bases 1 to 9497)
AUTHORS      Rust, S., Rostler, M., Funke, H., Reil, J., Amoura, Z., Piette, J. C.,
              Deleuze, J. F., Brewer, H. B., Duvrayer, N., Denefle, P. and Assmann, G.
TITLE        Direct Submission
JOURNAL      Submitted (01-JUL-1999) Genomics, Rhone-Poulenc Rorer, 2 rue Gaston
              Crémieux, Evry 91006, France

FEATURES
source      Location/Qualifiers
              1..9497
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /chromosome="9"
              /map="9q31"
              1..9497
              /gene="ABCI"
              121..6726
              /gene="ABCI"
              /note="ABC transporter; ABC1 protein"
              /codon_start=1
              /product="ATP cassette binding transporter 1"
              /protein_id="BAD49849.1"
              /db_xref="GI:5734101"
              /translation="WPSAGTLPWVGIGICANNPCFRIPPTGEGAPGVGNRNKSTVAR
              LPSDARRLILYSQKDTSMKMDKRVLRITLQOILIKSSSNLKLDDFLVNDTFEGFLYHNH

```

SLKPSYDOKMLRADYDILTKHVFYLOGOLHILTSJLNCNGSKSEEMJLOJGDEVESELGLPRE
KLAABERYLBNNDILKPLTLFPLTNPSTSPSPSKLAEAKTLTJLSHJGLOAELEKSMRSM
SDMKOEVMFLITVNNSSSTQITLYOASRVLVCGHPBGSKIKSLNWDENJNNYALRFG
NGEEDAEETFYDNTSTPYCNDLNMKNLESSPSTLITWKLAKLVLGKLLTYPDTPAIRO
VMAEVTPEQLEIAVFDHLEGMWEEELSPKMTITMENSOSMDLVRMLDZSRLNDHWEQO
LDGJEDTANQDIYAFELAKHEDVOSSNGSYGIRPEAFNETNOAITTIRFMEJCNLKL
LIPATFWMJLOKSMELLDREKTFMAGIVFEGIRPGSIELPHVKAITKIRMDIDNERTK
TKGTYWDPGRADPPEEDMRYWNGSPRYLODYVEOAIIKIVLTGTEKTKGYVMOOMPC
YVDOTIFRWMSRMLPMTLWMLTYSVAITIKCIYVEKARKETMRJLMDGNSLWFS
WJISLSJLPLBVSAGLLVLTJLGNLLPSYAVISVEFVSVAVVYTIQCEPISLHRS
ANLAACGAGIITFYLLPYLYCYAMQDYGPVFLKJFASLISPAVAFGCEXFLAFBEO
GIYOMUONFESPPEEDGPNLTYSVMMLPDPFLGVMTWYIEAVFGQYGIPIRWYF
PCJTSYMPGSEDESKSPGNSOKRISIELCEEPHLEKAGISIONKIRBMDGAKT
DGLNLTBEGQITSEIGHNCAKTTTMSJLTGFLPPTSGTAYLIGKROIBEMSTION
LGVCPOHNVLEDMITVEEHTWFAIRLKGJSEKVAEEMOALDVGRLPSKLSKTSQ
LSEGMOKRISALALAFSGSKVYVILDEPTNGOVPYYSRGIWELLKTYRGRITJLISTH
MDEVDJADRITAILISHKCLCVGSSILFELTNOGVTYLYLWKNVSSLSACRNSST
VSYLKEDSVSSODAGLGDHSEDTLIDVSAISNLTIRKHSARVEJDVAGETSGV
VLPYEAKEGAFVETLFEHIDRLDLSIGSYSEPTLEELFIRLKVARSLEGVADTSGV
TLPARNRRAFGDKOSCLRPFTEDDAANDPNOSDIDPESRENDILSGMDKGSYOVKGM
KLTYOQVVALMLMKRLIARSRKGFPAITVPAVRYCALNPLSILPFRGKYPSLEQ
PMTNBOEYTFVNSDAPEDTDTLELNAUKRDPGFCRGEHSGIPDYTCQAGEBETLQ
ADPOTIMDLFONGMTMNPSPACOCSSDKIKMLPVPSPAGGAPPOKROKMTADJ
LODITGNRISLIVKTYVYOILIAKSLNKIMVNEFIRGGEFSLCVSTMOALPOSEODNNA
TKOMKHLIKLAKOSSADRFLNLSGRMTGIDRNNVKTWNKGNHJALSIVFTAMVYNNNA
TLRMLDKGEMPHSYGTITAPRNPRLTKOOLSVYAMPVNSYVLSIVFTAMVYNNNA
SFEVFLIOERYSKAKHLOPISGVKPYITWLSNVDMCMTVPYPAVLVITIFIPICROKS
VYSSNLPJVALMLLLLGMSITPLMTPASVREIPSTAVVLTVNLTEGINGSVATP
VLEJETDKLNNINDILKSVFLIEPHRCCLRGJLMDNOAMADLBERGGERVSPAT
SMDJLGRNLFMAVEGVFPLTVILOYREFIPRPVANKLPLDNDEEDVREKORAR
LDGGDONLIEIKRKTJYKRRKRPANDRCLVCIPIGCEOGLJLGNAGKSTFKML
GDTYTRGDALFARNLSLNSLNEHYONMKCPOFDAITELJLGRVFEFLRNGVPR
KEVGVNEMALIRKLGIVKCEKTAGNTOGKNRKTAAALIGRRPVYFLDEPTTGMH
PKARFELNMCALSVYKGBRSVYLTSHSMECEKLTCPBAIMVNGRRCLGSVOHLKNN
FDGQGTIVYRIAGSNPDLKIVODFFGLAFGSPKXKHNNMOJLOPSSLSTLAFITF
ILSOSKRHLIEDYSQOTTLIDGVFVAFKDGSDDDHLKDLMLSHKNQVYVAVLTFS
LODEKVESYV"

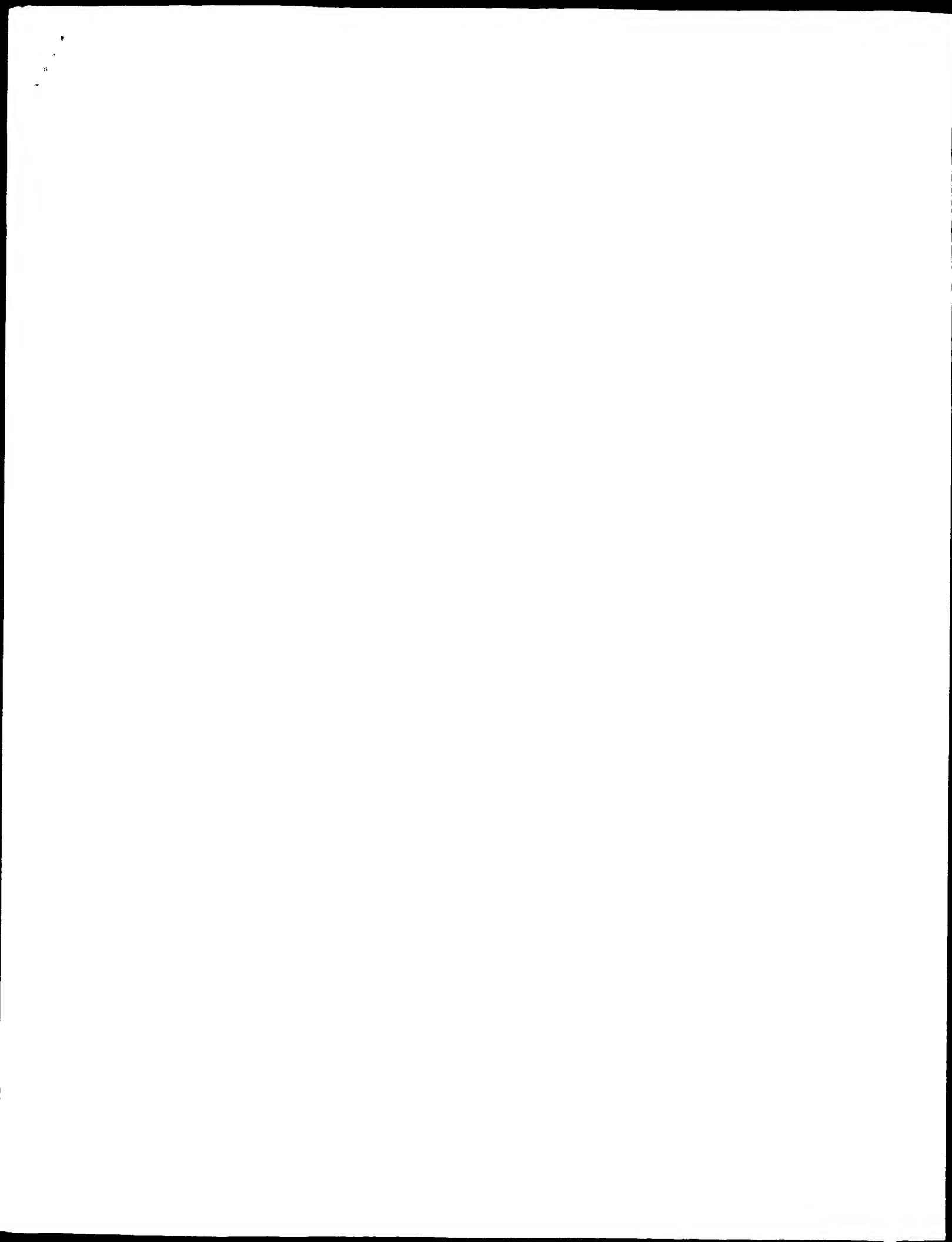
Query Match	90.4%;	Score 9444.6;	DB 9;	Length 9497;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 9464;	Conservative	0;	Mismatches 15;	Indels 1;
				Gaps 1;
Qy 351 caaacatgtaagctgttactggaagtgagcgtgcgtctattatcttcctgcattcggatc 410				
Db 1 CAAACATGTAGCTGTACTGGAAGGGCGCTGGCCTCTATTATCTTCGTAGCTGGATC 60				
Qy 411 tctgttcgctgtagcttaccacacccatgaaacaatgtagccatttccaataaagcc 470				
Db 61 TCTGTTCGGCTGAGCTACCCACCCTCTGAAACAATGAAATGCCATTTTCCAAATAAAGCC 120				
Qy 471 atgcccctcgaagaacacttcctcttggttcaaggagatcatctgtaatgccaacacccc 530				
Db 121 ATGCCCTCTCGAGAACACTCTCTTGGGTTCAAGGGGATTATCTGTAAATGCCAACACCCC 180				
Qy 531 tgttccgcttaccgcgactcctctggygaagctcccgagagttgttgaaacttaacaatcc 590				
Db 181 TGTTCGGTTACCCGACTCTCTGGGGAGCGCTCCCGGAGTGTGTGGAAATTTTAAACAAATTC 240				
Qy 591 atctggtctgcgcgtgttcctcagatgtctggaagcttccttataaagccagaagaaccc 650				
Db 241 ATTGTGCTGCCCTGTTCTCAGTACTCTCGAGGCTTCTTTATATACGCAAAAGACACC 300				
Qy 651 agcatgaagagacatgcgcaaaagttctgagaacattacagcagatcaagaatccagctca 710				
Db 301 AGCATGAAGGACAATGCCCAAAAGTTCTGAAATAATTACAGCGATCAAAAATTCAGCTCA 360				
Qy 711 aacttgaaagctcaaaagtttccgtgaggaacaatgaacacctctctggtttctctatcac 770				
Db 361 AACTTGAAGCTTCAAGATTTCTCGTGTGGACAAATGAACCTTCTCGGGTTCCTATACAC 420				



QY 771 aacctctctcccaagctctactgtgacaaagatgctgagggctgatactctccac 830
DB 421 AACCTCTCTCCCAAGCTCTACTGTGGACAAGATGCTAGGGCTGATTCATTTCTCCAC 480
QY 831 aaggtatttttgaaggaagctaccagttacatttgaacagctgtgcaatgatacaatca 890
DB 481 AAGGTATTTTGGCAAGGCTACAGTTACATTTCACAAAGTCTGTCGAATGATCAATAATCA 540
QY 891 gaagagatgattcaacttgttgacaaagaatttctgagctttgtgcttaccacaaagag 950
DB 541 GAAGAGATGATTCACATTGTGGACCAAGATTCTGAGCTTTGTGGCTTACCAAGAGG 600
QY 951 aaactgtctcagaagagagagtaacttcttccaaatgatacttccgaagccatccg 1010
DB 601 AAAGTGTCTCAGCAGAGGAGTCTGTTCCAACTGAGCAATCTGAAAGCCAAATCTG 660
QY 1011 agaacataacttatactatcccttcccgacgaagagagctgtgagccacaaataca 1070
DB 661 AGAACATAACTTACTATCTCTCTCCGAGCAAGAGAGCTGGCCGCAAGCAAAAACA 720
QY 1071 ttgtctgatagttcttggacttggccagagagctgttccagatgagaagctgtgagac 1130
DB 721 TTGTGTGATGTTTGGGACTGTGGCCAGAGCTGTTCAAGCATGAGAAGCTGGAGTAC 780
QY 1131 atgcgaagagagtgatgttcttgcacaaatgtgaaagcttccagcttccacccaatc 1190
DB 781 ATGCGACAGAGAGTGTGATGTTCTGACCAATGTGAACAGCTCCATCCATCCCAATC 840
QY 1191 taacagagtggtgtctgtattgtctgtcgagcatcccgagagaggggctgtaagaatcaag 1250
DB 841 TACCAAGGCTGTGTCTGATGTTCTGACCAATGTGAACAGCTCCATCCATCCCAATC 900
QY 1251 tctctcaactgtagtaggaacaaactaagaagccctcttggagggcaatgtgacatgag 1310
DB 901 TCTCTCAACTGGTATGAGAGACAACAACAAAGCCCTTGTGGAGGCAATGGCACTGAG 960
QY 1311 gaagatgtgaaacttctatgaaactctcaactcttactgaattgataag 1370
DB 961 GAGAGTGTGAAACCTTCTATGACAACTCTACACTCTTACTGCAATGATTTGATGAAG 1020
QY 1371 aattggaatcagtcctcttcccgcaatctatctgaaagctctgaaagccgtctgct 1430
DB 1021 AATTGGAGTCTAGTCTCTTCCGCAATATCTGAAAGCTCTGAAAGCCGTGCTGCT 1080
QY 1431 ggggaagatccgtatatacactgaaactccagccacaaagcagtgatgtgagtgaaac 1490
DB 1081 GGGAAATCTCTGTATACACTGTGACCAAGGCAAGGCAAGGCTGATGGTGAAGTGAAC 1140
QY 1491 aagaacttccagaaactgtgtgtctcagatctgaaagcagtgaggagaaactcagc 1550
DB 1141 AAGACTCTCCAGAGACTGTGCTGTCTGATGATCTGAAAGGCTGTGGAGAGCACTCAGC 1200
QY 1551 cccaagatcgtgacacttcatgagaaacagccaaagaatgaaactgttccgagatgtctgtg 1610
DB 1201 CCCAAGATCTGAGACTCTCATGAGAAACAGCAAGAAATGAGACTGTGCGGATGCTGTG 1260
QY 1611 gacagcagggacaatgacaacttctgggaacagcagtgatgagtgatgagtgaaagcc 1670
DB 1261 GACAGCAGGGACAATGACCACTTTTGGGAACAGCAGTTGGATGGCTTGAATTGACAGCC 1320
QY 1671 caagacatgtgtgtgttctggccaaagcaccagagagatctccagttcaataatgttct 1730
DB 1321 CAAGACATGCTGTGGCTTTTGGCCAAACACCCAGAGATCTCCAGTCCAAATATGCTGT 1380
QY 1731 gtgtacacccgtgagaagaagcttccaacgaaactaaccaggaatcccgaccataatctgc 1790
DB 1381 GTGTACACCTGTGAGAGAAAGCTTCAACGAGACTTAACAGCAATCCCGACATATCTCCG 1440
QY 1791 ttcatgtgagtgatgtaactcgtgaaagcagtgaaagccatagcaacagaagctgtgcatc 1850
DB 1441 TTCTATGAGTGTGTCAACCTGAGAAACCTTAAGCAACAGAAAGTGTGCTATC 1500
QY 1910 aacaagtcacatgagcgtgctgagtgagagagagcttctggtgtatgttactgga 1910

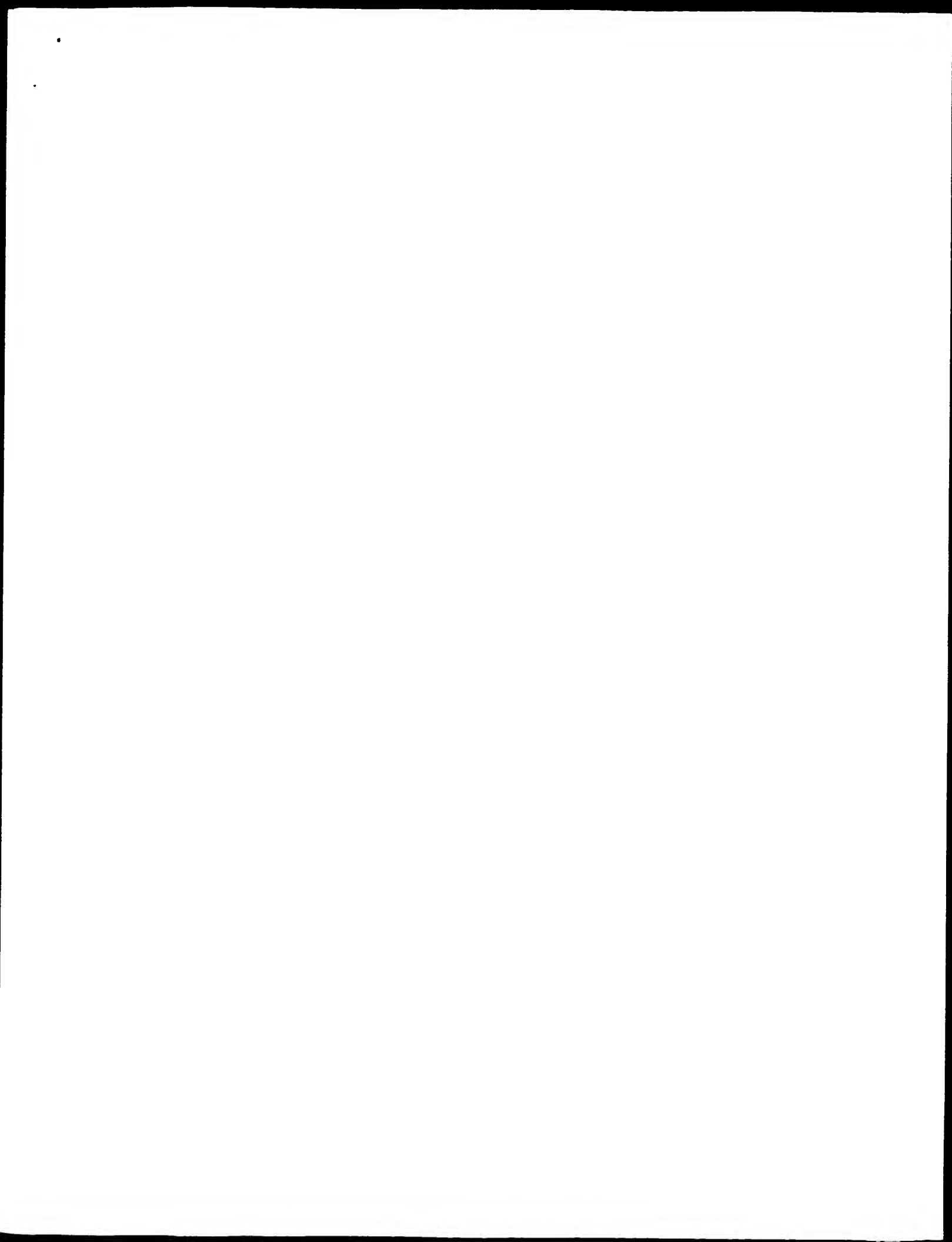
DB 1501 AACAAATCCATGAGCTGCTGGATGAGAGAAATTCGGGCTGTGTTTGTCTACTGGA 1560
QY 1911 attactcagcagcatttggatgtgtcccatcatgtaagaatccgaatgacatt 1970
DB 1561 ATTACTCCAGCAGCATGATGACTCCCATCATCTCATGATGACAAAGATTCGAATGACATT 1620
QY 1971 gacatgtgagagagacaataaatacaagatgtgtaactgtggaacctgtgtcctgaact 2030
DB 1621 GACATGTGAGAGAGACAATAATAAATCAAGATGTGATCTGGAGCCCTGTCTGAGCT 1680
QY 2031 gaaccttggagaaatgctgtaactgtgtgggggggcttccacttgaagatgtgtg 2090
DB 1681 GACCCCTTGAAGACATCGGTGAGCTGTGGGGGCTTCCCTTACTGCAAGATGTG 1740
QY 2091 gaggcgaatcatcaaggtgtgtgacggacccgaaagaanaactgtgtctatagcaa 2150
DB 1741 GAGCAGGCAATCATAGAGTGTGTGACGGGACCCGAGAAAGAAACAGGCTATATGCAA 1800
QY 2151 cagatgcccataccctgttaagtgtgacatcttctgtggtgtgtatgagccgttcaatg 2210
DB 1801 CAGATGCCCTATCCCTGTACCTGTATGATGACATCTTCTGGGGTATGAGCCGGTCAATG 1860
QY 2211 ccccttcatgagcgt 2270
DB 1861 CCCCTTATGACGCTGTGGCTGTGATTTACTCAGTGGCTGTATCATCAAGGGCATGCTG 1920
QY 2271 tatgagaagagagcagagctgtgaaagacatgagatcatgagccgtgacaacagcata 2330
DB 1921 TATGAGAAGAGGACAGGCTGAAAGAGACCATGCGGATCATGAGGCTGAGCAACAGCATC 1980
QY 2331 ctctgtttagctgtgtatcatagtagccatctccttctgtgtgtgtgtgtgtgtgtgt 2390
DB 1981 CTCGT 2040
QY 2391 gtgtgtatccttgaatgttagaaacccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2450
DB 2041 GTGTGTATCTGAGATGAGAAACCTGTCTCCTACAGTATGCCAGCGGTGTGTGTGTC 2100
QY 2451 ttctgtcgt 2510
DB 2101 TTCTGTGCGGTTGT 2160
QY 2511 tccagagcacaactgtgacagcagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2570
DB 2161 TCCAGAGCCAACTGTGAGAGAGCCCTGTGGGGCTTCATCTTCACTTCACTGCTGAC 2220
QY 2571 taagtctgt 2630
DB 2221 TACGTCTGT 2280
QY 2631 ctgtgtctcgt 2690
DB 2281 CTGCTGTCTCTGT 2340
QY 2691 ggcattgagtgagtgaggaacactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2750
DB 2341 GGCATTGAGTGACATGTGGAGCAACCTGTTTGAAGATCTGTGTGGAGAGATGTGCTTAAT 2400
QY 2751 cccacacacttgatctcatatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2810
DB 2401 CTACACACTCTGCTGT 2460
QY 2811 tacattgagcgt 2870
DB 2461 TACATTGAGAGCTGTCTTCCAGGCAAGCAAGCAATCCAGGCTGTGTATTTCTCTTGC 2520
QY 2871 accaagctcactgt 2930
DB 2521 ACCAAGTCTCTACTGT 2580
QY 2931 aagagaatgtcagaatcgtgagtgagagagagcaccacttgaagctgtgtgtgtgtgt 2990

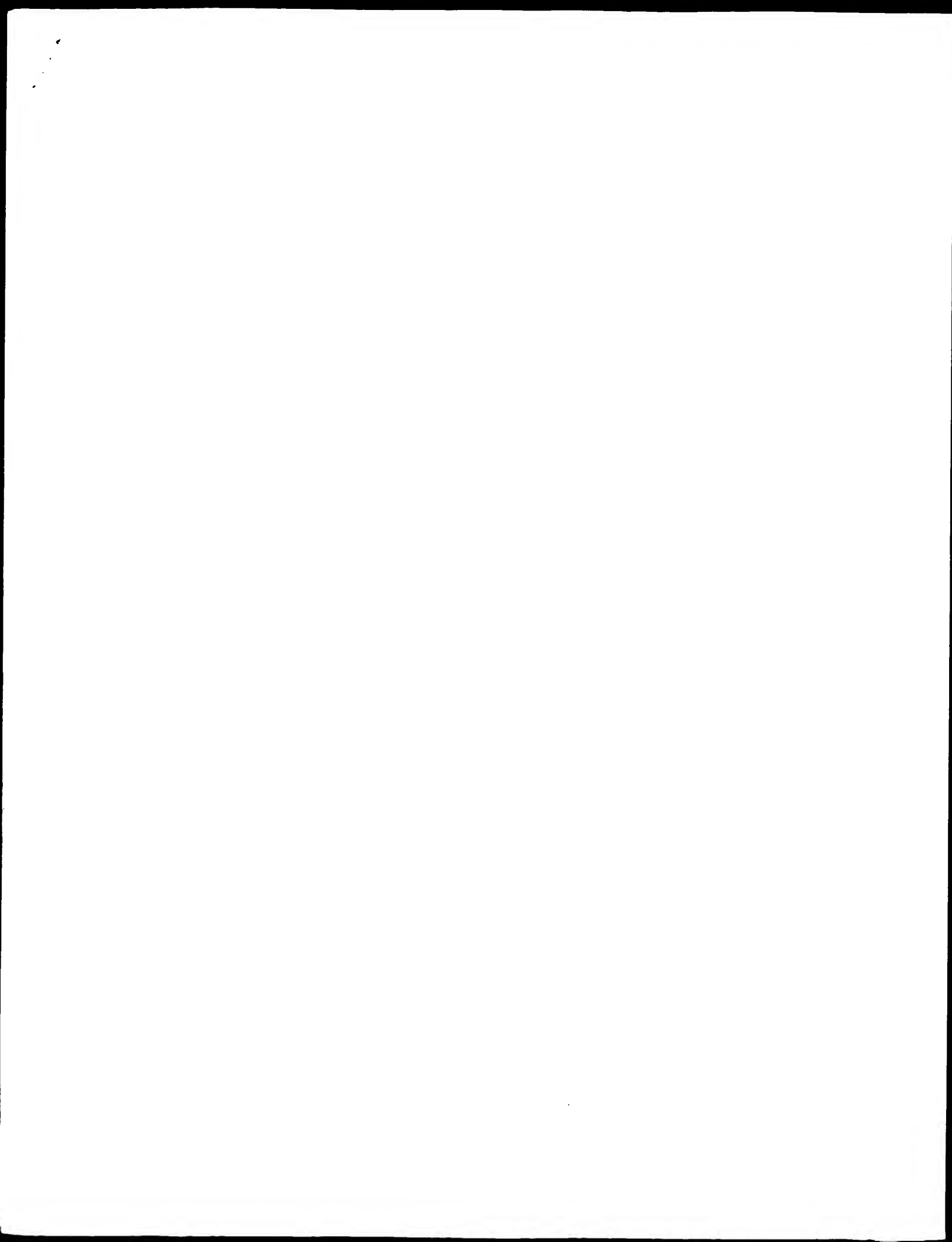
04
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100



5131 gggaggaacccatagcaatggaatcctgcttcaatcaatcccccgaatccaccag 5210
4801 ggaggaacccatagcaatggaatcctgcttcaatcaatcccccgaatccaccag 4880
5211 cagagccctcagagagtgctcctgcatgacacacatcagtgagtgctccttgctcctatgt 5270
4861 cagcagcctcagagagtgctcctgcatgacacacatcagtgagtgctccttgctcctatgt 4920
5271 gtcaccttgcaatgctcctgctcctcagcagccttgctcctgcatcctcagtcagagcag 5330
4921 gtcaccttgcaatgctcctgctcctcagcagccttgctcctgcatcctcagtcagagcag 4980
5331 gtcagcaagcaaaac 5390
4981 gtcaccaaaac 5040
5391 tctaatcttgctcagagatgagcaatcagtgctcctcagcagccttgctcctcagtcagag 5450
5041 tctaatcttgctcagagatgagcaatcagtgctcctcagcagccttgctcctcagtcagag 5100
5451 ttcacatgctcagcagcaagtcctatgctcctcagcagccttgctcctcagtcagagcct 5510
5101 ttcacatgctcagcagcaagtcctatgctcctcagcagccttgctcctcagtcagagcct 5160
5511 ctaacttgctcagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 5570
5161 ctaacttgctcagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 5220
5571 aagatcccccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 5630
5221 aagatcccccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 5280
5631 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 5690
5281 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 5340
5691 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 5750
5341 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 5400
5751 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 5810
5401 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 5460
5811 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 5870
5461 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 5920
5871 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 5930
5921 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 5980
5931 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 5990
5981 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 6050
5991 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 6050
6051 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 6110
6061 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 6170
6111 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 6170
6171 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 6230
6231 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 6230
6241 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 6290
6291 ggcagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 6290

5881 atccatgaagatgacatgacatgacatgacatgacatgacatgacatgacatgacatgacatg 5940
6291 tgcag 6350
5941 tgcag 6000
6351 gtcag 6410
6001 gtcag 6060
6411 gtcag 6470
6061 gtcag 6120
6471 gtcag 6530
6121 gtcag 6180
6531 gtcag 6590
6181 gtcag 6240
6591 gtcag 6650
6241 gtcag 6300
6651 gtcag 6710
6301 gtcag 6360
6711 gtcag 6770
6361 gtcag 6420
6771 gtcag 6480
6421 gtcag 6540
6481 gtcag 6540
6541 gtcag 6600
6551 gtcag 6660
6601 gtcag 6660
6661 gtcag 6700
6701 gtcag 6720
6721 gtcag 6780
6781 gtcag 6840
6841 gtcag 6900
6901 gtcag 6960
7311 gtcag 7370





GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2002, 12:54:11 ; Search time 55.68 Seconds
(without alignments)
4510.378 Million cell updates/sec

Title: US-09-595-526B-2

Perfect score: 11797
Sequence: 1 MACWPQLRLIMKMLTFRRR.....VDAVALTSFLDEKVESYV 2261

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11797	100.0	2261	22	AA1981361 Amino acid sequenc
2	11797	100.0	2261	22	AA1981365 Amino acid sequenc
3	11793	100.0	2261	21	AA1981117 Human ABC1 cholest
4	11793	100.0	2261	22	AA1981362 Amino acid sequenc
5	11793	100.0	2261	22	AA1981366 Amino acid sequenc
6	11792	100.0	2261	21	AA1981109 Human ABC1 cholest
7	11789	99.9	2261	21	AA1980882 Human ABC1 cholest
8	11789	99.9	2261	22	AA1981749 Human ABC1 protein
9	11789	99.9	2261	22	AA1981363 Amino acid sequenc
10	11789	99.9	2261	22	AA1981367 Amino acid sequenc
11	11786	99.9	2261	21	AA1981111 Human ABC1 cholest

12	11786	99.9	2261	21	AA1981114 Human ABC1 cholest
13	11786	99.9	2261	21	AA1981115 Human ABC1 cholest
14	11785	99.9	2261	21	AA1981105 Human ABC1 cholest
15	11785	99.9	2261	21	AA1981110 Human ABC1 cholest
16	11784	99.9	2261	21	AA1981113 Human ABC1 cholest
17	11784	99.9	2261	21	AA1981116 Human ABC1 cholest
18	11783	99.9	2261	21	AA1981112 Human ABC1 cholest
19	11777	99.8	2261	21	AA1981104 Human ABC1 cholest
20	11774.5	99.8	2260	21	AA1981016 Human ABC1 cholest
21	11771	99.8	2261	22	AA1982183 Human ABC1 mutant
22	11767	99.7	2259	21	AA1983107 Human ABC1 FHA-3 m
23	11767	99.7	2261	22	AA1983022 Human ATP binding
24	11767	99.7	2261	22	AA1985028 Human ABC1. Homo
25	11767	99.7	2261	22	AA1982176 Human ABC1 mutant
26	11764	99.7	2261	22	AA1982188 Human ABC1 mutant
27	11764	99.7	2261	22	AA1982189 Human ABC1 mutant
28	11763	99.7	2261	22	AA1982181 Human ABC1 mutant
29	11761	99.7	2261	22	AA1982181 Human ABC1 mutant
30	11760	99.7	2261	22	AA198550 Human ABC1 homolo
31	11760	99.7	2263	22	AA19811956 Human ABC1 homolo
32	11760	99.7	2263	22	AA198534 Human ABC1 mutant
33	11759	99.7	2261	22	AA1982182 Human ABC1 mutant
34	11759	99.7	2261	22	AA1982186 Human ABC1 mutant
35	11433	96.9	2201	21	AA198380 Human ATP binding
36	11433	96.9	2201	21	AA1983021 Human ATP binding
37	11433	96.9	2201	21	AA1985027 Human ABC1 binding
38	11398	94.9	2143	21	AA1983108 Human ABC1 cholest
39	11015	93.4	2130	22	AA1982187 Human ABC1 mutant
40	7988	67.7	1525	22	AA1982187 Human ABC1 mutant
41	5858.5	49.7	2273	19	AA19870398 ATP binding cassel
42	5849	49.6	1144	22	AA1982184 Human ABC1 mutant
43	5849	49.6	1144	22	AA1982185 Human ABC1 mutant
44	5755.5	48.8	2146	22	AA1980483 Human PD-ATP-bind
45	5715	48.4	1089	22	AA19862691 Human ABC1 protein

ALIGNMENTS

RESULT 1
AAB31361 AAB31361 standard. Protein; 2261 AA.
XX
AC AAB31361;
XX
DT 20-APR-2001 (first entry)
XX
DE Amino acid sequence of a human ABC1 polypeptide.
XX
XX Human: adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilization; cholesterol; Tangier disease;
KW chromosome 9q22-q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport.
XX
OS Homo sapiens.
XX
PN WO200078972-A2.
XX
PD 28-DEC-2000.
XX
PE 16-JUN-2000; 2000MO-US16765.
XX
PR 18-JUN-1999; 9905-0140264.
PR 14-SEP-1999; 9905-0153872.
PR 19-NOV-1999; 9905-0166573.
XX
PA (CVTH-) CV THERAPEUTICS INC.
XX
PI Lawn RM, Wade D, Garvin M;
XX WPI; 2001-137812/14.
XX
PT Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide;

PT useful for the development of agents for the treatment of heart disease
 CC and other disorders associated with hypercholesterolemia and
 PT atherosclerosis

PS Disclosure: Page 128-143; 215pp; English.

XX The present sequence represents a human adenosine triphosphate (ATP)
 CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
 CC membranes and utilizes ATP hydrolysis to transport a wide variety of
 CC substrates across the plasma membrane. ABC1 is a pivotal protein in
 CC the apolipoprotein-mediated mobilization of intracellular cholesterol
 CC stores. ABC1 is defective in Tangier disease, a genetic disorder
 CC characterized by abnormal HDL-cholesterol metabolism. The ABC1 gene is
 CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
 CC useful for developing pharmaceutical agents for the treatment of heart
 CC disease and other disorders associated with hypercholesterolemia and
 CC atherosclerosis. The genes are useful for developing screening assays to
 CC screen for compounds that regulate the expression of genes associated
 CC with cholesterol transport. The genes and proteins are also useful for
 CC are also useful as diagnostic indicators of cardiovascular disease and
 CC other disorders associated with hypercholesterolemia.

XX Sequence 2261 AA:

Query Match 100.0%; Score 11797; DB 22; Length 2261;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACHPQLRLMKMLTTRRRQTCOLLVAMPFLFLLISVRLSYPPYQHECHPNKA 60
 Db 1 macpqlrlrlmkmlttrrrtqcollvampflfllisvrlsyppyechechfnka 60
 QY 61 MPSAGTLPWVGITICNNANPCFRYPTRPEAGVGVGNFNKSVARLSEADARLLLSYKOT 120
 Db 61 mpsagtlpwwggitcnnanpcfryptrpeagvgyvgnfnksivarllsadarlllyskdt 120
 QY 121 SMKMRVLTLOQIKKSSNMLKLODFLVNETSGFLYNLSPKSTVDMKLADVILH 180
 Db 121 smkmrvltrlqgikksnmlkldflvnetsgflynlspkstvdmklradvllh 180
 QY 181 KVFLOGLVHLTSCNKSSEEMQLQDOVSELCGPKFKLAAEFVRLSNMDILKPL 240
 Db 181 kvflqglvhltsicnksseemqlqdgveselcgpkfklaaaevrlsnmdilkp1l 240
 QY 241 RLINSTSPFSKELAEATKTLHSLGLTAELEFSMRSWMDROVMEITVNSSSSTOI 300
 Db 241 rlinstspfskelaetktrlhslgltaelcfsmrswsmdrvmefltvnsststql 300
 QY 301 YQAVSRIVCGHPBGGLIKISLWMEEDNNYKALFGNGTEDEAEETFDNSTTPYCNLDMK 360
 Db 301 yqavsrlvcghpbgglkikslwmednnykalfgngteedaetfydnsttpycondlkm 360
 QY 361 NLSSPSRLITIMKALKLIVGKITVTPDPATQVMAEVNKKTOELAVHDLFGMEELIS 420
 Db 361 nlespsrlitlmkalklilvgkitvtpdpqtrqmaevnkktoelavhldlegmweels 420
 QY 421 PKIWTMENSOEMDLVRLMLDSRDNDHFWEQDGLDMLTADIVAFIAKHPEDVSSNGS 480
 Db 421 pkiwtmensoemdlvrmldsrndhfwegqldgladivafiahphedvsgsngs 480
 QY 481 VYTWRAFNNTNQAIRTISFMECVNLKLEPLATEVWLINNSMELIDERRKFWAGIVFTG 540
 Db 481 vytwrafnntnqairtisfmevcvnlkleplatevwlinsmeliderrkfwagivftg 540
 QY 541 ITPGSITELPHHVVYKTRMDIDNVERNTKIDGKWDPGRADPEEDMRVYWGFAFLQDNY 600
 Db 541 itpgsitelphhvvktrmdidnverntkldgkwdpgradpedemrwywgafaylqdv 600
 QY 601 EDAIIVLTGTEKTKGVYQOMPYPDYVDILFRLVWSRSMPLFMTLAWISYAAVILKGIY 660
 Db 601 eqaiivltgtekkgvymqypdyvdfilfrymsrsmplfmltawisyavvilkgiy 660

QY 661 YEKEARLKEWTRIMGDINSTIMSWFISLIPLLVSAGLLVYLKGNLLPDSQSVFV 720
 Db 661 yekearlketumimgdinstimswfislipllvsagllvylkgnllpdsqsvfv 720
 QY 721 FLISFAVAVTLQCFLLISTLFSRANLAAAGGIIYFTLYPYVYCVAMQDYGETLKIFPS 780
 Db 721 flisfavavtlqcfllistlfsranlaaaggiiyftlypyvycvawqdyvflkifas 780
 QY 781 LLSPVAFEGCEYFALFEEOGIGVQMDNLFESPFEEDGPNLTTSISMJLDTFLYGVMT 840
 Db 781 llspvafegceyfalfeegigvqmdnlfespeeedgpnlttsismjldtflylvmt 840
 QY 841 YIYAVPQGYIPRPYFFCTSYWNGESDEKSHGSKQKMSLCEMEEPYHLKLGVS 900
 Db 841 yiyavpogyiprpyffctsywngesdekshgskqkmslcemeepthlklgvs 900
 QY 901 IQMLVYVYRDKMVAVDGALNLFEGQIRSFIGNHAGKTTMTSLITGFPSTGAVIL 960
 Db 901 iqmlvyvyrdkmvavdgalnlfegqirsfignhagkttmtslitgfpstgavil 960
 QY 961 GKDISEMSTIRONLGVCPQHNVLFDMLTVEEHIMFYARLKLSEKHVKAEMQALDVG 1020
 Db 961 gkdiseemstironglvcphnvlfdmltveehimfyarlklsekhvkaemqaldvg 1020
 QY 1021 LPSSKILSKTSQSGMOKSLVALAFVGSKVYVILDEPTAGVDPRYSRKGIWELLKTRQ 1080
 Db 1021 lpskilsksqsgmqklsvalafvgskvvyldeptagvdprysrkgiwellkkyrq 1080
 QY 1081 GRTIILSTHMDADVLDGRIRALISHGKLCYSSSLFLKNQIGTYVTLVKKDVESLS 1140
 Db 1081 grtilsthmdeadvldgriralishgkccyssslflknqigtyvtilvkdvessls 1140
 QY 1141 SCRNSSTSYLKKEDSVOSSSDAGLGSDBHSDTLTIDVSAISNLIRKHVSEARLYEDT 1200
 Db 1141 scrnsstsyllkedsvosssdaqlgsdhesdtlidvsaaisnlirkhvsearlyedi 1200
 QY 1201 GHELTLYVLYPEAKGAEFELFHEIDDRSDLGISYSEPTLEIFLKAESGVDAE 1260
 Db 1201 gheiltyvlypeakgaevelfheidrrsdlgisysseptleiflkaesgvdae 1260
 QY 1261 TSDGTLPARNRRAFGDKQSLRPPTEDDADPNDSIDPESRETDLSGMDGSGSYOVK 1320
 Db 1261 tsdgtlparnrtrafgdqslrppteddaadpnstdpesredtlsgmdgsgsyovk 1320
 QY 1321 GKKLTQOQFVALMKRLILARSRKGFQAQIYLAVFCTIALVSLYPPPGKPSLELQ 1380
 Db 1321 gkkl tqoqfvalmkrlilarsrkgfqaqiylavfctialvslpppgkpslelq 1380
 QY 1381 PMVNEQYTFVSNDAPEDTGLTELNLALTKDPGCTRCMBGNPIPDPPCOAGEEWMTAP 1440
 Db 1381 pmvneqytfvsnadpedtgltelnlaltkdpgctrcmbgnpi dpdpcoageewmtap 1440
 QY 1441 VPQITMDLFPQNGNMTWQNPSPACQSSDKIKMLPVCPPGAGLPPQKQKNTADILQDL 1500
 Db 1441 vpgitmdlfpqngnmtwqnp spacqssdkikmlpvcppgaglp p p q k q k n t a d i l q d l 1500
 QY 1501 TGRNISTDLVTVYQOIIKSLKINKIWEERFYGGFSGVSTQALPPSOEVNDAIKQMK 1560
 Db 1501 tgrnistdlvtyyqoii kslkink iweerfyggfsgvstqalppsgevn da ik q m k 1560
 QY 1561 HLKLAQSSADRLNLSLGRFMTGLDTRNNYKVPWNNKGWHAISFLVANNALIRANLQK 1620
 Db 1561 hllakdssadrlnls lgrf mt gl dtr nny k v p w n n k g w h a i s f l v a n n a l i r a n l q k 1620
 QY 1621 GENSHGITAENPPLNLTQOOLSEVALMTTSDVVLVSICVIFAMSFVSPVFLIOER 1680
 Db 1621 genshgitaenpplnltqo olsevalmttsdvvlvsicvifamsfvspvflioer 1680
 QY 1681 VSKAKHLOEISGVKPVYVYVSNFWMDCNVVPATVITIFIFEOOKSSYSSNLPVIAL 1740
 Db 1681 vskakhloeisgvkpvvyvysnfwm dcnvvp atv it i f i f e o o k s s y s s n l p v i a l 1740
 QY 1741 LLLLYGWSITPLMYPASFVERKIDSTAVVVLTVNLFTGINGSVATFVLELFTDNKNININ 1800

Db	1741 ygsstclpmjpaafvfkipsdyavltsvnlfingvsatvflelftdnklnnn	1800
OY	1801 DILKSFLLFPFHLGRGLIDWVKNQAMADALEREGENREVSPLSMDLVGNLFMAAVES	1860
Db	1801 dlksvflifpfclcgslldmynqamadaletfgenfvspiswldvgnlfamaveg	1860
OY	1861 VVEFLITVLIOYRFFIPRPVNAKLSPLNDEDEDVRERORILLDGGGNDLLEIKELTKI	1920
Db	1861 vvflilvtvllygrffllprpvnaklsplndededvrerqrilldgsgndlleikeltk	1920
OY	1921 YRRKKRPAYDRICVGIPPECEFGILLGVNGAKSKSPFKMLTGDTVTYRGDAFLKNSILSN	1980
Db	1921 yrrkrkpavdricvygippcefgllgvngakskstfkmltgdtltvrgdaflnksilsn	1980
OY	1981 IHEHVHNMGCYCPQPAITEILLTGEHEHEFPALLRGVEKEVKVGEEMAIRKLGLVKYGEK	2040
Db	1981 ihelvhnmgycpqdaiteelltgehevefallrtypekevykygewairklglivkyek	2040
OY	2041 YAGNYSGNKRRLSTAMALLIGPPEVPLEDEPTTGMDPKARFLMNCALSIVYKEGSVLT	2100
Db	2041 yaegnysgnrkrlstamalligpppevpledepttgmpkarflimncalsivykesrvlt	2100
OY	2101 SHMECECALCTRRMALIMVNGFRCLGSVOHLKRNPGDGTYTIVARIGSNPDLPKPDPFG	2160
Db	2101 shmececalcterrmalmvngrfrclgsvoqlknrtfdgytlvvrtlaagsnpdlkpyqdfg	2160
OY	2161 LAFPGSVLKKEKHRRNMILOYQLPSSLSLARIFSLISQSKRKLHIEDYSVQTTLDOVFYNF	2220
Db	2161 lafpgsvlkekhhrrnmloyqlpsslslarifslisqskrcrlhedysvqtlldqvfynf	2220
OY	2221 AKDQSDDLKLDLSLHKNGTVYDVAVLTSTFLODEKKVESYV	2261
Db	2221 akdqsddhlkdlslnkngtvdvavltstfldgekvesyv	2261
 RESULT 2		
AABJ31365		
ID	AABJ31365 standard; Protein: 2261 AA.	
XX		
AC	AABJ31365;	
XX		
DT	20-APR-2001 (first entry)	
XX		
DE	Amino acid sequence of a human ABC1 polypeptide.	
XX		
KM	Human: adenosine triphosphate binding cassette protein 1; ABC1;	
KM	apolipoprotein-mediated mobilization; cholesterol; Tangier disease;	
KM	chromosome 9q22-q31; heart disease; hypercholesterolemia;	
KM	atherosclerosis; cholesterol transport.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200078971-A2.	
XX		
PD	28-DEC-2000.	
XX		
PF	16-JUN-2000; 2000MO-US16591.	
XX		
PR	18-JUN-1999; 99US-0140264.	
PR	14-SEP-1999; 99US-0153872.	
PR	19-NOV-1999; 99US-0166573.	
XX		
PA	(CVTH-) CV THERAPEUTICS INC.	
PA	(UNITV) UNITV WASHINGTON.	
XX		
PI	Lawn RM, Wade D, Oram JF, Garvin M;	
XX		
DR	WPI; 2001-137811/14.	
DR	N-PsDB; AAF24702.	
XX		
PT	Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides useful for treatment of heart disease	

Query Match	100.0%	Score 117971	DB 22	Length 2261
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2261	Conservative 0	Mismatches 0	Indels 0	Gaps 0
1	MACWQPLRLILMKMLNLFRRRQTCOLLLEVAMPFLIFLILISVRLSYPRYEQHECHPNKA	60		
1	macwqplrlilwkhnlfrtrrctqlllevampfliflilsvrlsypryqhechfnka	60		
61	MSAGTLPWVOGIIICNANNPCFRPPRPGAPGVNGFNKSTVARRLFSPARALLYSOKDT	120		
61	msagtlpwvogiicnannpcfrpprpgapgvngfnkstvarlfsparallilysqkdt	120		
121	SMKDRKVLRLTQQIKRSSNLKLDQFLVDNENFSGFLYHNLSLPKSTVDKMLRADVYLH	180		
121	smkdrkvlrltqqikrssnlkldqflvdnfnsgflyhnlslpkstvdckmlradvylh	180		
181	KYFLOGIQLHLTSLCNGSKSFEMQLQDDQVSLGCLPKXILAAERYLRSMQILPIL	240		
181	kyflogiqlhltslcngsksfemqlqddqvslgclpkxilaerylrsmqilpil	240		
241	RTLNSTSPPSKEIAEATKTLHSLGTLAQLDELPSMSWSMDMQEYVPLTNVNSSSSTOI	300		
241	rtlnstsppskeiaeatktlhslgltlaqldelpsmswsmdmqeyvpltnvnsssstoi	300		
301	YQAVSRIVCGHPGGGGLIKSLNMYEDNNYKALFGNGTNEBAEFYDNTSTPYCNQMLK	360		
301	yqavsrivcghpggglikslnmeyednnkalfngntnebaefydnsttpyqcnmlk	360		
361	NLSSPSLRILIKALKKPLLVGKILYTPEDPFRATQVAAVNAKTFQELAVAFHDLGKMEELS	420		
361	nlsspslrilikalpkllvgkilypdpfratqvaaavnaktfqelavafhdlgkmeels	420		
421	PKTWTMENSQEMDLVRMLLDSRDNHFWEQQLDGLDWTAAQDIAVAFIAKHPEDVOSSNGS	480		
421	pktwtmnsqemdlvrmlldsrndhfweqqldglwdttaaadiavafiakhpedsngs	480		
481	VYTWRAPEFETNOAIRTSIREMECVNLNKLEPATAETEWMLINKSMELLDLRKFMAGIVTGG	540		
481	vytwrapefetnoairtsiremevcvnlklepataetewmlinksmelldlrkfmagivtgg	540		
541	ITPGSIELPHAHYKXIRMDINVERTNKIKGVDPPRADPEEDMARVYWGCFAYLADVV	600		
541	itpgsielephahyxirmdinvertnkikgvdppradpeedmarvywgcfayladvv	600		
601	EQAILIRVLGTEKTKGVYMQQMPICVYDDIFLAVMSRNPALPMTLAMIYSAVAIIKKTIV	660		
601	eqailirvlgtektkgvyymqmpicvyddiflvmsrnpalpmatlamiysaavaiikktiv	660		
661	YKEEARLKEKMRIMRGIDNSILMFMSNFISSLPLLVASGVLVITLKGNLPLPYSDPSVYVF	720		

```

Db 661 yekearlketmrimjdnslwfwfssslpvlvsagllvvlkqglpypsdpsvfv 720
QY 721 fLSVFAVWVTLQCFLLISTLFSRANLAAACGGIIVFTLIPVYLCAVAMDYGFLLKJPAS 780
Db 721 fLSVFAVWVTLQCFLLISTLFSRANLAAACGGIIVFTLIPVYLCAVAMDYGFLLKJPAS 780
QY 781 LLSPVAFGCGEFALEFEOGIGVOMDINFESPEDEGNLTTSISMLFDTPLYGWTV 840
Db 781 LLSPVAFGCGEFALEFEOGIGVOMDINFESPEDEGNLTTSISMLFDTPLYGWTV 840
QY 841 YLEAVPQGYIPRPMYFECTKSYWFCESDEKSHPGSNOKRMSHCIEEPTLKLKGS 900
Db 841 YLEAVPQGYIPRPMYFECTKSYWFCESDEKSHPGSNOKRMSHCIEEPTLKLKGS 900
QY 901 IONLVYVRDGMKAVNDGIALNFYEGQTTSLGHNGAKRTTMSLTGLPPTSGIAYIL 960
Db 901 IONLVYVRDGMKAVNDGIALNFYEGQTTSLGHNGAKRTTMSLTGLPPTSGIAYIL 960
QY 961 GKDISEMSTIRQNLGVCPOHNVLPDMLTVEEHLMPYARLKLSEKHVKAEMQMALDVG 1020
Db 961 GKDISEMSTIRQNLGVCPOHNVLPDMLTVEEHLMPYARLKLSEKHVKAEMQMALDVG 1020
QY 1021 LPSSKLKSTQSLSGGMQRKLSVALAEVGSKVYILDEPTAGVDPYSRRGIWEILLKYRQ 1080
Db 1021 LPSSKLKSTQSLSGGMQRKLSVALAEVGSKVYILDEPTAGVDPYSRRGIWEILLKYRQ 1080
QY 1081 GRTIILSTHMHDEADYLDRTAITSHGKLCCVSSSLFKMLQNGYVLTLYKKDVSSLS 1140
Db 1081 GRTIILSTHMHDEADYLDRTAITSHGKLCCVSSSLFKMLQNGYVLTLYKKDVSSLS 1140
QY 1141 SCRNSSTVTVLKKEDSVSSGSSDAGLSDHESDTLTIDVSALSMLRKHVSARLVEDI 1200
Db 1141 SCRNSSTVTVLKKEDSVSSGSSDAGLSDHESDTLTIDVSALSMLRKHVSARLVEDI 1200
QY 1201 GHELTYYLPYPAKGAFAVELHEIDRLSDLGISSGISETLLEETFLKVAEESGVDAE 1260
Db 1201 GHELTYYLPYPAKGAFAVELHEIDRLSDLGISSGISETLLEETFLKVAEESGVDAE 1260
QY 1261 TSDGTLPARRRRAFGDKQSLRPFETEDDAADPNDSIDPESREPTLLSGMCKGSYQK 1320
Db 1261 TSDGTLPARRRRAFGDKQSLRPFETEDDAADPNDSIDPESREPTLLSGMCKGSYQK 1320
QY 1321 GWTLOOQFVALLMKRLILARRSKGFFAOIYLPANVCIALVSLTVPFGKYSLEQ 1380
Db 1321 GWTLOOQFVALLMKRLILARRSKGFFAOIYLPANVCIALVSLTVPFGKYSLEQ 1380
QY 1381 PMWYNEQYTFVSNDAPEDTGTELELNAITKDPFGTRCMHGNPIPTPCQAEEETAP 1440
Db 1381 PMWYNEQYTFVSNDAPEDTGTELELNAITKDPFGTRCMHGNPIPTPCQAEEETAP 1440
QY 1441 VPOTIMLFQNGWMTQNSPACQSSDKIKKMLPVCPPGAGGLPPQKQNTADILDL 1500
Db 1441 VPOTIMLFQNGWMTQNSPACQSSDKIKKMLPVCPPGAGGLPPQKQNTADILDL 1500
QY 1501 TGRNISDYLVKTIVVQIIAKSLKNIKWNNEFRYGGFSLGVSNTQALPPSQEVDAIKOMK 1560
Db 1501 TGRNISDYLVKTIVVQIIAKSLKNIKWNNEFRYGGFSLGVSNTQALPPSQEVDAIKOMK 1560
QY 1561 HULKADSSADRFLNSLGRPTGLDTRNNVXWVFNKKGMHAISPLANNALIRANLQK 1620
Db 1561 HULKADSSADRFLNSLGRPTGLDTRNNVXWVFNKKGMHAISPLANNALIRANLQK 1620
QY 1621 GENPSHYGITAENHPLNLTAKOOLSEVALMTSVVDVLSICVTFAMSFPASVFLIOER 1680
Db 1621 GENPSHYGITAENHPLNLTAKOOLSEVALMTSVVDVLSICVTFAMSFPASVFLIOER 1680
QY 1681 VSKAKLQFISGVKVIYWLNSNFVDMCMNVVPATLVIIIFCFOOKSYVSTNLPVAL 1740
Db 1681 VSKAKLQFISGVKVIYWLNSNFVDMCMNVVPATLVIIIFCFOOKSYVSTNLPVAL 1740
QY 1741 LLLLGWSTPLIMYASFEFKIPSTAYVVLVSNIETINGSVATFVLELFTDKNLNIN 1800
Db 1741 LLLLGWSTPLIMYASFEFKIPSTAYVVLVSNIETINGSVATFVLELFTDKNLNIN 1800

```

```

Db 1741 LLLYGWSTPLIMYASFEFKIPSTAYVVLVSNIETINGSVATFVLELFTDKNLNIN 1800
QY 1801 DILKSYFLFEPFCLGRGLIDYKQAMADALERGENRFPVSLSDLVGRNLFPAAVEG 1860
Db 1801 DILKSYFLFEPFCLGRGLIDYKQAMADALERGENRFPVSLSDLVGRNLFPAAVEG 1860
QY 1861 VVEFLITVLIQYRFRTRPVNAKLSPLNDEDEVREPRKOTILDGGQNDILEKELTKI 1920
Db 1861 VVEFLITVLIQYRFRTRPVNAKLSPLNDEDEVREPRKOTILDGGQNDILEKELTKI 1920
QY 1921 YRRKRKPAVDRIQVIGIPGEECFGLGVNAGKSSTFMLTGDVTVTRGDAFLKNSTLSN 1980
Db 1921 YRRKRKPAVDRIQVIGIPGEECFGLGVNAGKSSTFMLTGDVTVTRGDAFLKNSTLSN 1980
QY 1981 IHEVQNNQYQOPQATIELLTGREHEFFALLGVGEKVGKVEWAIKKLGVYGEK 2040
Db 1981 IHEVQNNQYQOPQATIELLTGREHEFFALLGVGEKVGKVEWAIKKLGVYGEK 2040
QY 2041 YAGNYSGGNKRRLSTAMALIGCPPVFLDEPTGMDPKARRPLMNCALSVYKGRSVLT 2100
Db 2041 YAGNYSGGNKRRLSTAMALIGCPPVFLDEPTGMDPKARRPLMNCALSVYKGRSVLT 2100
QY 2101 SHSMECALCTRAIMVNGFRCLGSVOHLKNRFGDYITIVRIAGSNPDLKPVDFFG 2160
Db 2101 SHSMECALCTRAIMVNGFRCLGSVOHLKNRFGDYITIVRIAGSNPDLKPVDFFG 2160
QY 2161 LAFPSVLEKERNMLQYOLPSSLSLARLFSTISOSKRLHIEDYSQOTRIDOVFVNE 2220
Db 2161 LAFPSVLEKERNMLQYOLPSSLSLARLFSTISOSKRLHIEDYSQOTRIDOVFVNE 2220
QY 2221 AKDQSDDDHLKDLSLKHNQTVVDVAVLTSFLQDEKVEKYV 2261
Db 2221 AKDQSDDDHLKDLSLKHNQTVVDVAVLTSFLQDEKVEKYV 2261

RESULT 3
AAB38117
ID AAB38117 standard; Protein; 2261 AA.
AC AAB38117;
DT 29-JAN-2001 (first entry)
DE Human ABC1 cholesterol transporter mutant, I883M.
XX
KW Human ABC1 cholesterol transporter; chromosome 9q31;
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW cardiovascular disease; coronary artery disease; coronary restenosis;
KW cerebrovascular disease; peripheral vascular disease;
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW prognosis; prophylaxis; drug screening; transgenic animal; mutant;
KW mutant.
XX
OS Homo sapiens.
XX
PN WO200055318-A2.
XX
PD 21-SEP-2000.
XX
PE 15-MAR-2000; 2000WO-IB00532.
XX
PR 15-MAR-1999; 99US-0124702.
PR 08-JUN-1999; 99US-0138048.
PR 17-JUN-1999; 99US-0139600.
PR 01-SEP-1999; 99US-0151977.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (XENO-) XENON BIORESEARCH INC.
XX
PI Hayden MR, Wilson AR, Pimstone SN.
XX

```

DR WPI: 2000-587528/55.

XX New ABC1 polypeptide is useful for treating diseases associated with
PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
PT disease and cancer -

PS Examples: Page -: 229pp; English.

XX The invention relates to the human ABC1 cholesterol transporter protein
CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC a member of the ATP-binding cassette (ABC transporter) superfamily of
CC proteins, and plays a crucial role in cholesterol transport, particularly
CC intracellular cholesterol efflux from the cell. The gene encoding ABC1 is
CC located on chromosome 9q31, and mutations in this gene are associated
CC with two genetic HDL (high density lipoprotein) deficiency disorders,
CC Tangier disease (TD) and familial HDL deficiency (FHD). These diseases
CC are distinguishable in that TD is an autosomal recessive disorder, while
CC FHD is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC cholesterol") in the blood correlate with a high risk of cardiovascular
CC disease, particularly coronary artery disease, but also cerebrovascular
CC disease, coronary stenosis, and peripheral vascular disease.
CC Conversely, a high level of HDL has protective effects against
CC cardiovascular disease. The invention provides genetic constructs and
CC transgenic cells and non-human animals comprising human ABC1 nucleic
CC acids, and methods of gene therapy for the treatment or prevention of
CC cardiovascular disease comprising the administration of an expression
CC vector encoding ABC1 or an active fragment thereof. The invention also
CC encompasses compounds which mimic ABC1 activity, compounds which
CC stimulate ABC1 expression and methods of screening for such compounds.
CC It further relates to methods for determining whether a patient has an
CC increased risk for cardiovascular disease due to polymorphisms in the
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
CC or prevent cardiovascular disease, especially coronary artery disease,
CC cerebrovascular disease, coronary stenosis or peripheral vascular
CC disease. They may also be used in the treatment of diseases associated
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC The invention specifically excludes proteins with the exact amino acid
CC sequences of Genbank Accession No: CAA10005.1 and X75926, and the nucleic
CC acid with the exact sequence as Genbank Accession No: A012376.1. The
CC present sequence represents a mutant human ABC1 cholesterol transporter
CC associated with an altered cholesterol level and therefore an altered
CC risk of cardiovascular disease.
CC Note: The present sequence is not shown in the specification, but is
CC derived from the native human ABC1 shown on pages 152-157.

XX Sequence 2261 AA;

Query Match 100.0%; Score 11793; DB 21; Length 2261;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2259; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACWPORLLLKNNLFFRRROTCOLLEAVAMPFLFLLILISVRLSPYEOHECHFPNKA 60
DB 1 macwpglrlllknnlffrrrotcolleavampflfllilsvrlspyyechechfpnka 60
QY 61 MPASAGTLPMVVGITICNANNPCFRYPPTGEPAGVGNFNKSIYARLESARLLLYSQKDT 120
DB 61 mpaagtlpmvvgiticanannpcfrypptgpagvgnfnksiyarlesarlllysqgdt 120
QY 121 SMDKMKVRLTLOQIKKSSNKLQDELVDNTEFSGFLYHNLSPKSRVYDKMLRADVILH 180
DB 121 smdkmkvrltloqikkssnklqdelvdntefsgfllyhnlspksrvydkmlradvilh 180
QY 181 KVFLOGYQLHLISLNGSGSSEEMTQLGDOVESLGLPEKELAAERVLRSNMDILKPDIL 240
DB 181 kvflogyqlhlislngsgsseemtqlgdoveslglpekelaervlrsnmdilkpdl 240
QY 241 RLLNLSPPPSKELAEATKTLHLISLGLTQAELEFSKMSGMDMROEYVFLTNVSSSSSROI 300
DB 241 rllnlspppskelaeatkthlslgltlqaelifsmrswsmdrmgevmltnvssssscqi 300

QY 301 YQASRTVCGHPGGGGLIKSLNMYEDNNV KALFGSGNGTEEDAEFTYDNSTPYCNDLAK 360
DB 301 yqasrtvchgphgggglkkslnmyednnvkalfgsgngteedaefthydnstpycndlak 360
QY 361 NLESSPLSRIILWALKPLVGLKILYTPDPATROVAEYNTKTFDELAVHDEGMIBELS 420
DB 361 nlessplsriilwalkplvglkilytpdpatrovaeyntktdelavhdegmibels 420
QY 421 PKITFENSGENDLVMLDSDNDHFWRCQDGLDMADQADIVAFIAHPPDVOSSNCS 480
DB 421 pkitfensgendlvmlsdndhfwrcqdgldmadqadivafiahppdvoSSNCS 480
QY 481 VYTWREAFENNOAIRTSRMECVNLKLEPIATEFWMLINKSMELLDBRKFWAGIVETG 540
DB 481 vytwreafennoairtsrmevcvnlklepiatefwmlinksmelldbrkfwagivetg 540
QY 541 ITPGSIELPHHVKYKIRMDIDNVERTNKIKDGTWDEPPRADPEEDMKRYWGGFAYIQDVV 600
DB 541 itpgsielphhvkkykirmidnvertnkikdgtwdeppradpeedmkrywggfayiqdv 600
QY 601 EQATIRVLTGTEKKTGYVMOOMPYCVVDIPLKVRMSRMLFMTLAMIYSVAIITKGIY 660
DB 601 eqatirvltgtekktgyvmoompycvvdiplkvrmsrmlfmtlamiySAIITKGIY 660
QY 661 YEKEARLKEFRIMGDLNLSILFMSPTSSLLPLVSAGLLVILKLGNTLPSDPSVFEV 720
DB 661 yekearlkefrimgdlNLSILFMSPTSSLLPLVSAGLLVILKLGNTLPSDPSVFEV 720
QY 721 FLISVPAVVTIQCGLISTLFSBRANLAACGGITFTYLYLRYLVCAVMODVGTGTLTIPS 780
DB 721 flisvpaVVtIQCGLISTLFSBRANLAACGGITFTYLYLRYLVCAVMODVGTGTLTIPS 780
QY 781 ILSPVAFGCEGYRALFEGOGIGVOMDLFESPEDEGFMNLTSISMALDFLYGMVMTW 840
DB 781 ilspvafgcegyralfegogigvomdlfESPEDEGFMNLTSISMALDFLYGMVMTW 840
QY 841 YIEAVFPQGYCIRPWPYPCRTKSYWFGESDEKSHPSGNCKRMEGTMEEPRLHKLIGVS 900
DB 841 yieavfpqgyCIRPWPYPCRTKSYWFGESDEKSHPSGNCKRMEGTMEEPRLHKLIGVS 900
QY 901 IONLYKVRDQKAVAVDGLALNFYGCOTSPFLGNNGAKTTYSILGLRPPSTGYAIL 960
DB 901 ionlykVRDQKAVAVDGLALNFYGCOTSPFLGNNGAKTTYSILGLRPPSTGYAIL 960
QY 961 GMDISEMSTIRONCGVCPQHNVLFDMLTVEEHIMFYARLKGISEKHVKAEMDQALDVG 1020
DB 961 gmdiseMSTIRONCGVCPQHNVLFDMLTVEEHIMFYARLKGISEKHVKAEMDQALDVG 1020
QY 1021 LPSSKILKSTQSLSGGMOKRISVALAPYVGSKVYLDEPTAGVDPYSRRIWELLKTRQ 1080
DB 1021 lpsskILKSTQSLSGGMOKRISVALAPYVGSKVYLDEPTAGVDPYSRRIWELLKTRQ 1080
QY 1081 GRITILSTHMDADYLGRIALISHGKLCGSSFLKNOLGUYTLTKKRVESLS 1140
DB 1081 gritilSTHMDADYLGRIALISHGKLCGSSFLKNOLGUYTLTKKRVESLS 1140
QY 1141 SCRNSSTVSYLKKEDYSQSSSDAGLSDBHESDPLTIDVSAISNLRKHVSEARLVEDI 1200
DB 1141 scrnsstVSYLKKEDYSQSSSDAGLSDBHESDPLTIDVSAISNLRKHVSEARLVEDI 1200
QY 1201 GHEILTVLPEYAAKESGAVELFHEIDRLSDLGISYSGISETTLEETLKAESSGVDAE 1260
DB 1201 gheilTVLPEYAAKESGAVELFHEIDRLSDLGISYSGISETTLEETLKAESSGVDAE 1260
QY 1261 TSDGTLPARNRAPGDKSCIRPTEDDAAPNOSDIDPESRETDLSGMDGSGSYOVK 1320
DB 1261 tsdgTLPARNRAPGDKSCIRPTEDDAAPNOSDIDPESRETDLSGMDGSGSYOVK 1320
QY 1321 GWRLTQOQFVALLKRLILARRSRKGFQAVILPAVFCIALVFSLYIPPGKIPSLLEQ 1380
DB 1321 gwrlTQOQFVALLKRLILARRSRKGFQAVILPAVFCIALVFSLYIPPGKIPSLLEQ 1380


```

QY 1381 PMVNEQYTFVSNDAPEDTGLELNLALTKDGFSGTCEMEGNPDPDTCQAGEEEMTAP 1440
    |||
Db 1381 pmvneqytfvsnadapedgtglellnaltkdpgfgtrcmegnplpdpdcqageeemtap 1440
QY 1441 VPQTIMDLFQNGNMTWQNPSPACQSSDKTKKMLPVCPPGAGGLPPPKQKNTADIIQDL 1500
    |||
Db 1441 vpgtlimdlfqngnwtmnpqspacqssdktkmlpvcppgagglpppqrkqntadliqdl 1500
QY 1501 TGNRTSDYLVKTYVQIANKSLKNIWNEPFYGGFSLGVSNTQALPPSQEVNDAIKQMK 1560
    |||
Db 1501 tgnrtsdylvktyvgliakslknkwnefryggfslgvsntqalppsqevndaikqmk 1560
QY 1561 HLEKADSSADREFNLNLSGFMTGLDTRNNVKKWENKNGMHAISSEPLANTINALLRANLQK 1620
    |||
Db 1561 hlekadsadreflnlnlsgrfmgtdtrnnvkwfnkghasissflnlnallranlqk 1620
QY 1621 GENPSHYGTITANHPNLNLTKQOLSVALMTTSSVDLVSTICIFAMSEVPASFVVELIQER 1680
    |||
Db 1621 genpshygtitahnpnlntkqolsevalmtssvdvlsicvifamsfvpasfvveliqer 1680
QY 1681 VSKAKHLDFISGVKPVYIWNLFNVDKCNVVPATVYIIFICPOQSSYSTNLPLYAL 1740
    |||
Db 1681 vskakhldfisgvkpvylwnlfndkcnvvpatlviifictqgksystnlplyal 1740
QY 1741 LLLLGKSTPLPLMPASVFKIPSTAYVLTSMVLTGINGSVATFVLELFTDNKLNIN 1800
    |||
Db 1741 llllygswltpmlmpasfvfkfstayvltsmvltginsvatfvelftdnklnin 1800
QY 1801 DILKSVFLIFPHCLGRLIDMKVKNQAMADALEEFGENRPSPLSMVLVGRNIFANAEG 1860
    |||
Db 1801 dilksvflifphclgrlidmkvknqamadaleregenrpsplsmvlvgrnifanaevg 1860
QY 1861 VWFELITVLIOYRFFIRPVPNAKLSPLNDEDEVRERORILDDGGGONDILEIKETLTKI 1920
    |||
Db 1861 vwfelitvlioyrffirpvnaklsplnededvrerorilddgggondileiketlki 1920
QY 1921 YRRKKRPVDRICGIRPGEFGILGYNAGKSSFTMLTGDITVTRGDAFLNKNSTLSN 1980
    |||
Db 1921 yrrkkrpvdricgirpgefgilgynagkssftmltgditvtrgdaflnknstlsn 1980
QY 1981 IHEVQNNQYCPQPDATTELTLTGREHEFPALLRGVEREFGVGVGMARFKLGIVYVYGRK 2040
    |||
Db 1981 ihevqnnqycpqpdatteletltgrehefpallrgverefvgvgvmarrkglgivyvgrk 2040
QY 2041 YAGVNSGCKRKKLSTAMALIGGPPVWFLDEPTTGMDPKARRLWMCALSVYKGRSVLT 2100
    |||
Db 2041 yagvnsqckrklstamaliqppvwldepttgmdpkarrlwmcalsvykegrsvlt 2100
QY 2101 SHSMECEALCTRMAIWNNGRFRCTGVSQHLKRRFGGYTIIVRIGSNPDLKPVQDPFG 2160
    |||
Db 2101 shsmecealctrmaiwnngfrctgvsqhllkrrfggytliivrigrsnpdlkpvqdfpg 2160
QY 2161 LAFPGSVLKEKRRNMIOYLPSSISLARLFSILSOSKRLHLEDVSQSOTLDOFVNF 2220
    |||
Db 2161 lafpgsvlkekrrnmioyqlpssislarlfsilsgskrlhledvsvsqtldofvynf 2220
QY 2221 AKDQSDDDHKLKSLKHKNQYVAVLTFSLDDEKKESTY 2261
    |||
Db 2221 akdqsdddhklklskhknqyvaavltsflddekkesty 2261

```

RESULT 4

AAB31362 standard; Protein; 2261 AA.

XX AAB31362;

XX 20-APR-2001 (first entry)

DE Amino acid sequence of ABC1 polypeptide from Tangier disease patient.

KW Human; adenosine triphosphate binding cassette protein 1; ABC1;

KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;

```

KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KM atherosclerosis; cholesterol transport.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 597
FT /note="this is changed from Glu to Arg in Tangier
FT disease"
PN
XX MO200078972-2.
XX
XX 28-DEC-2000.
XX
XX 16-JUN-2000; 2000WO-US16765.
XX
XX 18-JUN-1999; 99US-0140264.
XX 14-SEP-1999; 99US-0153872.
XX 19-NOV-1999; 99US-0166573.
XX
XX (CVTH-) CV THERAPEUTICS INC.
XX
XX Lawn RM, Wade D, Garvin M;
XX
XX WPI. 2001-137812/14.
XX
XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
XX useful for the development of agents for the treatment of heart disease
XX and other disorders associated with hypercholesterolemia and
XX atherosclerosis -
XX
XX Example 5; page 154-169; 215pp; English.
XX
XX The present sequence represents a human adenosine triphosphate (ATP)
XX binding cassette protein (ABC) 1 polypeptide, and is isolated from
XX a Tangier disease patient. ABC1 resides in cell membranes and utilises
XX ATP hydrolysis to transport a wide variety of substrates across the
XX plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
XX mobilisation of intracellular cholesterol stores. ABC1 is defective in
XX Tangier disease, a genetic disorder characterised by abnormal
XX HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
XX 9q22-9q31. The ABC1 genes and proteins are useful for developing
XX pharmaceutical agents for the treatment of heart disease and other
XX disorders associated with hypercholesterolemia and atherosclerosis. The
XX genes are useful for developing screening assays to screen for compounds
XX that regulate the expression of genes associated with cholesterol
XX transport. The genes and proteins are also useful for are also useful
XX as diagnostic indicators of cardiovascular disease and other disorders
XX associated with hypercholesterolemia.
XX
XX Sequence 2261 AA:
XX
QY 1 MACCPOLRLILMKNLFRRRQTCQILLFVAMPFLIFLLISVRLSYPRYEQHECHFENKA 60
    |||
Db 1 maccpqlrlilwknltfrrrqtcqillfvaupliffllisvrlsypryppqhechfpka 60
QY 61 MPASGTLIPWVOGILCNANPCFRYPPTPGAPGVGNFNKSIIVARLFSFARLLILYSQDT 120
    |||
Db 61 mpsagtlipwvgilcnaNPCfrypptpgapgvgnfnksivarlfsfarrllilysqdt 120
QY 121 SMKDKRKVLRTIQQIKKSSSNLKIDPFLVDNETFSGFLYHNI.SLPKSTVDMKLRADYILH 180
    |||
Db 121 smkdmrkvlrtlqqikksnllkqdfldvnetfsgflyhnlslpkstvdmlraadvilh 180
QY 181 KYFLQGYOHLTSLONGSKSFEEMTOLGDPVSELCGLPKKELAABERYLANSNDIIPIL 240
    |||
Db 181 kvflqgyqlhtslongsksseemlqldqvseclcgpkelaabervylansndiipil 240

```

Query Match 100.0%; Score 11793; DB 22; Length 2261;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2260; Conservative 1; Mismatches 0; Indels 0; Gaps 0;


```

QY 241 RTLNSTSPSPSKELAEATKTLHSLGTLAQELFSMSRSDMROEYFELTNVSSSSSTOI 300
Db 241 rlnstspfskselaetkltlslgltlaqelfsmrswdmrcewfltnvsssstqi 300
QY 301 YQAASTRVCGHPRGGGKIKLSLWYEDNNYKALFGNGRGEDEAFRYDSTPYCNDLMLK 360
Db 301 yqaastrvchgprgggkiklslwedydnnykalfgngredeafrydstpycndlmlk 360
QY 301 YQAVSTRVCGHPRGGGKIKLSLWYEDNNYKALFGNGRGEDEAFRYDSTPYCNDLMLK 360
Db 301 yqavstrvcghprgggkiklslwedydnnykalfgngredeafrydstpycndlmlk 360
QY 361 NLESSPLSLRIIWKALKPLVGLKILYTPDPATROVAEYNTFOELAVEHDELEGMWELS 420
Db 361 nlessplslriiwwalkplvglkilypdpatrovaeeyntfoelavehdelegmwels 420
QY 421 PKITFENSGEMDLVYMLLDSRDNDHFWEQOJDGLDWTARODIYALAKHPREVQSSNS 480
Db 421 pkitfensgemdlvymlldsrdndhfweqojdglwdtarodiylalakhprevqssns 480
QY 481 VYTRREAFNEFNQAIKRTISREMECVNLKLEPIATEYWLINSMELDEREKFWAGIVFEG 540
Db 481 vytrreafnefnqairtisremecvnlklepiateywlinsmelderekfwagivfeg 540
QY 541 ITPSIELPHHVKYKIRMDIDNVERTNKIKDGYWDGPRADPEDMKRYWNGFAYLQDYY 600
Db 541 itpsielphhvkkykirmdidnvertnkikdgywdgpradpedmkrwymngfaylqdyv 600
QY 541 ITPSIELPHHVKYKIRMDIDNVERTNKIKDGYWDGPRADPEDMKRYWNGFAYLQDYY 600
Db 541 itpsielphhvkkykirmdidnvertnkikdgywdgpradpedmkrwymngfaylqdyv 600
QY 601 EOAIIITVLTGKTKGYVMQOMPRCYVDIIFLRVMSRMPFLMTLAWISVAVIITKGYV 660
Db 601 eoaaiitvltgktkgyvmqomprcyvdiiflrvmrsmplmtlawnisvaviiikgyv 660
QY 661 YEKEARKETMRIGLDSILFMSFISLPLVLSAGLLVILKGNLTPSDPSVPEV 720
Db 661 yekearketmriglslfmsfislplvlsagllvilkgnltpsdpsvpev 720
QY 661 YEKEARKETMRIGLDSILFMSFISLPLVLSAGLLVILKGNLTPSDPSVPEV 720
Db 661 yekearketmriglslfmsfislplvlsagllvilkgnltpsdpsvpev 720
QY 721 FLVFAVNTLIQCELLISTFLSRANLAAACGIIYFTLYLPVLCVAMQDYVETLKIFAS 780
Db 721 flsvfavntliqcellistflsranaaaagiiyftlylpvlycvamqdyvetlikifas 780
QY 781 ILSPAFGECEYALFEEDGIGVOMNLFPSPEDEGFLNTSISMWLEDTFLYGMW 840
Db 781 ilspafgeceyalfeedgigvomnlfpspedegflntsismwledtfllygmw 840
QY 841 YLEAFVPCOYGIIPRWYPPCTKSYWFGESDEKSHPGSNOKRMSEICMEEPHTLKIGVS 900
Db 841 yleavfpcoygiiprwypptksywfgesdekshpgsnokrmseicmeephtlkigvs 900
QY 901 IONLVYTRDGMKAVAVDGLALNFYBGOITPSFLGNHAGKTTMTSITNGLPPTSGTYIL 960
Db 901 ionlvtrdgmkavavdglalnfybgotpsflgnhagkttmtsitinglpptsgtyil 960
QY 961 GKDISEKSTIRONGVPCOHNVLEFDMLTVEEHIMFYARKLGISEKHVKAEMEQMALDVG 1020
Db 961 gkdisekstirongvpcohnvlefdmltveehimfyarklgisekhvkaemeqmaldv 1020
QY 1021 LPSKSLKSTQSLSGGMORLUSVALAFVGSKVYILDEPTAGVDPYSRRGIIWELLKTYRQ 1080
Db 1021 lpskslksktsqslsggmorlusalafvgskvyldeptagvdpysrrgiiwellktyrq 1080
QY 1081 GRTIISTHMEADVLDRIALISHGKLCVSGSLFLKNOLGYYVTLTKKRVESLS 1140
Db 1081 grtiisthmadvldrialishgklcvsgslflknoigyvtlkkrvessls 1140
QY 1141 SCRNSSSTVYLLKEDSVSSSSDAGLSDHESDITLIDVSAISNLTIRKHVSEARLVEDI 1200
Db 1141 scrnssstvyllekedsvsqsssdaglsdhesdiltidvasaisnltirkhvsearlved 1200
QY 1201 GHELTIVLPEYAKAGAVELFHEITDDRSLDGLISSYISSTYLETFLTKAAESSVDAAE 1260
Db 1201 gheiltivlpeyakagavelfheitddrslsdglissyisstyletfltkaaessvd 1260
QY 1261 TSDGTLPARNRRAFGDKOSCLRPTEDDAADPNDSIDDPESRETDLSGMDGKSGSYQVK 1320
Db 1261 tsdgtlparnrtrafgdkosclrpfeeddaadpndsiddpesretllsgmdgksgsyvk 1320
QY 1321 GWKLTQOQFVALLWKRLLIARRSRKGFPAQIVLPAVFCIALVSLIIVPPGKIPSLQLQ 1380

```

```

Db 1321 gwkltdqgfvallwkrlllarrtskffagivlpavfcialvslivppfgkypslqlq 1380
QY 1381 PMYIIEQYTFVSDNADPEDGTLELALNLRKDPEGFCIRMEGNIPIDPTQOAGEEWTAP 1440
Db 1381 pmyiiieqytfvsnadpedgtlelalnlnrkdpdegfcirmegnipidptqoageewt 1440
QY 1441 VPQITMDLFGNGWMTKONPSBPACOSSDKRKMLPVCPPAGGLPPQKQNTADILQDL 1500
Db 1441 vpgitmdlfgngwmtnkpsbpacossdkrkmlpvcppagglppqkqntadilqdl 1500
QY 1501 TGRNIDSLVKTYYQIILAKSLKNNKIMWNEFRYGSFSLGVSNTOALPPSOEVDAIKOMK 1560
Db 1501 tgrnidslvktyyqiilakslknnkimwnefrygslgvsnতোalppsoevdaikomk 1560
QY 1561 HLKIAKSSADRFINSIGRMTGLDTRNNKVMFNNKGMHAISSFLANVINNALIRANLQK 1620
Db 1561 hlkiakssadrfinsigrmtgltrnnkvmmfnnkgmhaisflvnnaliranlqk 1620
QY 1621 GENSHGITAFNHPNLTKQOOLEVALMTTSYDVLSICVIFAMSFPVAFVFLQER 1680
Db 1621 genshgitafnhpnltkqoolvalmttsydvlsicvifamsfpvafvflqer 1680
QY 1681 VSKAKHLQFTISGVKPVYIWLNSFWYDMCNVVPATVLIIFICEQOKSYVSTNLPLVAL 1740
Db 1681 vskakhlqftisgvkpvylwlnsfwydmcnvvpatlviificeqoksyvstnlplval 1740
QY 1741 LLLYGVNSTPLPKTPASVFRIRPSTAVVLTSVNLFGINGSVATVLEFPNTKLNNTN 1800
Db 1741 llllygvnstplpktpasvfrirpstaavltsvnlfgingsvatvlefpntklnntn 1800
QY 1801 DILKSVLIFPHFCIGRLIDMVKNQAMADALERFGENREVSPLSMDLVGRNLFAMAVG 1860
Db 1801 dilksvliifphfcigrldimvknqamadalerrfgenrevsplsmdlvgrnlfamav 1860
QY 1861 VWFLLITVLIOYRFFIRPYNNAKLSPLNDEDEDVREPORIILDGQONDILEIKELTKI 1920
Db 1861 vwfllitvlloyrffirpynnaklsplndevedvrrporiildgqondileikeltki 1920
QY 1921 YRRKRKPVADRIQVGIIPGECFGLLVGNAGKSTFPMLGDTVTWRGDAFLKKNSTLS 1980
Db 1921 yrrkrkpvadriqvgiipgecfglvgnagkstfpmldgtvtwrgdafllkknstls 1980
QY 1981 IHEVHQNNGYCPQOPDAILTELLTGREHVEFFALLKGVPEKEVGKVENAIRKLGLVYGEK 2040
Db 1981 ihevhnngycpqpdailltelgrehveffallkgvpekevgkvenairklglvygek 2040
QY 2041 YAGNTSGGNKKRLSTAMALIGPVPVFLDEPTTGMDKARREFLMNCALSVYKGRSVLFT 2100
Db 2041 yagntsggnkkrlstamaligpvpvfldepttgmdkarreflmncalsvykgrsvlft 2100
QY 2101 SHSMEECEALCTRNAIMVNGRPRLGVSQVHLKNFGDGYTIVIRIAGSNPDLRPVODFFG 2160
Db 2101 shsmeecealctrnaimvngprlgsqvhlknfgdgytivririagsnpdlrpvodffg 2160
QY 2161 LAFPGSVLKEKHNNMLQYQLDSSLSLARIFSLSQSKKRLIHEDIVSYQTTLDQVYVF 2220
Db 2161 lafpgsvlkekhnmlqyqldsslslarifslsqskkrlihedivsyqttldqvvyvf 2220
QY 2221 AKDQSDHDLKDLSTHKNOTVVDVAVLNSPLODEKVKRSYV 2261
Db 2221 akdqsddhldkdlsthknotvvdvavlntspodekvkrsyv 2261

```

RESULT 5

AAB31366 standard: Protein: 2261 AA.

AAB31366;

20-APR-2001 (first entry)

Amino acid sequence of ABC1 polypeptide from Tangier disease patient.

XX Human: adenosine triphosphate binding cassette protein 1: ABC1;
 KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
 KW chromosome 9q22-9q31: heart disease; hypercholesterolemia;
 KW atherosclerosis; cholesterol transport.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 597
 FT /note= "this is changed from Glu to Arg in Tangier
 XX disease"
 XX
 PN MO200078971-A2.
 PD 28-DEC-2000.
 XX
 PF 16-JUN-2000; 2000MO-US16591.
 XX
 PR 18-JUN-1999; 9905-0140264.
 PR 14-SEP-1999; 9905-0153872.
 PR 19-NOV-1999; 9905-0166573.
 XX
 PA (CVTH-) CV THERAPEUTICS INC.
 PA (UNITM) UNIV WASHINGTON.
 XX
 PI Lawn RM, Wade D, Oram JF, Garvin M;
 XX
 DR WPI: 2001-137811/14.
 DR N-PSDB: AAF24707.
 XX
 PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
 PT polynucleotides and polypeptides, useful for treatment of heart disease
 PT and other disorders associated with hypercholesterolemia and
 PT atherosclerosis -
 XX
 PS Claim 25: Page 150-165; 211pp: English.
 XX
 CC The present sequence represents a human adenosine triphosphate (ATP)
 CC binding cassette protein (ABC) 1 polypeptide, and is isolated from
 CC a Tangier disease patient. ABC1 resides in cell membranes and utilises
 CC ATP hydrolysis to transport a wide variety of substrates across the
 CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
 CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
 CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
 CC 9q22-9q31. The ABC1 genes and proteins are useful for developing
 CC pharmaceutical agents for the treatment of heart disease and other
 CC disorders associated with hypercholesterolemia and atherosclerosis. The
 CC genes are useful for developing screening assays to screen for compounds
 CC that regulate the expression of genes associated with cholesterol
 CC transport. The genes and proteins are also useful for are also useful
 CC as diagnostic indicators of cardiovascular disease and other disorders
 CC associated with hypercholesterolemia.
 CC
 XX Sequence 2261 AA:
 SQ

Query Match 100.0%; Score 11793; DB 22; Length 2261;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2260; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 181 KVFAGYQYHLTLSTLONCSKSEEMTQDQVEYSEICGLPEKEXIAAERYLRNMILKPII 240
 DB 181 kvfagylqyhlhltsloncskseemiqldqveyselcgjpkexiaaerylrnmilkpil 240
 QY 241 RTINSTSPFSPKELAEAKTLLHSLGTLAQELFSMRKSDMRQEWMLJNVNSSSSSTQI 300
 DB 241 rtlnstspfpkselaekatlhlslgtlaqelfsmrksdmdrqewmljnvnsststqj 300
 QY 301 YQAVSRIVCGHPEGEGGLTKIKSLANWYEDNNYKALGSGTEDEATFEDNSTTTPYCNIDMK 360
 DB 301 yqavsrivcghpegggltkikslanwyednnkalgsgteedatfednsttptycndlmk 360
 QY 361 NLESPSLRITWKAALKPLVGLIYTPDPATROVAEAVNKTFOELAVFHDLEGRMEELS 420
 DB 361 nlespslrltwkaalkplvgliytpdpatrovaeavnktfoelavfhdlgrmeels 420
 QY 421 PKITFMENSOEMDLYMMLLDNRNDHFHQQLDGLMTQODIYAPLAKHPEVQSSNGS 480
 DB 421 pkitfmensogmdlymmlldnrndhfhqqldglmtqodiyaplakhpevqssngs 480
 QY 481 VYTWREAFNETQAIKRTISRMECVNLKLEPLATEVWLINKSMELDERKFWAGIYFTG 540
 DB 481 vytwreaenetqairtisirfmeecnlnkplatevwlinskmeelderkfwaagiylftg 540
 QY 541 ITPGSIELPHHVKKYKIKIMQDIDNVERTKIKDGTWDEGPRADPEDMRYWVGFAVYLDVY 600
 DB 541 itpgsielphhvkkkykikimqdindvertnkikdgtwdegprradpedmrywvgfaylrdv 600
 QY 601 EOAIIRVLTGTEKKTGYVMQMPYPCVDDIFRNVASRSPMLPMTLAMYISVAVIILKGIY 660
 DB 601 eoaairvltgtekktgyvmqmpypcvddifrvnasrspmlpmtlamyisvaviilkgiy 660
 QY 661 YEKBAKLEKEMRLMGDNLSTLWFSWFTSSLIPLVASGLIYVLKGNLIPYSDPSVAVY 720
 DB 661 yekearlkeemrlmgdnlstlwfsfssliplvasgliyvlkgnlipydspsvayv 720
 QY 721 FLVFAVNTTLOCFILSTFSRANLAAAGGIIYFLYLYVCAMQDYVFTLKIRAS 780
 DB 721 flvfavnttlocfilstfstranlaaaggiiyflylyvcamqdyvftlkirafas 780
 QY 781 LLSVPAFGCEYFALFEEOGIGVQWMDNFESPVEEDGQNLTTSSIMLFDPEFLGVMTW 840
 DB 781 llsvpafigceyfalfeegigvqwdnlfespevedgqnltsismldfpeflgvmtw 840
 QY 841 YIEAVPFGYGIPIRPWYFECTSYNFEESDKSHPSQNMKMSIEICMEEPTHILKGV 900
 DB 841 yieavpfgygiiprpyfictksywnfeesdkshpsqnmkseicmeepthilkigs 900
 QY 901 IONLVVYRDGMKAVNDGLANFEYEQUTSPFGHAGAGTTMSTLITGLFPPTSGTAYIL 960
 DB 901 ignlvvyrdgmkvavndglanfeyequtspfghagagttmstlitglfpptsgtayil 960
 QY 961 GKDISEKSTTRQNLGVCPQHNVLFDMLTVEEHLWYARLKLSEKHKAEQMAQDVG 1020
 DB 961 gkdirseksttrqnlgvcpqhnlfdmltveehlwyarlklsekhkaeqmadvg 1020
 QY 1021 LPSSKLKSTQSLGSGMQRKLSVALAFYGGSKVYILDEPTAGVDPYSRKGILWELLKTRQ 1080
 DB 1021 lpsklkstqslsgsmqrklsvalafyggskvyilddeptagvdpysrkgilwellktrq 1080
 QY 1081 GRTIILSTHMDADVLDRIALISHGKLCVGSGLFLKKNLGGYVTLVKKRVESLS 1140
 DB 1081 grtilsthdadvldriailshgklcvgssglflkknlggyvtlvkkrvessls 1140
 QY 1141 SCRNSSSTVSTLKEDSVSGSSDAGLGSDESDTLTIDVSAISNLTRKHVSEARLVEDI 1200
 DB 1141 scrnssstvtlkkedsvsgssdaglgsdesdtltdvsaisnltrkhvsearlvedi 1200
 QY 1201 GHETLYVPEYAEAKGAEVLEFHEIDRLSPLGSSSISGISTTLEELFLKVAEESGVDAE 1260
 DB 1201 gheltlyvpeyaekgaevelfheidrlsplgsssisgsttleelflkvaeesgvdae 1260

QY 1261 TSDGTLPARNRRAFGDKSCLRPTEDDAADPNDSIDIPESHPEDLLSGMDKGSYQVK 1320
 DB 1261 tsdgtlparnrtrafgdkscrlrpteddaadpnstdidipeshtedllsgmngkgsyqvk 1320
 QY 1321 GWRKLTQOOFPVALMKRLILARRSRKGFPAQIVLPAVFVCIALVSLVPPFGKPSLEIQ 1380
 DB 1321 gwrltqoofvalmkrlilarrsrkgfpaqivlpavfvciavslvppfgkpsleiq 1380
 QY 1361 PMWTNEQTYVSNAPEDTGTLELINALTRDPFGRCMGNGNITPTPOAGEEWTAP 1440
 DB 1361 pmwtnetyvsnapedtgtlelinaltrdpfgrcmgngnitptpoageewtarp 1440
 QY 1441 VPORTIMDFONGNWTQMNPSAPCCSSDKIKKMLPVCPPGAGGLPPORRONTADILQDL 1500
 DB 1441 vportimdfongnwtqmnpsapccssdkikkmlpvcppgagglpporrontadilqdl 1500
 QY 1501 TGRNIDSLVKTVOIILAKSLKNKIWNERRIGGFSLGVSNTQALPPSQVNAIQQMK 1560
 DB 1501 tgrnidslvktvooiilakslknkiwnerriggfslgvsntqalppsqvnaaiqqmk 1560
 QY 1561 HLKTLAKOSSADRFINSIGREMTGLDTRNNYKVMFNKNGMAHSSFLVNNALIRANKQK 1620
 DB 1561 hlktlakossadrfinsigrmtglptrnnnykvfnknngmahssflvnnalirankqk 1620
 QY 1621 GENPSHYGITAFNHPNLNLTQOLSEVALMTTSDVLSICVIFAMSFVPAFVFLIOER 1680
 DB 1621 genpshygitafnhpnlntqolsevalmttsdvlsicvifamsfvpafovflioer 1680
 QY 1681 VSKAKHLOPISGKRVYIWNLFNFWDMKNYVVPATVITIIIFICQOOSYSSTNPLPAL 1740
 DB 1681 vskakhlopisgkrvyiwnlfnfwdmknyvvpativitiiificqoosysstnplpal 1740
 QY 1741 LLLLGWSTPTPLMYPASVFEKIPSTAYVLTVMLEFGINGSVATFLELFTDKLNIN 1800
 DB 1741 llllgwstptplmypasvfekipstayvltvmlefgingsvatflelftdklnin 1800
 QY 1801 DILKSVFLIPEHFCIGRLIDMKWKNOMADALERGENRFPSPISMDLNGENLFAMAVEG 1860
 DB 1801 dilksvflipehfcigrldmkwknomadalergenrfpspismdlnngenlframaveg 1860
 QY 1861 VVEFLITVLIQYRFRIRPPVNAKLSPLNDEDEDEVRRERQRILDGGGONDILEIKELTKI 1920
 DB 1861 vveflitvliqyrfrirppvnaaklsplndevedevrrerqrildgggondileikeltki 1920
 QY 1921 YRRRRKPAVDRIQVIGPECEFGLLGVNGAKSSTFKMLTGDYTVTRKDAFLANKNSILSN 1980
 DB 1921 yrrrrkpavdriqvigpecefgllgvngakssstkmltgdtytvtrkdaflanknsilsn 1980
 QY 1981 IHEVHONMGYCPQFOAITELLGREHVEFFALLRGVPEKEVGKVGEMAIIRKILGLVKYGEK 2040
 DB 1981 ihevhnmgycpfoaiteellgrehveffallrgvpekevgkvgemairkilglvkygek 2040
 QY 2041 YAGNSYGNKRLSTAMALIGSPVVEIDEPPTGMDPKARFLMNCALSVYKESRSVLT 2100
 DB 2041 yagnsygnkrlstamaligspvveidepptgmdpkarflmncalsvykesrsvlt 2100
 QY 2101 SHMECEALCTFMAIMWNGFRRCISYQHLNRRGDGTYTVIRAGSNPDLKPVQDEFG 2160
 DB 2101 shmecealctfmaimwngfrrcisyqhl nrrgdgtytviragsnpdlkpvqdeffg 2160
 QY 2161 LAEPGSVLKEKHNNMLQOYLPSSLSLARIFSLISQSKRLHIEDYSVSQTTLDGVFVN 2220
 DB 2161 laepgsvlkekhnnmlqoylpsslslarifslisqskrlhiedysvsqttldgvfnf 2220
 QY 2221 AKDQSDDLKLDLSLHKNOTVDVAVLTFSLQDEKKESEYV 2261
 DB 2221 akdqsddhlkldlslhknqtlvavavltfslqdekkesyvv 2261

RESULT 6
 AAB38109
 ID AAB38109 standard; Protein; 2261 AA.
 XX

AC AAB38109;
 XX 29-JAN-2001 (first entry)
 DT
 XX
 DE Human ABC1 cholesterol transporter mutant, R219K.
 KW Human ABC1 cholesterol transporter; chromosome 9q31;
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
 KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
 KW cardiovascular disease; coronary artery disease; coronary restenosis;
 KW cerebrovascular disease; peripheral vascular disease;
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
 KW prognosis; prophylaxis; drug screening; transgenic animal; mutant;
 KW muten.
 OS Homo sapiens.
 PN W0200055318-R2.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-1B00532.
 XX
 PR 15-MAR-1999; 99US-0124702.
 PR 08-JUN-1999; 99US-0138048.
 PR 17-JUN-1999; 99US-0139600.
 PR 01-SEP-1999; 99US-0151977.
 XX
 PA (UYBR-) UNITI BRITISH COLUMBIA.
 PA (XENO-) XENON BIORESEARCH INC.
 PI Hayden MR, Wilson AR, Pimstone SN;
 DR WPI; 2000-587528/55.
 XX
 PT New ABC1 polypeptide is useful for treating diseases associated with
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
 PT disease and cancer -
 XX
 PS Examples; Page --: 229pp; English.
 XX
 CC The invention relates to the human ABC1 cholesterol transporter protein
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of
 CC proteins, and plays a crucial role in cholesterol transport, particularly
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
 CC located on chromosome 9q31, and mutations in this gene are associated
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,
 CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
 CC are distinguishable in that TD is an autosomal recessive disorder, while
 CC FFA is inherited as an autosomal dominant trait. Low levels of HDL ("good
 CC cholesterol") in the blood correlate with a high risk of cardiovascular
 CC disease, particularly coronary artery disease, but also cerebrovascular
 CC disease, coronary restenosis, and peripheral vascular disease.
 CC Conversely, a high level of HDL has protective effects against
 CC cardiovascular disease. The invention provides genetic constructs and
 CC transgenic cells and non-human animals comprising human ABC1 nucleic
 CC acids, and methods of gene therapy for the treatment or prevention of
 CC cardiovascular disease comprising the administration of an expression
 CC vector encoding ABC1 or an active fragment thereof. The invention also
 CC encompasses compounds which mimic ABC1 activity, compounds which
 CC stimulate ABC1 expression and methods of screening for such compounds.
 CC It further relates to methods for determining whether a patient has an
 CC increased risk for cardiovascular disease due to polymorphisms in the
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
 CC or prevent cardiovascular disease, especially coronary artery disease,
 CC cerebrovascular disease, coronary restenosis or peripheral vascular
 CC disease. They may also be used in the treatment of diseases associated
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
 CC The invention specifically excludes proteins with the exact amino acid

CC sequences of Genbank Accession No: CAA10005.1 and X75926, and the nucleic
 CC acid with the exact sequence as Genbank Accession No: AJ012376.1. The
 CC present sequence represents a mutant human ABC1 cholesterol transporter
 CC associated with an altered cholesterol level and therefore an altered
 CC risk of cardiovascular disease.
 CC Note: The present sequence is not shown in the specification, but is
 CC derived from the native human ABC1 shown on pages 152-157.
 XX
 Sequence 2261 AA:

Query Match 100.0%; Score 11792; DB 21; Length 2261;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2259; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACPOLRLMLKNTERRRQTCQLLEFVAMPFLITLISVRLSPREDECHPEPKA 60
 Db 1 macpolrlmlknterrrqtqqllefvampflitlissvrlsyppeghechfpka 60
 QY 61 MRSAGTLPWVQGITCANNPCFRYPPTGPAPGVGNFNKSIVARLFSDARRLLTSOKDT 120
 Db 61 mrsagtlpwvggitcannpcfrypptgpapgvgnfnksivarlfdsarrlltysqdt 120
 QY 121 SMKDMKRYRTLOOTIKSSSNKIQDFLVNTEFSGFLYHNI SLPKSTVDKMLRADVTLH 180
 Db 121 smkdmkryrtlootiksssnkldqdflvntefsgfllyhnlslpkstvdkmlradvllh 180
 QY 181 KVFLOGYQLHLTSLNGSKSEEMIQLDQVESELGCLPREKLAARLRLSMDILKPTL 240
 Db 181 kvflogyqlhltslنگskseemiqldqvselcglpreklaaerlrlsmdllkpl 240
 QY 241 RFLNSTSPPEKELAEARKTLHLISGLTIAQELFSMRSDMKQEVMLFTLVNNSSSSTQI 300
 Db 241 rflnstsppekelaektlhlshgltagel fsmrswdmrkmqevmlftlvnsssstqi 300
 QY 301 YQAVSRIVCGHPEGGLKTKSLNMYEDNNYKALFGNGTEEDAEFYDNGSTTPYCNLDMK 360
 Db 301 yqavsrivcghpeggklkkslnmyednnkalfgngteedaefydnsttpeyndl mk 360
 QY 361 NLESPLSLRIIWKALKPLLVGKIILYPTDPATROYMAEVNKTFOELVAFVHLEGMWELS 420
 Db 361 nlesplslriiwlkpllvvgkiilyptdpatroymaevnktfoelvafvhl egmwels 420
 QY 421 PKITFMENSOEMDLVRRLDSDRNDHPWEQDLGLDWTADIVAFIAKHPEDVOSSNGS 480
 Db 421 pkitfmensoemdlvrldsd rndhpweqdlgl dwtadivafiakhp edvo ssngs 480
 QY 481 VYTRERAPNETNOAIRTSRFMECVNLKLEPTATEVWLINKSMELDERKFNAGIYFTG 540
 Db 481 vytrerafnetnqairtsrfmecvnlkleptatevwl linksmellder kfnagi yftg 540
 QY 541 ITPGSIELPHHVKKIKMDIDNVERTKIKDGVWDPEGRADPFEDMKRYWGGFAYLQDVV 600
 Db 541 itpgsielphhvkkikmdidnvertkikdgvwdpegradpfedmkrywggfayl qdvv 600
 QY 601 EQAIRVLVTGTEKKTGYVMOQMPYPCYVDIIFLRVMSRSMPLMTLAMIYSVAVITKGY 660
 Db 601 eqairvlvtgtekktgyvmoqmpy pcyvdiiflrvm srsmplmtlamiysvav itkgy 660
 QY 661 YEKEARLKEKRMIMGIDNSITLMSWFTSSILPLVSAGLLVLTKLGNLTPVSDPSVVV 720
 Db 661 yekearlkekrimgidnslt lmswftssilplvsagllvllkgnltpv sdpssvvv 720
 QY 721 FLTSVFAVVTILOCFILSTLFSFRANLAACGGITFTLYL PYVLGVAMQDYVGFILKTPAS 780
 Db 721 fltsvfaavvtilofcflstlfsfranlaacggitftlylpyvl gvamqdyv gfilkt pas 780
 QY 781 LLSPAVAFGCGEYFALFEQOGIGVOMDNLFESPVEEDGFNLTSTISMMFLDFELGVMTM 840
 Db 781 llsparafgceyfalfeeqogigv omdnlfes pveedgfnltstismm fldfelgvmtm 840
 QY 841 YLEAVFGCGYIPRPWYFPCCTKSYMFGEESDEKSHFGSNQKMSKTCMEEPETHLKCVS 900
 Db 841 yleavfgcgyiprpwyfpctk sywfmfgeesdekshfgsnqkmsctme eepethlkcv s 900

Db 841 yleavfpgqyiprpwyfpctk sywfmfgeesdekshfgsnqkri seicmeeepthlkigvs 900
 QY 901 IONLVKRYRDGKAVVDGALNFEYEGOTTSLGHNGAGKTTTMSLTGLFPPTSGTAYIL 960
 Db 901 ionlvkryrdgkavvdg alnfe yegottslghngagktttmsltglfpptsgt ayil 960
 QY 961 GKDIRESEMTIRONLVGCPQHNVLFDMLTVEEHITFWYARLKGLESEKHVKAEMQMALDVG 1020
 Db 961 gkdiresemtironlv gcpqhnlfdmltveehitfwyarlkglsekhvkaemqma ldvg 1020
 QY 1021 LPSSKLSKTSQSLSGGMOKRISVALAPYGSKVYILDEPPAGVDYPSRRCIGITWELLKRYQ 1080
 Db 1021 lpsksksktsqslsggmokr isvalap ygskvyldeppagvdypsrrcig itwellkryq 1080
 QY 1081 GRTIILSTHNDMDVDLGDRIATISHKCLCCVSSSLKKNOLGXYLTLYKKDYESLS 1140
 Db 1081 grtilsthnmdvdldgria tishkclccvssslkknolgxy ltllykkdyesls 1140
 QY 1141 SCRRSSSTVSTLKKEDSVSOGSSSDAGLSDHESDITLIDVSAISNLRKHVSARLVEDI 1200
 Db 1141 scrrssstvsylkkedsvsogsssdaglsdhsedltlidvsaisnlrk hvsarlv edi 1200
 QY 1201 GHEFTYVLPYEAKEGAFVELFHEIDRLSDIGTSSISGSETTLEELFLKVAEESGVDAE 1260
 Db 1201 gheftylvpyeakegafv elfheidrlsdigtssisgsettleelflkvae esgvdae 1260
 QY 1261 TSQGTLPARRNRRAFGDKOSCLRPFTEDAADPNDSIDIPESREPTDLSGMDCKSGSYOK 1320
 Db 1261 tsdgtlparrnrraf gdkosclrpftedaa dnpndsidip esreptdls gmdcksgsyok 1320
 QY 1321 GKKLTQOQFALLMKRLRLIARRSRKGFPAQIYLPANFVCIALVSLVPPCKYPSLEIQ 1380
 Db 1321 gkltqoqf allmkrlrl iarrsrk gfpaiy lpanfvcialvslvppckyp sleiq 1380
 QY 1381 PMYNDQYTFVNSDAEDTGTLELNLATFKDPGFRGCEGNPIPTPOQAGEEEMTAP 1440
 Db 1381 pmyndqytfvnsdaed tgtlelnlatfkdp gfrgcegnpiptpoq ageeemt ap 1440
 QY 1441 VPQTIMDLQONGWITQONSPACQSSDKIKKMLPVCPPGAGLPPPOKQOTADILDL 1500
 Db 1441 vpqtimdlqongw itqonspacqssdkikm lpvcppgaglp ppokqotadil dl 1500
 QY 1501 TGRNISDYLVKTYVQDIASLKNKTIWVNEFRYGSGLGVSQNALPPOEVNDAIKOKKK 1560
 Db 1501 tgrnisdylvktyv qdiaslknk tiwvnefr ygs glgvsqnalp poevndai k okkk 1560
 QY 1561 HLKLAQSSADRLNSLGRFMTGLDTRNNVYKWFNNKGWHAISSFLANYINNAILRANLQK 1620
 Db 1561 hlkl aqssadrlnslgrf mgtl dtrnnv ykwnnkgw hais sflanyinna ilranl qk 1620
 QY 1621 GENPSHYGTAFNHNPLNLTKOQLSVALMTTSVDVLSICYIFAMSFPVPSFVFLIOER 1680
 Db 1621 genps hygtafn hnpnlntk oqlsvalmttsvdvls icyifamsfpvpsf vfl ioer 1680
 QY 1681 VSKAKHLQFISGVKPVYIWLNSFWDMCNVYVPATLVIIIFICQOQSYSTSLPVLAL 1740
 Db 1681 vskahlqf isgvkpv ywl nswfwdm cnvyvpatlvi iif icqoqsy stslp v lal 1740
 QY 1741 ILLIYGSITPLAMPASVFKIPSTAYVLTSLVLFGLINGSVATFVLELFTDNKLNIN 1800
 Db 1741 illiygsitplamp asvfkips taya vltslv lfg lingsvatfvlelft dnklnin 1800
 QY 1801 DILKSVFLIFPHFCIGRLIDMVKNOAMADALEFGENRFPSPIMPLVGRNLFAMAVEG 1860
 Db 1801 dilksvflifphfc igrlidmv knoamada lefg enrfpspim plvgrn lfamaveg 1860
 QY 1861 VVEFLIVLLOYRRFIRPRYNAKLSPLNDEDEDVRRERORIIIDGGQNDILEIKELTKI 1920
 Db 1861 vveflivlloyrrf irpryna klspln dedevrrerori idggqndilei keltki 1920
 QY 1921 YRRRKRPAVDRIICGIPGECFGLGVNAGKSTFPMILGDTTVYRGAFLKKNLSLN 1980
 Db 1921 yrrkrpavdr icgipgecf glgvnagk stfpmilgdttvyrga flkknlsln 1980

QY 1981 IHEVHONMGYCPQFIDAITELLTGREHVEFPALLRGVPEKEVGKGMARLGLVYGEK 2040
 DB 1981 Ihehqmgycpqfidaiteilgrehvefallyrpekevgkgevalrlglvkygek 2040
 QY 2041 YAGNYSGGNRRKISTMTMALIGCPVVEFLDEPTTGDMPKARFLMNCALSVYKEGRSVLT 2100
 DB 2041 yaqnysgnrrkistmtaligcpvvefldeptgmprkarrflmncalsvkegrsvlt 2100
 QY 2101 SHSMECEALCTMAIMWNGRECLSGVOHLKNRREDGTTIVYRAGSNPDLKPYQDFEG 2160
 DB 2101 shsmeecealctmairmngreclsgvohlknrrdgytlvyragsnpdlkpyqdfeg 2160
 QY 2161 LAPPGSVLKEKHNMLQYOPLSPSSLSLARIFFSLISQSKRHLIEDYVSQTTLDQVFN 2220
 DB 2161 lafpqsvlkekhnmlyqplspsslsarlffslisqskrhlhedyvsqttldqvfn 2220
 QY 2221 AKDQSDDDLKDLSLRKNQTVDAVLTSFLQDEKYSYV 2261
 DB 2221 akdqsddhldkdlslrknqtvdaavltsflqdekysyv 2261

RESULT 7
 ID AAB38082 standard; Protein; 2261 AA.
 AC AAB38082;
 XX 29-JAN-2001 (first entry)
 DE Human ABC1 cholesterol transporter.
 XX Human ABC1 cholesterol transporter; chromosome 9q31;
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
 KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
 KW cardiovascular disease; coronary artery disease; coronary restenosis;
 KW cerebrovascular disease; peripheral vascular disease;
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
 KW prognosis; prophylaxis; drug screening; transgenic animal.
 XX Homo sapiens.
 OS WO200055318-A2.
 XX 21-SEP-2000.
 PD 15-MAR-2000; 2000WO-IB00532.
 PF 15-MAR-1999; 99US-0124702.
 PR 08-JUN-1999; 99US-0138048.
 PR 17-JUN-1999; 99US-0139600.
 PR 01-SEP-1999; 99US-0151977.
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON BIORESEARCH INC.
 XX Hayden MR, Wilson AR, Pimstone SN;
 DR MPI: 2000-587528/55.
 DR N-PSDB: AAC69120.
 XX New ABC1 polypeptide is useful for treating diseases associated with
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
 PT disease and cancer -
 XX Claim 5; Page 152-157; 229pp; English.
 XX The invention relates to the human ABC1 cholesterol transporter protein
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of
 CC proteins, and plays a crucial role in cholesterol transport, particularly
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being

CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
 CC located on chromosome 9q31, and mutations in this gene are associated
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,
 CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
 CC are distinguishable in that TD is an autosomal recessive disorder, while
 CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
 CC cholesterol") in the blood correlate with a high risk of cardiovascular
 CC disease, particularly coronary artery disease, but also cerebrovascular
 CC disease, coronary restenosis, and peripheral vascular disease.
 CC Conversely, a high level of HDL has protective effects against
 CC cardiovascular disease. The invention provides genetic constructs and
 CC transgenic cells and non-human animals comprising human ABC1 nucleic
 CC acids, and methods of gene therapy for the treatment or prevention of
 CC cardiovascular disease comprising the administration of an expression
 CC vector encoding ABC1 or an active fragment thereof. The invention also
 CC encompasses compounds which mimic ABC1 activity, compounds which
 CC stimulate ABC1 expression and methods of screening for such compounds.
 CC It further relates to methods for determining whether a patient has an
 CC increased risk for cardiovascular disease due to polymorphisms in the
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
 CC or prevent cardiovascular disease, especially coronary artery disease,
 CC cerebrovascular disease, coronary restenosis or peripheral vascular
 CC disease. They may also be used in the treatment of diseases associated
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
 CC The invention specifically excludes proteins with the exact amino acid
 CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
 CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The
 CC present sequence represents the human ABC1 cholesterol transporter.
 XX Sequence 2261 AA:
 SO

Query Match 99.9%; Score 11789; DB 21; Length 2261;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2258; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MACMPQLRLILMKNLFFRRQTCOLLLEVAMPLEFIPLILSVRLSYPPYQHECHFPNKA 60
 DB 1 macmpqlrlilwkhltfrrtqqlilevampfifililsvrlsyppyeqhechfpnka 60
 QY 61 MPSAGTLPWVGITICMANNPCFRIPPTGEBAPGVYGNKKSIVARLPSDARILLYSQXDT 120
 DB 61 mpsagtlpwwvgitlonanmpcfrptpggabpyvgnknksivarlpsdarilllysqdkt 120
 QY 121 SMKMKRKLRLTLOQIKKSSSNLKLQDFVDEPFGCLYNNLSLPKSTVDKMLRADVILH 180
 DB 121 smkkmrkvlrltloqikksssnlklqdfvdehltsgfllynnlsipksvtdkmlradvilh 180
 QY 181 KVFLOGYQLHLTSLCNGSKSSEMTQLDQEVSELGSLPKKLAARVLRSMNDILKPL 240
 DB 181 kvflgylqlhltslncgskssemtqlgdqevselcgslpreklaaervlrsnmndilkp11 240
 QY 241 RLINSTSPPKSEKLEAEAKRTLLHSIGTLAQLFEMRBSMSMDROCVMLRTVWNSSSSTOI 300
 DB 241 rlinstspfskelaekclllhsigtlaqlfsmrwsmdrvgmflrvwnssstql 300
 QY 241 RLINSTSPPKSEKLEAEAKRTLLHSIGTLAQLFEMRBSMSMDROCVMLRTVWNSSSSTOI 300
 DB 241 rlinstspfskelaekclllhsigtlaqlfsmrwsmdrvgmflrvwnssstql 300
 QY 301 YQAVSRIVCGHPGEGGLKIKSLNWEYEDNNYKALGSGNTERDADTFYDNSTTPYCDNLMK 360
 DB 301 yqavsrivcghpegglkikslnwedyednnkalgsgnterdaetfndnstpycndlmk 360
 QY 361 NLESSPLSRITWKALKPLLVGKILYTPDTPATROYMAEVNKTFOELAVFHDLSGMWELS 420
 DB 361 nlessplsrilwkalppllvgkilytpdtpatroymaevnktfodelavfhdlegmwels 420
 QY 421 PKIWTFMENSQEMDLRYRLMLDSRDNDHFWEOQLGDLMTADIDYAAFLAKHPEDVQSSNGS 480
 DB 421 pkiwtfmenqemdlryrlmldsrdndhfwegldgldmtadidyaafakhpdevqssngs 480
 QY 481 VYTWREAFNETNOAIIKTSRMECVNLNKLKLEPIAEVWLINKSMLLDERKFWAGIVFTG 540
 DB 481 vytwreafnetnolaitsrmevcvnlknkllepiavevwlinskmllderkwagivftg 540

QY 541 ITPGSIELPHHKYKIRMDINVERTNKIKGICYWDGPRADPFEDMRVWGFAVLODPUV 600
 Db 541 ITPGSIELPHHKYKIRMDINVERTNKIKGICYWDGPRADPFEDMRVWGFAVLODPUV 600
 QY 601 EGAIRIVLTGTEKTKGVYMOQMPYCYVDJIELRVMSMSMLPMTLMTIYSVAITIKGIV 660
 Db 601 EGAIRIVLTGTEKTKGVYMOQMPYCYVDJIELRVMSMSMLPMTLMTIYSVAITIKGIV 660
 QY 661 YEKERLKEVNRKMGJLONSILMSFWSISLLPLLVSAQLLVVILKLGNIJPSDPVAVFV 720
 Db 661 YEKERLKEVNRKMGJLONSILMSFWSISLLPLLVSAQLLVVILKLGNIJPSDPVAVFV 720
 QY 721 FLVSFAVVTIIQCFILISLFSRANLAAAGGIIYFTIYLPVLCVANOVDYVGFLLKIFAS 780
 Db 721 FLVSFAVVTIIQCFILISLFSRANLAAAGGIIYFTIYLPVLCVANOVDYVGFLLKIFAS 780
 QY 781 LLSVPAEGCEGEPALFEEDGIGVOMDNLFPESPEEDGFNLITISIMMLEFTPLFYGVMT 840
 Db 781 LLSVPAEGCEGEPALFEEDGIGVOMDNLFPESPEEDGFNLITISIMMLEFTPLFYGVMT 840
 QY 841 YIEAVFGQVGIIPRPWFPCKKSTWFEESDEKSHPSNOKRMSEICMEEPHLLKLGVS 900
 Db 841 YIEAVFGQVGIIPRPWFPCKKSTWFEESDEKSHPSNOKRMSEICMEEPHLLKLGVS 900
 QY 901 IONLVKYYRQGMKVAVDGLALNFEQGITSEFLGHNGAKTTISILTLGLPPTSGRAYIL 960
 Db 901 IONLVKYYRQGMKVAVDGLALNFEQGITSEFLGHNGAKTTISILTLGLPPTSGRAYIL 960
 QY 961 GKIDRSKSTIRONLGYCPOHNVLFDMIVBEHITWFIARLKLSEKHVKAEMBOMLDVG 1020
 Db 961 GKIDRSKSTIRONLGYCPOHNVLFDMIVBEHITWFIARLKLSEKHVKAEMBOMLDVG 1020
 QY 1021 LPSKSLKSTKTSOLSGMQRKLSVALAFVGGSKVYIIDEPAAGVDPVSRKRTIWLILKYRQ 1080
 Db 1021 LPSKSLKSTKTSOLSGMQRKLSVALAFVGGSKVYIIDEPAAGVDPVSRKRTIWLILKYRQ 1080
 QY 1081 GRTIISTHMDADVLGDRIRAIISHGKLCVSSLEFLKNQJGTGYLLTVKKDVESSIS 1140
 Db 1081 GRTIISTHMDADVLGDRIRAIISHGKLCVSSLEFLKNQJGTGYLLTVKKDVESSIS 1140
 QY 1141 SCRNSSSTVYLYKKESSVSOSSSDAGISDHSDELTIIVSAISNLIRKHVSARLVEOI 1200
 Db 1141 SCRNSSSTVYLYKKESSVSOSSSDAGISDHSDELTIIVSAISNLIRKHVSARLVEOI 1200
 QY 1201 GHELTIVLYPEAKEGAFVELFHEIDRLSDLGISISYGISETTLEIFLKAEESSGVDAE 1260
 Db 1201 GHELTIVLYPEAKEGAFVELFHEIDRLSDLGISISYGISETTLEIFLKAEESSGVDAE 1260
 QY 1261 TSDGTLPARNRRAFGDKOSCLRPETEDDADPNDSIDPESRETDLSGMDGKSGYQVK 1320
 Db 1261 TSDGTLPARNRRAFGDKOSCLRPETEDDADPNDSIDPESRETDLSGMDGKSGYQVK 1320
 QY 1321 GWKLTQOQFVALLMKRLLIARSRKGFQAOIVLPAFVCIALVFSIIVPFGKYPSLEIQ 1380
 Db 1321 GWKLTQOQFVALLMKRLLIARSRKGFQAOIVLPAFVCIALVFSIIVPFGKYPSLEIQ 1380
 QY 1381 PMMYNBOQYTFVNSDAPEDGTGLELNAITKDPGFGTRCMEGNPDPDTPCOAGEEBMTAP 1440
 Db 1381 PMMYNBOQYTFVNSDAPEDGTGLELNAITKDPGFGTRCMEGNPDPDTPCOAGEEBMTAP 1440
 QY 1441 VPQITMDLFPQNGNMTMQUONSPACOCSSDKIKKMLPVCPPGAGGLPPQKQKOTADILDL 1500
 Db 1441 VPQITMDLFPQNGNMTMQUONSPACOCSSDKIKKMLPVCPPGAGGLPPQKQKOTADILDL 1500
 QY 1501 TGRNLSIDTIVKTYVOIIAKSLKNKIWNEFRYGFSTIGVSNTOALPPSOEVDAITKQMK 1560
 Db 1501 TGRNLSIDTIVKTYVOIIAKSLKNKIWNEFRYGFSTIGVSNTOALPPSOEVDAITKQMK 1560
 QY 1561 HLKLAQSSADGFLNSLGFPMGLDTRNNVYKWFNNKGMHAISPLVANNALIRANIOK 1620
 Db 1561 HLKLAQSSADGFLNSLGFPMGLDTRNNVYKWFNNKGMHAISPLVANNALIRANIOK 1620
 QY 1621 GBNPSHYGITAEFNHPLNTKQOLSEVALMTTSVDVLVSIQVIFAKSFVAFVFLIGER 1680

Db 1621 GBNPSHYGITAEFNHPLNTKQOLSEVALMTTSVDVLVSIQVIFAKSFVAFVFLIGER 1680
 QY 1681 VSKAKHLQISGVKPVYIWLNSFNWDMCNVVPATLVIIIFTCFOQKSYVSTNPIVAL 1740
 Db 1681 VSKAKHLQISGVKPVYIWLNSFNWDMCNVVPATLVIIIFTCFOQKSYVSTNPIVAL 1740
 QY 1741 LLLLYGMSITPLMYPASFEFKIPSTAYVVLTSVNLFIINGSVAIFVLELFDNKLNNIN 1800
 Db 1741 LLLLYGMSITPLMYPASFEFKIPSTAYVVLTSVNLFIINGSVAIFVLELFDNKLNNIN 1800
 QY 1801 DLKSVFLIFPHECLRGJLIDWKYNOAMADALEREGENFVPLSDVLGRNLFMAAVEG 1860
 Db 1801 DLKSVFLIFPHECLRGJLIDWKYNOAMADALEREGENFVPLSDVLGRNLFMAAVEG 1860
 QY 1861 VYFELLTVLIQRFIRPRPVNAKISPLNDEBEDYRREKORILDGCGONDILEIKELTKI 1920
 Db 1861 VYFELLTVLIQRFIRPRPVNAKISPLNDEBEDYRREKORILDGCGONDILEIKELTKI 1920
 QY 1921 YRRKRKPAVDRLCYGIPGCEGFLGVNGAGKSTFEKMLTGDTTTRGDAPLNKSLISN 1980
 Db 1921 YRRKRKPAVDRLCYGIPGCEGFLGVNGAGKSTFEKMLTGDTTTRGDAPLNKSLISN 1980
 QY 1981 IIEHONMGYCPQDAILTELLTGREHVEFFALLRGVPEKEVGKGEWAIRKILGVYGEK 2040
 Db 1981 IIEHONMGYCPQDAILTELLTGREHVEFFALLRGVPEKEVGKGEWAIRKILGVYGEK 2040
 QY 2041 YAGNYSGGNKRKLTAMALIGSPVYFLDEPTGMDPKARFLNNCALSYKBEGRSVLT 2100
 Db 2041 YAGNYSGGNKRKLTAMALIGSPVYFLDEPTGMDPKARFLNNCALSYKBEGRSVLT 2100
 QY 2101 SISMEECEALCTRMAIMVNGREFCLGSVOHLKNRGRDGYTIVRIAGSNPDLKPVODFFG 2160
 Db 2101 SISMEECEALCTRMAIMVNGREFCLGSVOHLKNRGRDGYTIVRIAGSNPDLKPVODFFG 2160
 QY 2161 LAIFGSVLYKEKRNMLQYOLPSSLSLARISISOSKRRKHIEDYSQITLLQOVYNE 2220
 Db 2161 LAIFGSVLYKEKRNMLQYOLPSSLSLARISISOSKRRKHIEDYSQITLLQOVYNE 2220
 QY 2221 AKDOSDDHLKDLKRNQYVAVLVNLSFLQDEKVESYV 2261
 Db 2221 AKDOSDDHLKDLKRNQYVAVLVNLSFLQDEKVESYV 2261

RESULT 8
 ID AAB71749 standard; protein: 2261 AA.
 XX AAB71749:
 AC 17-MAY-2001 (first entry)
 DT 17-MAY-2001 (first entry)
 DE Human AbC1 protein.
 KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; AbC1.
 XX Homo sapiens.
 OS Homo sapiens.
 PN W0200115676-A2.
 XX 08-MAR-2001.
 PD 08-MAR-2001.
 PF 01-SEP-2000; 2000MO-IB01492.
 PR 01-SEP-1999; 99US-0151977.
 PR 15-MAR-2000; 2000US-0526193.
 PR 23-JUN-2000; 2000US-0213958.
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON GENETICS INC.
 PI Hayden MR, Brooks-Walson AR, Pimstone SN, Clee SM;
 XX

DR WPI: 2001-244356/25.
XX Treating a lower than normal high density lipoprotein-cholesterol
PT (HDL-C) level, a higher than normal triglyceride level, or a
PT cardiovascular disease, by administering a compound that modulates LXR-
PT or RXR-mediated transcriptional activity -
XX Claim 16: Fig 2: 317pp: English.
PS
XX
CC The present invention relates to a method for treating a patient
CC diagnosed as having a lower than normal high density
CC lipoprotein-cholesterol (HDL-C) level, a higher than normal
CC triglyceride level, or a cardiovascular disease, involving
CC administering a compound that modulates LXR- or RXR-mediated
CC transcriptional activity or ABC1 expression or activity.
CC The LXR gene product may be used in an assay to identify
CC compounds useful for the treatment of a disease or condition selected a
CC lower than normal HDL cholesterol level, a higher than normal
CC triglyceride level, and a cardiovascular disease.
CC
XX
SQ Sequence 2261 AA:

Query Match 99.9%; Score 11789; DB 22; Length 2261;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2258; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACGPQRLRLMKNTLERRRQTCOLLLEVAMPFLIFLLISVRLSYRPEQHECHFPNKA 60
DB 1 macgpqrlllwnklfrrrrtqcolllevawpflflllsvrlsyppqeghechfpnka 60
QY 61 MPSAGTLPMWOGIITCANNANPCFRPPPGAPGVYGNFNKSIYARLPFSQARLLIYSQDT 120
DB 61 mpsagtlpmwvgigllcannanpcfrpppgapgvynfnksiyarlfpsdarlllysqdt 120
QY 121 SMKMRKVLTIOQIKSSSNLKLDFLVNDFSEFLVHNLSLPSTYDKMLRADVILH 180
DB 121 smkmrkvltlqgiksssnlklqdfldvnefsgflvhnlsipkstydmlradvilh 180
QY 181 KVFLOGYOLHLTSLCNGSKSEEMIQLODQEVSELGCLPKEKLAARVLRSMNDILKPL 240
DB 181 kvflogylhltslcnsgskseemiqldqevselcglpkeklaaerlvrsmdilklpl 240
QY 241 RFLNSTSPFSPKELAEATKTLHSLGLAOLFSMSMSWSMRQEWELTNVNSSSTQI 300
DB 241 rflnstspfskelaektktlhslglaelfsmswsmrqewmflcnvsssstqi 300
QY 301 YQAVSRIVCGHPGEGGLIKISLMWYEDNNYKALFGNGTEDEAEFYDNSTTPYCDLNMK 360
DB 301 yqavsrivcghpgegglkikslmwedydnnykalfgngteedaeftydnsttpcndlmk 360
QY 361 NLESSPSRIITWALKLPVVGKILYTPDPATROVAEAVNKTQEOBLAVFHDEGMMDEIS 420
DB 361 nlesspsriitwalklpvvgkilytpdpatrovaevnktqeoelavfhdeggmdeis 420
QY 421 PKIYTFMNSQBMOLVRLMLDSRDNDHPWGOULDGLWMTQDIAVFLAKHPEDVOSSNGS 480
DB 421 pkiytfmnsqbmolvrlmldsrdndhpwgouldglwmtqodiavflakhpedvoSSNGS 480
QY 481 VYTMREAFENETNOAIRTISRFMECVNLKLEPIATEVWLINKSMELLDERKFMAGIVTGS 540
DB 481 vytmreafeNETNOAIRTISRFMECVNLKLEPIATEVWLINKSMELLDERKFMAGIVTGS 540
QY 541 ITPGSIELPHVKKIRADINDVERTKIKDGYWDPGRADPFEDMRYVWGAGVADQVY 600
DB 541 itpgsielephvkkiradindvertkikdgywdpgradpfedmryvvgagvaydv 600
QY 601 BOAIIIRVLGTGKTKGVYMOOMPFCYVDIIFLRMSKSMPLFWTLAMITSVAIIKGIY 660
DB 601 boaiiirvlgtgktkgvymoompfcyvdiiiflrmsksmplfwtlamitsvayikgiy 660
QY 661 YKEEARLKETMRIMGLDINSILFWSFISLILPLVSAGLLVILIKGNLLPYSDPSVYV 720
DB 661 ykeearlketmrimgldinsilfwsfisslilplvsagllvilkgnllpySDPSVYV 720

DB 661 ykeearlketmrimgldinsilfwsfisslilplvsagllvilkgnllpySDPSVYV 720
QY 721 PLSVFAVVTIIOCFILSTLFSRANLAAACGGIYFTTLPLPVLCVANOVDVGGFTLKTFAS 780
DB 721 plsvfavvtiioCFILSTLFSRANLAAACGGIYFTTLPLPVLCVANOVDVGGFTLKTFAS 780
QY 781 LLSVPAFGGCVFPLAFEEGOGIGVQMDNLFESEVEDCFNLTTSISMLEPTFLYGMVTW 840
DB 781 llsvpaFGGCVFPLAFEEGOGIGVQMDNLFESEVEDCFNLTTSISMLEPTFLYGMVTW 840
QY 841 YIEAVPQGYGIPRPYFPCTRSYWFGEESDEKSHPGSNQKRMSEICMEEPHTLKIGVS 900
DB 841 yieavpQGYGIPRPYFPCTRSYWFGEESDEKSHPGSNQKRMSEICMEEPHTLKIGVS 900
QY 901 IQLVLVYVRDGMKAVNDGLALFVEGQITSEFGHGACKTTMTSLTNGLPPTSGTYIL 960
DB 901 iqlvlvYVRDGMKAVNDGLALFVEGQITSEFGHGACKTTMTSLTNGLPPTSGTYIL 960
QY 961 GKDIREMSTIRONLGVCPQHNVLPDMLTVEBHIWFYARLKLSEKHVKAEMEGNALDVG 1020
DB 961 gkdireMSTIRONLGVCPQHNVLPDMLTVEBHIWFYARLKLSEKHVKAEMEGNALDVG 1020
QY 1021 LPSSKLKSTQSLSGGMQRKLSVALAFVCGSKVILLDEPTAGVDPSRGTIMELLIKYRQ 1080
DB 1021 lpsklkstqsLSGGMQRKLSVALAFVCGSKVILLDEPTAGVDPSRGTIMELLIKYRQ 1080
QY 1081 GRTITLSTHMDADVLDGRLATITSHGKLCVGSSEFLTNQGTGYTLVKKDESSLS 1140
DB 1081 grtitlSTHMDADVLDGRLATITSHGKLCVGSSEFLTNQGTGYTLVKKDESSLS 1140
QY 1141 SCRNSSSTVSYLKREDVSQSSSDAGIGSDHESDITLIDVSAISNLIRKHSEARLVEDI 1200
DB 1141 scrnssstvsylKREDVSQSSSDAGIGSDHESDITLIDVSAISNLIRKHSEARLVEDI 1200
QY 1201 GHELTLYLPEAKKGAFLVLFHEIDRLSDIGISSYGSSETTLEIFLKVKEESGYVAE 1260
DB 1201 gheLTLYLPEAKKGAFLVLFHEIDRLSDIGISSYGSSETTLEIFLKVKEESGYVAE 1260
QY 1261 TSQDTLPARNRRRFAFGKQSCLEPTEEDADPNDDIPESRETDLSGMDKGSYQV 1320
DB 1261 tsqdtlpARNRRRFAFGKQSCLEPTEEDADPNDDIPESRETDLSGMDKGSYQV 1320
QY 1321 GWKLTQOOFVALLMKRLILARRSKGFPFOIYLPAYVCIALVSLIYPPFGKYSLEIQ 1380
DB 1321 gwklTQOOFVALLMKRLILARRSKGFPFOIYLPAYVCIALVSLIYPPFGKYSLEIQ 1380
QY 1381 PWMXNEQYTFVSNAPBDTGTLELNAITKDPGGRKMGNGPIPTPCOAGEEWTTAP 1440
DB 1381 pwmXNEQYTFVSNAPBDTGTLELNAITKDPGGRKMGNGPIPTPCOAGEEWTTAP 1440
QY 1441 VPOTIMDLFONGMNTKQNPSPACQSSSDKIKMLPYCPGAGGLPPORRONTADILQDL 1500
DB 1441 vpotIMDLFONGMNTKQNPSPACQSSSDKIKMLPYCPGAGGLPPORRONTADILQDL 1500
QY 1501 TGRNISDYLVKTYOIIAKSLKNIWNERRYGFSLGVSNTQALPSPQEVNDAITOMKK 1560
DB 1501 tgrNISDYLVKTYOIIAKSLKNIWNERRYGFSLGVSNTQALPSPQEVNDAITOMKK 1560
QY 1561 HXLAKDSSABRPLNSIGREPTGLDTRNNYKVMFNNGGMAIISFLVAINNATILRANLQK 1620
DB 1561 hxlAKDSSABRPLNSIGREPTGLDTRNNYKVMFNNGGMAIISFLVAINNATILRANLQK 1620
QY 1621 GENPSHYGITAFAFNHPLNLTKOOLSEVALMTTSDVDIVSICVIFAMSFVPSVYVFIQER 1680
DB 1621 genPSHYGITAFAFNHPLNLTKOOLSEVALMTTSDVDIVSICVIFAMSFVPSVYVFIQER 1680
QY 1681 VSKAHLQPIGSKVRYIWNLSNFWDMCNVYVPAITVLIIFICFOOKSYSSNPLVVAL 1740
DB 1681 vskAHLQPIGSKVRYIWNLSNFWDMCNVYVPAITVLIIFICFOOKSYSSNPLVVAL 1740
QY 1741 LLLYGWSITPLMYPASVFKIPSTAVVVLTVSMVLFTGINGSVATVLELFTDNKLNIN 1800
DB 1741 lllYgwsitPLMYPASVFKIPSTAVVVLTVSMVLFTGINGSVATVLELFTDNKLNIN 1800

```

QY 1801 DLKSVFLIFPHFCIGKGLIMVKNQAMADLBERGRENFSPLSMDLVGRNIPAMAVEG 1860
DB 1801 dILMSVfllfphfclgltglmVknqamadalErfgertfvsplswdlvgnllfamaVeG 1860
QY 1861 VVFFLTIVLIYRPFIRPRPNNAKLSPLNDEDEVRREPROBILINGGCONDLLEKELTKI 1920
DB 1861 vVfflTivLIyRpfIRprpNNAkLSplNdEdEvrrErqLIldg99qndllElkElTKI 1920
QY 1921 YRRKRKPAVDRIYVIGIPPECEFGILGVNAGAKSSFTFKMLTGDVTVTTRGDAFLNKNLSLN 1980
DB 1921 YrRkrKpAvDrIyVigIpPeCeFgIlLvNgAgKsStfKmlTgdTvtTrGdaFlNknSlSn 1980
QY 1981 IHEHOMNMGVPOPDATITELTSGREHEFFALLKGVEPEKGVKGEWAIRKLGIVKGEK 2040
DB 1981 iHeHOMnMGvPOpdATITeLTsGREHEffALLkGvEpEKgVKGewAIRkLGIVkGek 2040
QY 2041 YAGNYSGGNKRKLSTAMALIGBPVFLDEPTTGMDPKARFLMNCALSVKKEGRSVLTF 2100
DB 2041 YaGnYsGgNkrKlStAmAlIgGpVvFlDePtTgMdpKArRfLmNCaLSvKkEgRSvLtf 2100
QY 2101 SHSMECEALCTRAIMVNRFRIGISVQHKNRFGGTYTVRIAGSNPDLKPVODFG 2160
DB 2101 sHsMeCeAlCtTrAiMvNrFrIGiSVQHkNrFGGtyTVrIAGsNPdLKpVoDfG 2160
QY 2161 LAFPGSVLKKRHRNMLQYOLPSSLSLARIFSLISOSKRRLIEDYSVOTTLDQYFVNF 2220
DB 2161 lAfPgSVlKkRhrNmLqYolPssLSlArIFsLISgSkRRLhEdYsVgTtldQyFvNf 2220
QY 2221 AKQOSDDHLKDLSLHKNQTVVAVVLTSLDDEKVKESYV 2261
DB 2221 aKqoSdDdHlKdLSlHknQtVvAvVlTslDdEkvKesyv 2261

```

RESULT 9

AAB31363

ID AAB31363 standard; Protein; 2261 AA.

AC AAB31363;

DT 20-APR-2001 (first entry)

DE Amino acid sequence of ABC1 polypeptide from Tangier disease patient.

KW Human; adenosine triphosphate binding cassette protein 1; ABC1;

KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;

KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;

KW atherosclerosis; cholesterol transport.

OS Homo sapiens.

XX

FT Key Location/Qualifiers

FT Misc-difference 587

FT "note= 'this is changed from Arg to Trp in Tangier disease'"

PN WO200078972-A2.

XX

PD 28-DEC-2000.

XX

PF 16-JUN-2000; 2000WO-US16765.

XX

PR 18-JUN-1999; 99US-0140264.

PR 14-SEP-1999; 99US-0153872.

PR 19-NOV-1999; 99US-016573.

XX

PA (CVTH-) CV THERAPEUTICS INC.

XX

PI Lawn RM, Wade D, Garvin M;

XX

DR WPI; 2001-137812/14.

XX

PT Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide.

PT useful for the development of agents for the treatment of heart disease

PT and other disorders associated with hypercholesterolemia and

PT atherosclerosis -

XX

PS Disclosure; Page 176-191; 215pp; English.

XX

CC The present sequence represents a human adenosine triphosphate (ATP)

CC binding cassette protein (ABC) 1 polypeptide, and is isolated from

CC a Tangier disease patient. ABC1 resides in cell membranes and utilises

CC ATP hydrolysis to transport a wide variety of substrates across the

CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated

CC mobilisation of intracellular cholesterol stores. ABC1 is defective in

CC Tangier disease, a genetic disorder characterised by abnormal

CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome

CC 9q22-9q31. The ABC1 genes and proteins are useful for developing

CC pharmaceutical agents for the treatment of heart disease and other

CC disorders associated with hypercholesterolemia and atherosclerosis. The

CC genes are useful for developing screening assays to screen for compounds

CC that regulate the expression of genes associated with cholesterol

CC transport. The genes and proteins are also useful for are also useful

CC as diagnostic indicators of cardiovascular disease and other disorders

CC associated with hypercholesterolemia.

CC

XX

Sequence 2261 AA;

Query Match 99.9%; Score 11789; DB 22; Length 2261;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MACQWOLRLILMKNLTPRRROTCLLEVAMPFLFLLISVRSLSPYEDQHECHFPKA 60
DB 1 macwqolrlilmknltprrrotclllevampflfllisvrslspyedqhechfnpka 60
QY 61 MESAGTLFWVQGIICNANPCFRYPPTGEPAGVGVGNFKSIVARLFSPARLLYSOKDT 120
DB 61 mpsagtlfwvgiicnannpcfryptpggapvgvgnfkshivarlfsparllysoKdt 120
QY 121 SMKDKRKYLRTLQOIKKSSNLKLODFLVNDETSGFLYHNLSLPKSTVDKMLRADYLH 180
DB 121 smkdkrkyltrlqoikksnlnklodflvndetsgflyhnlslpkstvdkmradylh 180
QY 181 KYFLQGYOLHTSLCNGSKSEEMIQLGDQVESELCGPKEKLAAEVNLNNMDILKPTL 240
DB 181 kVflgYyOLhtslcngskseemIqlgdqVesElcgpKeklaaEvnlNnmDilKptl 240
QY 241 RTLNSTSPFSKELAEATKTLHSLGTLAQLFSMRSMWDMKROVMLTJNVNSSSSTQI 300
DB 241 rtlNstspfskelaEATKtlHslgTlaqlfsmrsmwDMkroVmlTjnvNssstQI 300
QY 301 YOAVSRIYCGHPEGGGLKIKSLNMYEDNNYKALFGNGTEDEAETFYDNSTTRYCNDLMK 360
DB 301 yGaVsRiYcghpegGglKikslNmyEdnnYkAlfgNgteDeaETfyDnSttrycNdLmk 360
QY 361 NLESSPLSRIIWKALKPLVKGKILYTPDTPATROVAEAVKKTQELAVFDLGGMWEELS 420
DB 361 nlessplsrIiWkAlKplVgkIlYtpDtpatRoVAeAvKktqElavfdlGgmweels 420
QY 421 PKITFMENSGEMDLVRLDSDRNDHFWEQDLDGLDWTADQIVAPLAKHPEDVSSNGS 480
DB 421 pKItfMenSgemdlVrldSDrNdHfweQdldglDwtAdQivApLakhpEdvssngs 480
QY 481 VYTWEAFNEFTNOAIRTISRFMECVNLNKEPIATEVWLNKSMELIDEEKFAGIVFNG 540
DB 481 vYtWeaFneftnOairtIsrfMecvnlNkePiAtEvwlNksMeLiDeekfAgIvFng 540
QY 541 ITPGSIELPHHVKKYKIRMDIDNVERTNKKIKGYWDBGPADPREDARYWGGFAYLQDPV 600
DB 541 iTpGsIeLphHvKkYkIrMdIdNvErtnKkIkGyWdbGpAdpRedArYwGgFaYlQdpv 600
QY 601 EOALIRVLGTGEEKTGYYNQOMPRPCYVDDIFLRWRSRMLPMTLAMIYSAVAIITKGIY 660
DB 601 eOaLiRvLgtGekTgYyNqOMpRcYvDdIFlrWrsRmLPmtLAmIySAvAIITkGIy 660

```



```

QY 661 YEKARLEKTRMIRGLDINSILFESWPTSSILPLIVSAGLLVILKIGNLPLISDPSEVAV 720
Db 661 yekarilektrmirdlnsilfswptssilplivsasgllvilkignlplisdpsevvav 720
QY 721 FLVSFAVYTIICQCLISTLSPSRALAAAGGIYFTLYEYVLCVAMODVGTLEKIFXS 780
Db 721 flsvfavytliqcclistspsrallaaaggiftlyeyvlcvamodvgtltkifxs 780
QY 761 LLSPAFGCEGFALFEEOGIGVOMDNLESPPEEDGFNLTTSSIMMLPDTLEYGMVMT 840
Db 761 llspafgcegfalfeeoigivomdnlesppeedgfnlttssimmlpdtleygmvtw 840
QY 841 YLEAVFPGQYIIPRWTFPCTKSTWFGESDEKSHPSNOKRMEICMEEPFHKLGVIS 900
Db 841 yleavfpgqyiprpwtfpctkstwfgesdekshpsnokrmeicmeeepfhklgvis 900
QY 901 IONLVKVRDGMKAVNOSLALNFEQGTSFLGHNGAKTTMSILTLGLPPTSGTAYIL 960
Db 901 ionlvkvrddgmkavnoslalnfeqgtsflghngakttmsiltlglpptsgtayil 960
QY 961 GKDISEKSTIKONLGVCPONHNVLFDMLTVEHIMFYARLKGISEKHVKAEMEQMALDVG 1020
Db 961 gkdisekstikonlgvcpohnvlfdmLTVEHIMFYARLKGISEKHVKAEMEQMALDVG 1020
QY 1021 LPSSKLKSTQSOLSGMQRKLSVALAEVGSKVYLDEPFAVUPYRSRGIMELLKXRO 1080
Db 1021 lpsklkstqsolsgmqrklsvalaevgskvyldepfavgupyrsgimellkxrv 1080
QY 1081 GRTIISTHMEADVLDRIAIIISHGKLCVGSLSFLKNOLGTGYITLVKRVESLS 1140
Db 1081 grtiisthmeadvldriaaishgklcvgslsflknolgtgyitlvkrvessls 1140
QY 1141 SCNNSSTVSYLKKEDSVSQSSSDAGLSDHESDITLIDVAISNLIRKHVSEARLEVDI 1200
Db 1141 scnnsstvsylkkedsvsqsssdaglsdhesdltldvasaisnlirkhsearlvdi 1200
QY 1201 GHELIYVLEFAKKEGAFVLEFHEIDRLSDLGISYGISFTLLEIFLKAESGVDAE 1260
Db 1201 gheliyvlefaakkegafvlefhaidrlsdlgisysyisftlleiflkaesgvdae 1260
QY 1261 TSDGTLPARNRRAFGDKOSCLRPFTEDDADPNDSIDDPESRETDLSGMDGKSYOVK 1320
Db 1261 tsdgtlparnrrafgdkosclrpfteddaadpndsiddpesretldlsmdgksyovk 1320
QY 1321 GWKLTQOQFVALLWKRLLIARSRKGFPAQIVLPAVFCIALVESLYPPRGKYSLELO 1380
Db 1321 gwkltgqfvalllwkrlliarstrkgfpaqivlpavfcialvlslypprgkyplelq 1380
QY 1381 PMMYNQYFPVSNDAPEDEGTLELINALTKDPFGRCMEGNIPDTPCOAGEEEMWTAP 1440
Db 1381 pmyneqyfpvsnadapedegtlelnalatkdpfgrcmegnipdtpcoageeemwtap 1440
QY 1441 VPQITMDLFONGMWTQONSAPACOSSDKIKKMLPYCPPGAGLPPORQONTADILDL 1500
Db 1441 vptitmdlfgngmwtqonsapacossdkikkmlpycppgaglpportqontadilddl 1500
QY 1501 TGRNISDYLVKTYVOIIAASLKKIYVNEFRGGFSLGYSNQALPPSGEVNDALIKOMK 1560
Db 1501 tgrnisdylvktyvoiiiaaslkkivynefrggfslgysnqalppsgevndalikkomk 1560
QY 1561 HLKLAQSSADRFNLNSIGRPMTGLDTRNNYKVFNNKGMHAISSEFLNVNNAILRANLOK 1620
Db 1561 hlklakqssadrfnlnsigrpmtgltdtrnnnykvfnnkgmhaissseflnvnnailranlo 1620
QY 1621 GENPSHYGITAFAHPLMLTQOOLSEVALMTTSDVLTVCYFAMFVAFASPVFLIDOR 1680
Db 1621 genpshygitafahplmltkqolsevalmttsdvltvcyfamfvafaspvflidorr 1680
QY 1681 VSKAKHLQFTSGVKKPVITWISNFWDMCNVVPATLVIIIFICFOOKSYVSSNTLPEVL 1740
Db 1681 vskakhlqftsgvkkpvitwvsnfwdmcnvvpatlviififcfooksyvssntlpevl 1740

```

```

QY 1741 LLLYGSITPELMYPAFSEVKEIPSTAYVVLTVSNLEFIGINGSVAFVLELFTDNKLNTIN 1800
Db 1741 llllygsitpelmypafsevkeipstayvvltsvnlefigingsvafvlelfdnklntin 1800
QY 1801 DILKSVFLIPHECLGGLIDMKRNQAMADALERFGENRVRSPSLMSDLDGRNLFAAAVAG 1860
Db 1801 dilksvflipheclgglidmkrnqamadalerrfgenrvrspslmsdldgrnlfaavaag 1860
QY 1861 VVEFLITVLIOYRFFIRPRPVNAKLSPLNDEDEDDVRERORILIDGGGQNDILEIKELTKI 1920
Db 1861 vveflitvlityrffirprpvnaklsplndeadedvrerorilidgggqndileikeltki 1920
QY 1921 YRRKRKPAVDRIICVGIIPPEGCEGLLVNGAGKSTFEMLTGDTTVTRGDAFLKNKNTLSN 1980
Db 1921 yrrkrkpavdricvgiippegceglvngagkstfemltgdtvtvtrgdaflnknntlsn 1980
QY 1981 IHEVHQNMGYCPQPDATITELLTGREHVEFALLMGVEKEVGKWEAIRKLGIVYGEK 2040
Db 1981 ihevhnmgycpqpdattitelltgrehvefallmgvekevkwewairklgivvygek 2040
QY 2041 YAGNYSGGKRRKLSFAMALLIGPPVFLDEPTTGMDPKARFIMNCALSVYKGRSVLT 2100
Db 2041 yagnysgkrrklsfamaalligppvfldepttgmdpkarflmncalsvykgrsvlt 2100
QY 2101 SHSMECEALCTPMAIMVNGRFRCLGSVOHLKNRFGDGYITIVRIAGSNPDLPYQDFEG 2160
Db 2101 shsmecealctpmaimvngfrclgsvohlknrfgdgyitivrriagsnpdlpyqdfeg 2160
QY 2161 LAFPGSVLKEKRKNMLQYQPSLSLARKRFSIIISQSKRLHIEDYSVSOOTLDQVVFNF 2220
Db 2161 lafpgsvlkekrrnmlqyqpslsllarkrfsiisqskrlhiedysvsotldqvvnf 2220
QY 2221 AKDOSDDHLKDLSLHRKNOTVVDVAVLTSFLODEKVKESYV 2261
Db 2221 akdosddhlkdlslhrknotvvdvavvltsfldekvkesyv 2261

RESULT 10
AAB31367
ID AAB31367 standard; Protein: 2261 AA.
XX AC AAB31367;
XX DT 20-APR-2001 (first entry)
XX DE
XX AA Amino acid sequence of ABC1 polypeptide from Tangier disease patient.
XX KW Human: adenosine triphosphate binding cassette protein 1; ABC1;
XX KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
XX KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
XX KW atherosclerosis; cholesterol transport.
XX OS Homo sapiens.
XX FH Key location/Qualifiers
XX FT MISC-difference 587 /note="this is changed from Arg to Trp in Tangier
XX FT disease"
XX PN MO200078971-A2.
XX PD 28-DEC-2000.
XX PE 16-JUN-2000; 2000MO-US16591.
XX PR 18-JUN-1999; 99US-0140264.
XX PR 14-SEP-1999; 99US-0153872.
XX PR 19-NOV-1999; 99US-0166573.
XX PA (CVTH-) CV THERAPEUTICS INC.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Lawn RM, Wade D, Oram JF, Garvin M;

```

XX WPI: 2001-137811/14.
 DR N-PSDB: AAF24708.
 XX
 PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
 PT polynucleotides and polypeptides, useful for treatment of heart disease
 PT and disorders associated with hypercholesterolemia and
 XX atherosclerosis -
 XX
 PS Claim 28; Page 172-187; 211pp; English.
 XX
 CC The present sequence represents a human adenosine triphosphate (ATP)
 CC binding cassette protein (ABC) 1 polypeptide, and is isolated from
 CC a Tangier disease patient. ABC1 resides in cell membranes and utilises
 CC ATP hydrolysis to transport a wide variety of substrates across the
 CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
 CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
 CC Tangier disease, a genetic disorder characterised by abnormal
 CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
 CC 9q22-9q31. The ABC1 genes and proteins are useful for developing
 CC pharmaceutical agents for the treatment of heart disease and other
 CC disorders associated with hypercholesterolemia and atherosclerosis. The
 CC genes are useful for developing screening assays to screen for compounds
 CC that regulate the expression of genes associated with cholesterol
 CC transport. The genes and proteins are also useful for are also useful
 CC as diagnostic indicators of cardiovascular disease and other disorders
 CC associated with hypercholesterolemia.
 CC
 XX Sequence 2261 AA:
 SO
 Query Match 99.9%; Score 11789; DB 22; Length 2261;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 541 icpgslelphhvkylzmdidnvertunkikdgywdpgradpfedimyywvgfaylqdv 600
 QY 601 FOAIRVLVGTGKRTGKYVMQMOOPYCYVDLFEIWMRSMPLEMTLAWISAVATIKGY 660
 Db 601 egairvlvtgkrtgkyvmqmqmpcyvddfltrvmsrmp1tmclawysavatlkgyl 660
 QY 661 YEKEARLEKEMRMIGLIDNSIIFSWFISLPLVLSAGLLVVLIKLGNLPPYDPSVVF 720
 Db 661 yekearlekmrmimglidsiifswfisslpllvssagllvvlklgnllpydpsvvt 720
 QY 721 ELSEFAVYTIQCELIISLFRANLAAACGIIYFTLYLPVLCVAMQDYVGTTLKIFAS 780
 Db 721 flsfaavytiqceliislfranalaaacgiiyftlylpvltcvamqdyvgttlkifas 780
 QY 781 ILSVPAFGCEYFALFEEDGIGVOMDNLFESEPEEEDFNLTISISMLPDTFLYCVMM 840
 Db 781 ilsvpafgceyfalfeedgigvowndnlfepegdfltsismlpdtflvyvmv 840
 QY 841 YLEAFPGQYGIIPRWPRPCKTSYFGESEDESKHPSNOKRMSEICMEEPHKLIGVS 900
 Db 841 yleavfpqygiiprwprpcktsyfwgesedekshpsnqkrmseicmeeephkligvs 900
 QY 901 IONLVKVRDGMKYAVDCLALNFEQITSGFNGAGTTFMSITLGLFPTSGTAYTL 960
 Db 901 ignlvkvrddgmkyavdclalnfeqitsgfngagtftmsitlglfptsgtaytl 960
 QY 961 GKDIRSEKSTIRONLGYCPOHNVLEDMITVEBHITWYARLKLSEKHVAEMDQALDVG 1020
 Db 961 gkdirsekstironglycpoahnvledmitvebhitwfarlklgsekhvkaemqaldvg 1020
 QY 1021 LPSSKLKSKTSQISGQMRKISVALAFVGSKVVIIIDEPAGVDVPSRGIMELLKAYQ 1080
 Db 1021 lpsklksktsqisgqmrkislvalafvgskvviiidepagvdvpsrgimellkayq 1080
 QY 1081 GRTIILSTHMDADVLDGRITAIISHGKLCQVSSSFLKNQLOTGYTLTVKKDYESSLS 1140
 Db 1081 grtilsthmdeadvldgritaiisbgklccvgsflknqlotgytltvkkdyessls 1140
 QY 1141 SCRRSSSTVSLKKEPSSVSSSSSDAGISGSHEDTLITIVSALSNLIRKHVEARLVEDI 1200
 Db 1141 scrssstvsylkkesvsssssdagisgshedtlitivsalsnlirkhvearlvedi 1200
 QY 1201 GHELTLYVLYPEAAKEGAFVLEFHEIDRLSDGISYSGISETTLERIFLAKVEESGVDAE 1260
 Db 1201 gheiltyvlypeakegafvlefhaidrlsdgisysgisettleeiflkaeesgvdae 1260
 QY 1261 TSDGTLPARNNRRAFGDKOSCLRPFTEDDAADPNDSIDPESRETDLLSGMDGKSYOVK 1320
 Db 1261 tsdgtlparnnrrafgdkgscrlrpfleddaadpndsidpesretdllsgmdgksgyvk 1320
 QY 1321 GMLTQOQFVALLMKRLIARSRKGFPAOTVLPVFCIALVESLIYPPGKTPSLEIQ 1380
 Db 1321 gmltqqgfvaallmkrliaarsrkgfpaotvlpvfciavelsiyppgktpslqliq 1380
 QY 1381 PMWYNEQYTFVNSDABEDGTLELNALTKDPGFCSTRGEGNPIDPFCQAGEEWTAP 1440
 Db 1381 pmwyneqytfvnsdapedgtlelnaltdkpgfcstrmegnpidpfcqageewtarp 1440
 QY 1441 VPQTIMDLFQNGWMTQONSPACQCSQKIKMLFVCPGAGAGLPPOKKNATDIIDL 1500
 Db 1441 vptqtimdlfqngwmtqonspacqcsdkikmlfpvcpgagaglppokknatdiidl 1500
 QY 1501 TGRNISDYLVKTYVOIIFASLKNKIMVNEFRYGSLSVSNQALPPOQEVNDALIKOMK 1560
 Db 1501 tgrnisdylvktyvoiiifaslknkimvnefrygslsvsnqalppsdevndalikomk 1560
 QY 1561 HUKLAOSSADRLNSLGEFTGLDTRNNVKKWFNNKGMHAISSFLVYNNAINARILQK 1620
 Db 1561 huklaossadrlnslgfimgltdtrnnvkwfnkghaissflvynnaianrlqk 1620
 QY 1621 GENPSHYGITAFNHPPLNLTIKOOLSEVALMTTSVYVYISCIYFAMSVYPASFVYLQER 1680
 Db 1621 genpshtygitafnnpplnltikoolsevalmttsvdyvysicifamsvypasfvylqer 1680

```

QY 1681 VSKAKHLQFISGVKPYIYWLNFVDMCNVYVPATLVIIIFICFOOKSVSSTNLPLVAL 1740
    |||||||
Db 1681 VSKAKHLQFISGVKPYIYWLNFVDMCNVYVPATLVIIIFICFOOKSVSSTNLPLVAL 1740
QY 1741 LLLVGSWSTPLMPYASVEFKIPSTAYVYLVSNLFIGINGSVAFFVLELPDNKLNIN 1800
    |||||||
Db 1741 LLLVGSWSTPLMPYASVEFKIPSTAYVYLVSNLFIGINGSVAFFVLELPDNKLNIN 1800
QY 1801 DILKSVLELFPKCGRLIDMKNQAMADALERGENSEFVPLSMDLVGRMLFMAVAG 1860
    |||||||
Db 1801 DILKSVLELFPKCGRLIDMKNQAMADALERGENSEFVPLSMDLVGRMLFMAVAG 1860
QY 1861 VVEFLITVLIOYRFFIRPPYNAKLSPLNDEDEDVRRERORILLDGGGNDLEIKELTKI 1920
    |||||||
Db 1861 VVEFLITVLIOYRFFIRPPYNAKLSPLNDEDEDVRRERORILLDGGGNDLEIKELTKI 1920
QY 1921 YRRKKRPANDRICVGIPECECGILGVNAGKSSFTFKMLTGPTVYRGDAFLNKSLISN 1980
    |||||||
Db 1921 YRRKKRPANDRICVGIPECECGILGVNAGKSSFTFKMLTGPTVYRGDAFLNKSLISN 1980
QY 1981 IHEVHOMGCGPOFDAITELTGREHVEFFALRGVPEKEVGKVGEMAIKLGKYGK 2040
    |||||||
Db 1981 IHEVHOMGCGPOFDAITELTGREHVEFFALRGVPEKEVGKVGEMAIKLGKYGK 2040
QY 2041 YAGNYSGKRRKLSTAMALIGBPVVFLEDPPTGMDPKARRELMNCALSVEKGRSVLT 2100
    |||||||
Db 2041 YAGNYSGKRRKLSTAMALIGBPVVFLEDPPTGMDPKARRELMNCALSVEKGRSVLT 2100
QY 2101 SHMECECALCTMAIMVNRFCISYOLKRRFGDGTIVYRIGSPNDLKPVDFFG 2160
    |||||||
Db 2101 SHMECECALCTMAIMVNRFCISYOLKRRFGDGTIVYRIGSPNDLKPVDFFG 2160
QY 2161 LAEPGVLKEKHNMLQYOLPSSLSLARIFSLISQSKRLHEDYSVSQTTLDQVFN 2220
    |||||||
Db 2161 LAEPGVLKEKHNMLQYOLPSSLSLARIFSLISQSKRLHEDYSVSQTTLDQVFN 2220
QY 2221 AKQSDDDHLKDLISLKNQNVVAVLTSPLQDEKYESYV 2261
    |||||||
Db 2221 AKQSDDDHLKDLISLKNQNVVAVLTSPLQDEKYESYV 2261

```

RESULT 11

AAB38111 standard; protein; 2261 AA.

AAB38111;

29-JAN-2001 (first entry)

Human ABC1 cholesterol transporter mutant, V771M.

Human ABC1 cholesterol transporter; chromosome 9q31.

ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;

Tangier disease; TD; familial HDL deficiency; FHD; polymorphism;

cardiovascular disease; coronary artery disease; coronary restenosis;

cerebrovascular disease; peripheral vascular disease;

Alzheimer's disease; Niemann-Pick disease; Huntington's disease;

X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;

prognosis; prophylaxis; drug screening; transgenic animal; mutant;

muteln.

Homo sapiens.

WO200055318-A2.

21-SEP-2000.

15-MAR-2000; 2000WO-1B00332.

15-MAR-1999; 99US-0124702.

08-JUN-1999; 99US-0138048.

17-JUN-1999; 99US-0139600.

PR 01-SEP-1999; 99US-0151977.

XX (XBR-) UNIV BRITISH COLUMBIA.

PA (XEN-) XENON BIORESEARCH INC.

XX Hayden MR, Wilson AR, Pimstone SN;

PI WPI: 2000-587528/55.

XX New ABC1 polypeptide is useful for treating diseases associated with

PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's

PT disease and cancer -

XX Examples; Page -: 229pp; English.

XX The invention relates to the human ABC1 cholesterol transporter protein

CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is

CC a member of the ATP-binding cassette (ABC transporter) superfamily of

CC proteins, and plays a crucial role in cholesterol transport, particularly

CC intracellular cholesterol trafficking in monocytes and fibroblasts, being

CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is

CC located on chromosome 9q31, and mutations in this gene are associated

CC with two genetic HDL (high density lipoprotein) deficiency disorders,

CC Tangier disease (TD) and familial HDL deficiency (FHD). These diseases

CC are distinguishable in that TD is an autosomal recessive disorder, while

CC FHD is inherited as an autosomal dominant trait. Low levels of HDL ("good

CC cholesterol") in the blood correlate with a high risk of cardiovascular

CC disease, particularly coronary artery disease, but also cerebrovascular

CC disease, coronary restenosis, and peripheral vascular disease.

CC Conversely, a high level of HDL has protective effects against

CC cardiovascular disease. The invention provides genetic constructs and

CC transgenic cells and non-human animals comprising human ABC1 nucleic

CC acids, and methods of gene therapy for the treatment or prevention of

CC cardiovascular disease comprising the administration of an expression

CC vector encoding ABC1 or an active fragment thereof. The invention also

CC encompasses compounds which mimic ABC1 activity, compounds which

CC stimulate ABC1 expression and methods of screening for such compounds.

CC It further relates to methods for determining whether a patient has an

CC increased risk for cardiovascular disease due to polymorphisms in the

CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat

CC or prevent cardiovascular disease, especially coronary artery disease,

CC cerebrovascular disease, coronary restenosis or peripheral vascular

CC disease. They may also be used in the treatment of diseases associated

CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick

CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.

CC The invention specifically excludes proteins with the exact amino acid

CC sequences of Genbank Accession No: CAA10005.1 and X75926, and the nucleic

CC acid with the exact sequence as Genbank Accession No: A7012376.1. The

CC present sequence represents a mutant human ABC1 cholesterol transporter

CC associated with an altered cholesterol level and therefore an altered

CC risk of cardiovascular disease.

CC Note: The present sequence is not shown in the specification, but is

CC derived from the native human ABC1 shown on pages 152-157.

Sequence 2261 AA:

Query Match 99.9%; Score 11786; DB 21; Length 2261;

Best local similarity 99.8%; Pred. No. 0;

Matches 2257; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MACWPQRLILMKNLFFRRQTCQLLEVAWPLIFLLISVRLSPYRHOEHCPPNKA 60
    |||||||
Db 1 macwpqrlilwknltfrrtqcllleawplifllilsvrlsyppeqnechfpnka 60
QY 61 MPSAGTLPWVOGITCANANNPCFRYPPTGEPAGVGVGNFNKSIYARLFSDARLLLSQKDT 120
    |||||||
Db 61 mpsagtlpwvvgitcanannpcfryptpgpavgvgnfnksiyarlfsdarllllyskdt 120
QY 121 SMKDMRKVRLTIOQIKSSNKLQDFLVNDFSGFVHNSLSPSYTDKMLRADVILH 180
    |||||||
Db 121 smkdmrkvrltlqikssnklqdfvlvndfsgfvlhnlslpsvtdkmlradvilh 180

```

QY 181 KVFLOGLYTLTSLCNGSKSEEMTOLGDOVESELCGLPKRKLAAARVYLRSMNDILKPLT 240
 Db 181 kvflqyqlhltslcnsgskeemqldgdevselcglprcklaaaveftrsmndllkpll 240
 QY 241 RTLNSTSPFPPSKELAEATKTLHLSTGLAOLEFSMRSMDSMDROEVMFLTNVSSSTJOI 300
 Db 241 rtlnstspfskelaektlhls]gllaqel fsmrswdsmdrmqevmfltnvsssstq 300
 QY 301 YOAVSRIVCGHPGGGKIKTSIMMYEDNNKALFGNGTPEDEAETTYDNTTPYCDMLAK 360
 Db 301 ygaavsrivcghppeggkiktslmymyednnkalfgngtpeedaetlydntstpycdmlak 360
 QY 361 NLESSLRLIIMKALPLVGLTLYTPDTPATROVAEVMKTRPOELAVPHDLGMEELS 420
 Db 361 nlessprliimkalkpllvglkllypdpdpactqmaenktqelavfhldlegmeels 420
 QY 421 PKIWTFMENQEMDLYRMLLDSRDNHFEQOLGDLMTAODIVAFLAHHPEDVOSSNGS 480
 Db 421 pkltwmensqemdlyrmlldsrndhfewqldgldmtaodivafiahhpedsngs 480
 QY 481 VYTWREAFNETNOAIRTISRFMECVNLNKLPRATPEVNLINSMELDERKTFMAGIVFTG 540
 Db 481 vytwreafeinetnairtisrfmecnlnklepratevnlinsmellderkltwaglvftg 540
 QY 541 ITPGSIELPHVVKYKLRMDIDNVERTNKIKDGYMDPGPRADPFEDMRVWGGFAYLQDYY 600
 Db 541 itpgsielphvvykkrmdidnvertnkikdgywdpgrpadfedmrvwggtfaylqdyv 600
 QY 601 EOAIIIVLTGTEKKGTVQOQMPYPCYVDIFLRVWSRSMPLFPLTAWIYSAVAIIRKIV 660
 Db 601 eoaIIIVltgtekkgtvqoqmpypcyvddiflrwsrsmplfpltwaiysaavaiirkiv 660
 QY 661 YEKREARKETRMIMGDNLISLWFSFISLRLVLSAGLLVYLKLGNLPLSDSVYVY 720
 Db 661 yekearketrmimgdnlislwfsfissrlplvsaqlvlvylkgnlplsdsvyv 720
 QY 721 ELISVAVVITLQCFILISLFSRANLAAACGGIITFTLYLPLVLCVAMODVYFTLKIRAS 780
 Db 721 flsvavvitlqcfilislfsranlaaacggiiyftlypylvcvamdvyftlkirast 780
 QY 781 LLSPVAFGCEFFALFEEOGIGVOMDNLFSRVEDGDNLTTSMMILFDFILYGVMTW 840
 Db 781 llsprafgceyfalfeeoglgvqvdnlfsrveedgdnlttsvmmldfilygvmtw 840
 QY 841 YLEAVFPGQYIPRPWYFPCIKSYWFGESDEKSHPGSNOKRMSEPTCMEEPETHLKLVS 900
 Db 841 yleavfpgqyiprpwyfpciksywfgesdekshpgsnqkriseimeeepthklvys 900
 QY 901 IONLVKVVYDGMKVAVDGLAIFVEGOTTSPFGHNGACKTTMTSLTGLFPPTSGTAYTL 960
 Db 901 ignlvkvvydgmkvavdglaifvegottsplghngackttmtsltgllfpptsqtaytl 960
 QY 961 GKDISEMSTJRONLGVOPHNVLFDMLTVEEHIMFVARLKGISEKHAKAMEQALDVG 1020
 Db 961 gkdiseemstjronlgvophnvlfdmLTVEEHIMFVARLkgisekhvkaemeqaldvg 1020
 QY 1021 LPSKLTAKTSQLSGGMORISVALAFVGGSKVYLDEPTAGVDYPSRGGTWELLKRYQ 1080
 Db 1021 lpskltaktsqsggmorkisvalafvgsksvyldeptagvdypsrrggtwellkryq 1080
 QY 1081 GRTIILSTHHMDEADVLDRIAITSHGKLCVGSSEFLKNLGGYLYTLVKKVVESLS 1140
 Db 1081 grtIILsthhmdeadvldriaITSHgklcvgsseflknlggylytlvkkvessls 1140
 QY 1141 SCRNSSTSVYLLKEDSVQSSDAGLGSDESHTLTIDVSAISNLRKHVSEARLVEDI 1200
 Db 1141 scrnsstsvyllkedsvqssdaglgsdeshltldvsaaisnlrkhvsearlvedi 1200
 QY 1201 GHELTLYVLPYAAKGAFFVEFHETIDRLSDLGISSTIGISTITTEELFLKYAESGVDAE 1260
 Db 1201 gheltlyvlpYaaKgaFFVEFHETIDRLsdlgisstigistitTEELflkyaesgvdae 1260
 QY 1261 TSDGTLPARNRRAFGDKOSCLRPFTEDDAADPNDSIDIPDESRTDILSGMDGGSYQVK 1320

Db 1261 tsdgtlparnrRAFGDKOSCLRPftEDdaADPNdsIDIPdesRTdILsgMDGGSyqvk 1320
 QY 1321 GKKLTQOQFVALLMKRLLIARSRKGFPAQIVLPVAFVCLIAVSLIYPPRGKXPSEIQ 1380
 Db 1321 gkkltqoqfvalLMKRllIARsrKGFpaQIVLPvAFVCLIAVslIYpprgKXPseIQ 1380
 QY 1381 PMWNEQYTFVSNDAPEDTGTLELLNALTKDPGEGTRCMENPILPDPCQAGEEETAP 1440
 Db 1381 pmwneqytfvsnDapedtGTlellnaLTkDpgEGtrCMENpILpdPCqAGEEetAP 1440
 QY 1441 VPOTINDLEONGNMTQMNPSPACOCSSDKIKKMLPVCPRGAGGILPPQKONTADITIDL 1500
 Db 1441 vpotlmdlEONGnMTQMNPSPACOCSSDKIKKMLPVCPrgAGGILppqKONTADITIDL 1500
 QY 1501 TGRNISDYLVTYVOIILKSLKNKIWVEEFYGGFSLGSVSTQALPPSOEYNDAIKOMK 1560
 Db 1501 tgrnIsdyLVktYqIILKslknKIwveEFYggfSLGSvSTQALppsoEYNDAIKomK 1560
 QY 1561 HLKIAKDSADRFLNSLGRFMTGLDTRNNKAVWFNKGWHAISSEFLVINNAILRANLQK 1620
 Db 1561 hlkIakdsadrflnsLgrfMTglDtrnnkvWFnkgwHAissEflvInnaILranlqk 1620
 QY 1621 GENPSHYGITAFNPNLNTKQOLSEVALMTSVYVLSICVIFAMSPVPSFVYFTLOER 1680
 Db 1621 genpsHYgitafNPNlNTKqOLseVALmtsvYVLSICVIFAMSPVpsfVYftLOER 1680
 QY 1681 VSAKHLQELISGVKPVYIWSNFWMDKONVVPATVLIIFIGFOOKSYVSTNLPLYAL 1740
 Db 1681 vsakhlqELISgvKpVYIwSNfWMDKONVVPATVLIIfIGfoOKsYvSTNLpLYal 1740
 QY 1741 LLLLYGMSITPPLAMPASVFKRIPSTAYVLTSVNLFGINGSVATPYLELFTONKLNIN 1800
 Db 1741 llllygmsITpPLAMPASvFKRIPstAYVLTsvNLFGINGSvATPYLElFTONkLNIN 1800
 QY 1801 DILKSVFLIPPHFCLRGILDMVKNQAMADALEFEGENRFRVPSLMDVLRNLFAAAVES 1860
 Db 1801 dlksvflIPPhfCLRGILdmvKNqAMADALEfEGENRFRVpsLMDVLRnlFAAAves 1860
 QY 1861 VVFFLITVLIOYREFTRPPVNAKLSPLNDEDEDVRERORILDDGGQNDILEIKELTRYI 1920
 Db 1861 vvfflITvlIOYrefTRppvNAKlsPLNDEDEDVRERORILddgGQNDILEIKELtrYI 1920
 QY 1921 YRRKRPAVDRICVIGIPGCGFLGYNAGKSGSTFRMLTGDVTYRGAFILKNKSLSN 1980
 Db 1921 yrrkrPAVdrICvIGIPGCGflGYNAGKSGstFRMLtGDVTYrgAFILKNKslSN 1980
 QY 1981 IHEVHQMGCYCPFDATTELLTGREHVEFPALLRGVPEKEVGKVGEMAIRKILQLYYGER 2040
 Db 1981 ihevHqMgcYcPfdATTEllTgrEHVEfALLrgVpeKEvgKVGEMAIrKILQlYYger 2040
 QY 2041 YAGNYSGGNRKRLSTAMALLGGPPVYFLDEPTGMDPKARRPLMNCALSVYKGRSVILT 2100
 Db 2041 yaGnySGgnRKrlSTaMALLgGppVYflDEPTGMDPKARRPLMNCALsvYKgrsvILT 2100
 QY 2101 SHSMECEALCTPMAIMVNGRFRCLGSVOHLKRNFPDGGTIVYRIAGSNPDJLKPVDFFG 2160
 Db 2101 shsMECEALctPMAIMvNGRFRclGSvOHLkRNfPDGGtIVYRIAGsNPdJLkpVdFFg 2160
 QY 2161 LAFPGSVLKKKHNMLQYQLPSSLARIFSLIOSKRLHIEDYSVSQTLDOVFVNF 2220
 Db 2161 lafpgsvlKkKHNmLQYqlPssLARIFsLIOSKRLHIEdYSVSQtlDOVFvNF 2220
 QY 2221 AKQSDDDHLKDLSTLKNQTVDVANLTSEFLDDEYKESYV 2261
 Db 2221 akqsdDdhlKdLstLkNqTVdVANLTseFLDdeYKesyv 2261

RESULT 12
 AAB38114
 ID AAB38114 standard; Protein; 2261 AA.
 XX
 AC AAB38114;

XX 29-JAN-2001 (first entry)

DE Human ABC1 cholesterol transporter mutant, E1172D.

XX Human ABC1 cholesterol transporter; chromosome 9q31.

KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;

KW Tangier disease; TD; familial HDL deficiency; FHD; polymorphism;

KW cardiovascular disease; coronary artery disease; coronary restenosis;

KW cerebrovascular disease; peripheral vascular disease;

KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;

KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;

KW prognosis; prophylaxis; drug screening; transgenic animal; mutant;

KW mutant.

OS Homo sapiens.

XX WO200055318-A2.

PN 21-SEP-2000.

PD 15-MAR-2000; 2000WO-IB00532.

PF 15-MAR-1999; 99US-0124702.

XX 08-JUN-1999; 99US-0138048.

PR 17-JUN-1999; 99US-0139600.

PR 01-SEP-1999; 99US-0151977.

XX (UYBR-) UNIV BRITISH COLUMBIA.

PA (XENB-) XENON BIORESEARCH INC.

PI Hayden MR, Wilson AR, Pimstone SN;

PI WPI: 2000-587528/55.

DR New ABC1 polypeptide is useful for treating diseases associated with

PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's

PT disease and cancer -

PT Examples: Page -; 229pp; English.

XX The invention relates to the human ABC1 cholesterol transporter protein

CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is

CC a member of the ATP-binding cassette (ABC transporter) superfamily of

CC proteins, and plays a crucial role in cholesterol transport, particularly

CC involved in cholesterol trafficking in monocytes and fibroblasts, being

CC located on chromosome 9q31, and mutations in this gene are associated

CC with two genetic HDL (high density lipoprotein) deficiency disorders,

CC Tangier disease (TD) and familial HDL deficiency (FHD). These diseases

CC are distinguishable in that TD is an autosomal recessive disorder, while

CC FHD is inherited as an autosomal dominant trait. Low levels of HDL ("good

CC cholesterol") in the blood correlate with a high risk of cardiovascular

CC disease, particularly coronary artery disease, but also cerebrovascular

CC disease, coronary restenosis, and peripheral vascular disease.

CC Conversely, a high level of HDL has protective effects against

CC cardiovascular disease. The invention provides genetic constructs and

CC transgenic cells and non-human animals comprising human ABC1 nucleic

CC acids, and methods of gene therapy for the treatment or prevention of

CC cardiovascular disease comprising the administration of an expression

CC vector encoding ABC1 or an active fragment thereof. The invention also

CC encompasses compounds which mimic ABC1 activity, compounds which

CC stimulate ABC1 expression and methods of screening for such compounds.

CC It further relates to methods for determining whether a patient has an

CC increased risk for cardiovascular disease due to polymorphisms in the

CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat

CC or prevent cardiovascular disease, especially coronary artery disease,

CC cerebrovascular disease, coronary restenosis or peripheral vascular

CC disease. They may also be used in the treatment of diseases associated

CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick

CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.

CC The invention specifically excludes proteins with the exact amino acid

CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic

CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The

CC present sequence represents a mutant human ABC1 cholesterol transporter

CC associated with an altered cholesterol level and therefore an altered

CC risk of cardiovascular disease.

CC Note: The present sequence is not shown in the specification, but is

CC derived from the native human ABC1 shown on pages 152-157.

XX Sequence 2261 AA:

QY Query Match 99.9%; Score 11786; DB 21; Length 2261;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2257; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

1 MACPQLRLIMKNTFFRRQTCOLLLEWAPDLFFILISVRLSPYRPOHCHFPNKA 60

|||||

1 macwpqlrlilwknltfrircqllleawpdlffililsvrlsyppeqhehfnka 60

61 mpsagtlpwwogciicnannpcfrpypgeapgvgnfnksivarlfsdarrlllyskdt 120

|||||

61 mpsagtlpwwogciicnannpcfrpypgeapgvgnfnksivarlfsdarrlllyskdt 120

121 smkdmrkvlrtlqotiksssnklodflvndfntsgfilyhnlslpkslvdkmlradvllh 180

|||||

121 smkdmrkvlrtlqotiksssnklodflvndfntsgfilyhnlslpkslvdkmlradvllh 180

181 kvflogyolhlslcngskseemioLGDVEVSELGLPKREKLAARLRNSMDILKPIIL 240

|||||

181 kvflogyolhlslcngskseemioLGDVEVSELGLPKREKLAARLRNSMDILKPIIL 240

241 rltlnstspfskelaeatklllshlsgtlaqelfsmrswmdkroeymlfLNNSSSSSTOI 300

|||||

241 rltlnstspfskelaeatklllshlsgtlaqelfsmrswmdkroeymlfLNNSSSSSTOI 300

301 yqavsrivcqhpeggllkkslnwgedmnykalrgnqgeedaeflynsftypcndlmk 360

|||||

301 yqavsrivcqhpeggllkkslnwgedmnykalrgnqgeedaeflynsftypcndlmk 360

361 nlespsrlriwkalppllvglkllypdtpatrymaevnkltfgelavfhndlegmwels 420

|||||

361 nlespsrlriwkalppllvglkllypdtpatrymaevnkltfgelavfhndlegmwels 420

421 pkiwtfemsqendlyrmlldsrndhfwegqldgldvdaqdivflakhpcedvssngs 480

|||||

421 pkiwtfemsqendlyrmlldsrndhfwegqldgldvdaqdivflakhpcedvssngs 480

481 vvmwreafnetnoairtisrpfmfcvmlnkilepatevmlinsmellBERKFMAGIVTG 540

|||||

481 vvmwreafnetnoairtisrpfmfcvmlnkilepatevmlinsmellBERKFMAGIVTG 540

541 itpgsilelphrvvkkirmdidnvertnkikdgywdrpadpfeDMRYVWGFAYLDVY 600

|||||

541 itpgsilelphrvvkkirmdidnvertnkikdgywdrpadpfeDMRYVWGFAYLDVY 600

601 EQAIRRLVLTGTEKTYGVMQMPYCYVDIFLRVRSRMPFLTAMLYSAVIRKIV 660

|||||

601 EQAIRRLVLTGTEKTYGVMQMPYCYVDIFLRVRSRMPFLTAMLYSAVIRKIV 660

661 yekEARLKETMRIMGDINSILMFSSFTSLIPLVSAGLVLKGNLIPYSDPSVVFV 720

|||||

661 yekEARLKETMRIMGDINSILMFSSFTSLIPLVSAGLVLKGNLIPYSDPSVVFV 720

721 flsvfavltilqcllsltlfsranlaacqgillyflylpylcvaawdqygfllklfas 780

|||||

721 flsvfavltilqcllsltlfsranlaacqgillyflylpylcvaawdqygfllklfas 780

781 llsVAAGFCGFALFEEDGICVQMDNLFESPEDEGDNLTSSMFLDFELFGWTW 840

|||||

781 llsVAAGFCGFALFEEDGICVQMDNLFESPEDEGDNLTSSMFLDFELFGWTW 840

841 YIEAVPGOYGIPIPPWFPCTKSYGGEESDEKSHPGSNOKRMSLECEEPETHLIGVS 900

|||||

841 YIEAVPGOYGIPIPPWFPCTKSYGGEESDEKSHPGSNOKRMSLECEEPETHLIGVS 900

841 yieavfpgygiPIPPWFPCTKSYGGEESDEKSHPGSNOKRMSLECEEPETHLIGVS 900

QY 901 IONLVKVVYRDGMKVAVDGLALNFEGYITSLGHNAGKTTTMSILTELPPTSGTAYIL 960
 Db 901 IqnlvkvrydgmkvavdglaInfyegqIlsfIghngagktttmsIlgtlpprsgtayaIl 960
 QY 961 GKDIRSMSTIROLGYCPCPHNHYFLDMLYVEBHIFWFAKLKGLSEKHVKAEMEQMALDVG 1020
 Db 961 gkdirsmstlrqldgyvcpnhnyflDmlYveehIwfyarIkglsekHvkemegmaIdvg 1020
 QY 1021 LPSSKLKSTQSOLSGMQRKLSVALAFVGSKVYLDEPTAGVDPYSRRIWELLYKRR 1080
 Db 1021 lpskklkstqsolsgmqrklsvalafvgskvyldeptagvdpysrrigweliIkyyr 1080
 QY 1081 CRTIILSTHMDADVLDGDIKAIISHGKCLCCVSSSLFLKNQGLGTGYVFLVKKDVSSLS 1140
 Db 1081 crtIilstHmdadvldgdiKaiIsHgkclccvssslflKnqglgtgyvflVkkdvssls 1140
 QY 1141 SCRRSSSTVSLKKEDESVSSSDAGLSGDSHEDTLTIDVSAISNLIRKHVSARLYEDI 1200
 Db 1141 scrrssstvsylkkesdsvsssdaglsghsdctltIdvsaIsnlIrkhvsarIyedi 1200
 QY 1201 GHETLYVLPYEAKEGAFVFLFHEIDRLSDLGISYGISSETTLEIPLKVAEESGVDAE 1260
 Db 1201 ghetlyvlpYeaKegafvflfheIdrIsdlgIssygiSettleIPlkvaEesgvdae 1260
 QY 1261 TSDGTLPARNRRAFGDKGQCLRPTEDDAADPNDSIDPESEFDLISGMGKGYQVK 1320
 Db 1261 tsdgtlparnrrafGdkgcrlPteddaadpndsidPeSEfdlIsGmgdkgyvqvk 1320
 QY 1321 GWRUTQOQVYALLMKRLIARRSRKGFPAQVLPVAFVCIALVFLSLVPEFGKYSLEIQ 1380
 Db 1321 gwrltqgfvallwkrliArtsrkGfpaqvlpavfvciAlvflslvPefgkysleIq 1380
 QY 1381 PMYNYNOCYFVNSDAEDDTGTELLNALTKDGFCTRCHEGNPDPDPCQAEEMETAP 1440
 Db 1381 pmynyNocYfvnsdaEdDTgTEllNALtkDgfcTrcheGnpDpdPcQaeEmetAp 1440
 QY 1441 VPQITMDLFQNGNWTMQNPSAPACOCSSDKIKKMLPVCPPGAGLPPPGKOTADILDL 1500
 Db 1441 vpqitmdLfQngnwtMqnpsapAcocssdkIKkmlPvcppgagLpppgkOtadilDl 1500
 QY 1501 TGRNTSDYLVKTYQIYIASKNKITVNFRRGGSGLGVSNTOALPPSOEVDAIKOMK 1560
 Db 1501 tgrntsdYlvktyqiYiAsknKITvNfRRggsGLgvSnTOalPpsOevdaIKomk 1560
 QY 1561 HUKLAKDSADREFLNSLGRFMTGLDTRNNVKVWPNKNGHAISSFLVNTNNAILRANLQK 1620
 Db 1561 hUklakdsadREflnsLgrfMTglDtrnnvKvWpNknGhAISsflvNtnnaIlraNlqk 1620
 QY 1621 GENPSHYGTITANNPLNLTKOOLSEVALMTTSVDVLSICVIFAMSEVPASFEVLQER 1680
 Db 1621 genpshygtITannPlnLTkoOLseValMTtsvDVlsICvIFamseVpasfEvlqEr 1680
 QY 1681 VSKRAHLOPISGVKPVYIWLNFVMDMCNYYVPAVLVIIIFCPOKSYVSSSTNLPVAL 1740
 Db 1681 vSkahloPiSgvkPvYiWlNfVmdMcNyyVpavlVIIIFcPoKsyvssstnlPval 1740
 QY 1741 LLLLYGNSITPLMAYSTVEFKIPSTAYVLTISVNLFIGINSVATFVLELFTDNKLNIN 1800
 Db 1741 llllygnsitPlmAYstVEfkIPstAYvLTisVnlfiGinsvatFvlelftDnKlnin 1800
 QY 1801 DILKSVFLIFPHFCGRGLIMVKNQAMADALERGENRFPSPISMDVGNLPRAMAVEG 1860
 Db 1801 dIlksvflIFphfcGRglIMvknQaMaDAleRgenrFPsPiswDvgnlPrAmaveg 1860
 QY 1861 VVEFLITVLIOYREFIRBPVNAKLSPLNDEDEVDYRERQRILDGGGONDILLETIKELTKI 1920
 Db 1861 vvEfliTvLIoYrEfIRBPvNAkLsPlnDEdeVDyRerQRilDggGondilLeTikEltkI 1920
 QY 1921 YRRKRKPVDRLCYGIRPGEOGGLGVNGAKSSFFKMLTDITVTYRKDAFLKNKSILSN 1980
 Db 1921 yrrkrkpvdrlCYgIRpgEOgGLgvNgakSSffKmlTDITvTYrkDAflKnksilSn 1980

QY 1981 THEVHONMGYCPQFPAITTELITGREHVEFPALLRGVPEKGVKXGEMAIRKLGLVYGEK 2040
 Db 1981 thevHonmgYcpqfPaITteLitGreHvefPallrgvPeKgvKxgEmairKlglvYgeK 2040
 QY 2041 YAGNYSGNKRRKLSSTAMALIGGPVFLDEPTTGMDPKARFELMNCALSVKESRVL 2100
 Db 2041 yaGnysgnkrrklsstAmalIGgpVfldePtTgmdPkARfElmncAlsvKESrvl 2100
 QY 2101 SHSMECEALCTRMAIMNNGRRCLGSVOHLKNRGGDGTITVIRAGSNPDLKRVODEFG 2160
 Db 2101 shsmecealCtRmaImnNgrrclGsvoHlknRgGdgtITvIRagSnPdlKrvODEfg 2160
 QY 2161 IAFPGSVLKEKHNNMLQYOLPSSLSLARIFSIQSOKKRIHEDYSVSOPTLDOVPNF 2220
 Db 2161 IaFpGsvlkeKhnnmlqYolPsslsLarIfsiQsokkriHedysvsoPtldOvpnf 2220
 QY 2221 AKDQSDHDLKDLSLHKQYVAVAVLTSFLQDEKVESYV 2261
 Db 2221 akdqsddhldkdlSlhkqYvavavLtsflQdekvesyV 2261

RESULT 13

ID AAB38115 standard; Protein: 2261 AA.

AC AAB38115;

DT 29-JAN-2001 (first entry)

XX Human ABC1 cholesterol transporter mutant, R1587K.

XX Human ABC1 cholesterol transporter; chromosome 9q31;
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
 KW Tangier disease; TD; familial HDL deficiency; FHL; polymorphism;
 KW cardiovascular disease; coronary artery disease; coronary restenosis;
 KW cerebrovascular disease; peripheral vascular disease;
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
 KW prognosis; prophylaxis; drug screening; transgenic animal; mutant;
 KW muton.

OS Homo sapiens.

PN W020005318-A2.

XX 21-SEP-2000.

PF 15-MAR-2000; 2000MO-IB00532.

XX 15-MAR-1999; 99US-0124702.
 PR 08-JUN-1999; 99US-0138048.
 PR 17-JUN-1999; 99US-0139600.
 PR 01-SEP-1999; 99US-0151977.

XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON BIORESEARCH INC.

XX Hayden MR, Wilson AR, Pimstone SN;
 DR WPI; 2000-587528/55.

XX New ABC1 polypeptide is useful for treating diseases associated with
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
 PT disease and cancer -

XX Examples; Page -: 229pp; English.

CC The invention relates to the human ABC1 cholesterol transporter protein
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of
 CC proteins, and plays a crucial role in cholesterol transport, particularly
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is

located on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, Tangier disease (TD) and familial HDL deficiency (FHD). These diseases are distinguishable in that TD is an autosomal recessive disorder, while FHD is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, particularly coronary artery disease, but also cerebrovascular disease, coronary restenosis, and peripheral vascular disease. Conversely, a high level of HDL has protective effects against cardiovascular disease. The invention provides genetic constructs and transgenic cells and non-human animals comprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also encompasses compounds which mimic ABC1 activity, compounds which stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease, cerebrovascular disease, coronary restenosis or peripheral vascular disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact amino acid sequences of GenBank Accession No: CA110005.1 and X75926, and the nucleic acid with the exact sequence as GenBank Accession No: AJ012376.1. The present sequence represents a mutant human ABC1 cholesterol transporter associated with an altered cholesterol level and therefore an altered risk of cardiovascular disease.

Note: The present sequence is not shown in the specification, but is derived from the native human ABC1 shown on pages 152-157.

XX Sequence 2261 AA:

Query Match 99.9%; Score 11786; DB 21; Length 2261;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2257; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACMPQRLRLMKNLFFRRQTCQLLEVAWPLFIFLILSVRLSPYEQHECHPNKA 60
Db 1 macmpqrlllwnlffrrqtcqlleavapllfllilsvrslsrypyeqhechfnka 60
QY 61 MPASGTPWVGITICANNNCFRPTTPEARPGVGNFNKSTVARLPSDARRLLYSQKOT 120
Db 61 mpsagtlpwvgiticanncfrrpttpearpgvgnfnksivarllisdarrlllysqkdt 120
QY 121 SMKMRVLTLOQIRKSSNLKLODLVNEFPFGFLYNNLSLPKSTVDMKLRAVDILH 180
Db 121 smkdmrvltlloqirkssnllkldlvnnefpfgflynnlsipkstkvmklradvllh 180
QY 181 KVLQGYQLHLTSLCNGSKSEEMIQLDQEVSELCGLPKREKLAARVRLSRNMDILKPL 240
Db 181 kvlqgyqlhltslcnsgskseemiqldqevselcglpreklaaervrlsrnmdilklpl 240
QY 241 RTLNSTSPSPSKELAEATKTLILSLGTLAQELFMSRSMQMRQVWMLTVNNSSSSTOI 300
Db 241 rltlnstspfskelaeatktilslgltaqelismrswdmrgevmlltvnnsstscq 300
QY 301 YQAVSRIVCGHPGEGGLIKISLAMYEDNNYKALFGNGTEDEATTFYDNSTTPYCNDLMK 360
Db 301 yqavsrivcghpeggglkikslamyednnykalfgngteedactfydnsttpcndlmk 360
QY 361 NLESSPSRIITWAKLKLPLVGLKILYTPDTPATROVMAEVNKTFOELAVFHDLSGMEELS 420
Db 361 nlesspsrliitwaklklplvglkilytpdtpatrgvmaevnktfoelavfhdlsgeeweels 420
QY 421 PKIPIFMFNSQMDLVRLMLDRNDHFHWEQOGLDGMTADDIYAFIAKHPEDVOSSNGS 480
Db 421 pkivfimefnsqemdlvrlmlsdrndhfhwEQGLDGLMTADDIYAFIAKHPEDVOSSNGS 480
QY 481 VYTWREAFENETNOAIRTISRMECVNLINKLEPIATEVWLINLSMELLDERKFWAGIVFTG 540

Db 481 vylwreafeneqngitrlisrimecvnlinkllepiaetevwlinsmellderkfwagivftg 540
QY 541 ITPGSIELPHVKKIRKMDIDNERTKIKDGYNDPPRPADPFEDMKVWVGAFYIADVV 600
Db 541 itpgsielephvkkirkmdidnertkikdgyndpprpadpfedmkvwwgafyayidvv 600
QY 601 BOAIRRVLTGTEKTKGVYMOOMPVCYVDIDFLVWMSRMLFMTLAMIYSAVITIGIV 660
Db 601 boairrvltgtektygmogmpvcyvdidflvwmsrmlfmltlamiysavitigiv 660
QY 720 YEKARLKEKIRKIMGLDNLISLFWFSISLIPLLVAGLVLILKGNLPLSPSYVFW 720
Db 720 yekarlkekirkimglDNLISLFWFSISLIPLLVAGLVLILKGNLPLSPSYVFW 720
QY 780 FLISVAVVTITQCLISLIFSRANLAAAGGIIFFTLPLPVLCVAMODYGFLLKIFAS 780
Db 780 flisvavvtitqclisllfstranlaaaggiiFFTLPLPVLCVawqdyvffllkifas 780
QY 840 ILSPVAFGFGCEYFALFEEOGIGVQMDNLFPSPVEDGFNLTTSTISMLFDTFLYGMTW 840
Db 840 ilspvafgfgceyfalfeEoGIGVqmdnlfpSPVEDGFnlTtstismlfDTFLYgMTw 840
QY 900 YTEAVFPGQYGIPTPWYTPCTKSTWFGESDEKSHPSGNOKRMSFICMEEPHTLKIGVS 900
Db 900 yteavfpgqygiprPWYtpctkstwfgesdeksHpsgnokrmsfiselmeephtlkigvs 900
QY 960 IONLKYVRDGMKVVAVDGLALNFYEGQITSPFGHAGAKTTMTSLITGLFPPTSGTATL 960
Db 901 ionlkyvrdgmkvavdglalnfyEGQITSPFGHAGAKTTMTSLITGLFPPTSGTATL 960
QY 1020 GMDISEMSTIKQNLGVCPOHNVLFDMLTVEEHWLFVARKGLSEKHAKMEQALDVG 1020
Db 961 gmdiseMstikqnlGvcPohnvlfDmlTveehwlfvArklglsekhakmeqalDvg 1020
QY 1080 LPSKLSKTSQLSGGMOKLSVALAFVGGKVVVILDEPTAGVDPYSRGIWELLKXRO 1080
Db 1021 lpsklksktsqlsGgmoklsvalafvGgkvvVildeptagvdpysrGiwellkXrG 1080
QY 1140 GGTIILSTFHMDADVLDGRIATISHGKLCYGSSEFLKNOUGTYTYTLVKKDESSLS 1140
Db 1081 ggtiilstfhmdadvldgriatishgklcygsseflknouGtytytlvKkdessls 1140
QY 1200 SCNNSSTVYLKEDSVQSSSDAGLGSDBESDTLTIDVSAISMLIRKHSEARLVEDI 1200
Db 1141 scnnsstvsylkedsvsqsSDaglgshesdtltIdvsaismliRkhsearlvEdi 1200
QY 1260 GHELYVLPEAAKEGAYVELFHEIDRLSDGISTGISETTLEPIFLKVAEESGVNAE 1260
Db 1201 gheLyvlpeaakegaYelFheidrlsdgIstgiseTtleepiFlkvaeesgvnae 1260
QY 1320 TSDGTLPARNRPAFCDDKQSLRPFTEDADPNDSIDIPESRETDLSGMDGKSSYQVK 1320
Db 1261 tsdgtlparnrpaFCDDKqslRpfTEDADPNdsidIPesREtdlsGmdgkssyqvk 1320
QY 1380 GWKLTQOQFVALMKRLILARRSRKGFQAOIVLPAVFCIALVFSILYPPFGKYSLELO 1380
Db 1321 gwklTqgfvalmkrlilARRsrkGFqaoiVlPAVfcIALVfsilYppfgkyslelG 1380
QY 1440 PMWYNQYTFVNSDAPEDGTLELNLAKTRDQFGTRCMEGNPIDPTPCQAGEEEMTAP 1440
Db 1381 pmwYnqyTFvnsDapEDgtleLnlAKtrDqfgTRcmEGNPIDptPCQAGEEEMtAp 1440
QY 1500 VPQITMDLPONGMWIWMQNSPACQSSDKIKKMLPVCPPGAGGLPPQKQKQNTADILODL 1500
Db 1441 vpqitmdlpONGmwIwmQnsPacqSSdkIKmlPvcPPgagglppPqkqkntadilOdL 1500
QY 1560 TGRNISDYLVKTYVOIITANSLSKNKIVWNEFRYGGFSLVGVSMTQALPPSOEVDALIKOKK 1560
Db 1501 tgrnisdyLVktyvOIITanslsKNkIvWnefrYggfslVsgvmtQalppseVdaLiKokk 1560
QY 1620 HUKLAKDSSADRLNLSGRMTGLDTRNNVYKWFNNKGWHAISSFLVNNALIRANLQK 1620

Db 1561 h1jakssadrfinsigrfmgtdtknnykvwfnkqwha1ssflnvlnaallranlqk 1620

QY 1621 GENPSHGTAFNHNPLNLTFRQOLSEVALMTTSDVLSTICVIFAMSVPAFVPLIOER 1680

Db 1621 genpshtgafnlnplntkqglevalmtstsdvlsicvifamsvpafvplioer 1680

QY 1681 VSKAKHOFISGVKPVYIWTLSNFWDMCNVVPATLVIIIFICFOOKSVYSTNLPVAL 1740

Db 1681 vskakhofisgvkpvwyiwtlsnfwdmcnvvpatlviifcfoqksystsnlpval 1740

QY 1741 LLLTGSMTPLMVPASFVKIPSTAVVLTSTNLTFTGINSATFVLETFNTKLNIN 1800

Db 1741 llltgsmtplmvpasfvkfstayvltstnltftginsatfvtlftntklnin 1800

QY 1801 DILKSVLTFPHHCLGGLIDMVKKNQADALERFGENFVSPLSMDVGRNLFAMAVES 1860

Db 1801 dilksvltfphclgglidmvyknqamadalertgenfsvplswdlvgrnlfamaveg 1860

QY 1861 VWFELITVLIOYRPFETPRPVNAKLSPNDEDEDVRERORITLDGGGNDILEKELTKI 1920

Db 1861 vwfllitvlioyrpfetprpvnaklsplndedevrretrqrlldgggndilekeltk1 1920

QY 1921 YRRKRPAVDRIKVGIPRGECEGILGVNGAKSSTFKMLTGDITVTRGDAFLNKSILSN 1980

Db 1921 yrrkrpavdrkvgiprgecgfllgvngakstfkmltgdltvtrgdaflnksilsn 1980

QY 1981 IHEVHOMGVCPQPDATITELLTGREHVEFPALLRGVPEKEVGVGEMAIKGLVYGERK 2040

Db 1981 ihevhomgvcpqpdattelltgrehvefalltgvpekevgvgemaitkglvlygerk 2040

QY 2041 YAGNYSGNKRLKSTAMALIGBPVVFLEDEPTTGMDPKARREPLMNCALSVYEGRSVLT 2100

Db 2041 yagnysgnkrkistamallgppvvfldeptgmprkarrellmncalsvnyegrsvlt 2100

QY 2101 SHSMECEALCTEMALIMVNRFRCLGSVOHLKMRPDDGTTIYRTAGSNPDILKPVODFPG 2160

Db 2101 shsmeecealctemalimvnrfrclgsvohlkmrpdgtyrtagsnpdilkpvodfpg 2160

QY 2161 LAFPGSVLKKRHRNMLQOYLPSLSLSLARIFSLISQSKRLHTEQSVSQTLLDOGVFNF 2220

Db 2161 lafpgsvllkchrnmlyqqlpslsislarifslisqskrlhedyvsqtlldgvfnf 2220

QY 2221 AKQSGDDHKLKSLKNOTVVDVAVLTSLFLODEKVESYV 2261

Db 2221 akqsgddhklkslknqtlvvdvavltslfdekykesyv 2261

RESULT 14

AAB38105

ID AAB38105 standard; Protein; 2261 AA.

XX AAB38105;

AC 29-JAN-2001 (first entry)

DT Human ABC1 cholesterol transporter Td-2 mutant protein (Q597R).

XX Human ABC1 cholesterol transporter; chromosome 9q31;

XX ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;

XX Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;

XX cardiovascular disease; coronary artery disease; coronary restenosis;

XX cerebrovascular disease; peripheral vascular disease;

XX Alzheimer's disease; Niemann-Pick disease; Huntington's disease;

XX X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;

XX prognosis; prophylaxis; drug screening; transgenic animal; mutant;

XX muten.

OS Homo sapiens.

XX WO200055318-A2.

XX 21-SEP-2000.

PF 15-MAR-2000; 2000MO-1B00532.

XX 15-MAR-1999; 9905-0124702.

PR 08-JUN-1999; 9905-0138048.

PR 17-JUN-1999; 9905-0139600.

PR 01-SEP-1999; 9905-0151977.

XX (UYBR-) UNIV BRITISH COLUMBIA.

PA (XENO-) XENON BIORESEARCH INC.

XX Hayden MR, Wilson AR, Plimstone SN;

PI WPI: 2000-587528/55.

DR N-PSDB; AAC69386.

XX New ABC1 polypeptide is useful for treating diseases associated with

PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's

PI disease and cancer -

XX Examples; Page -: 229pp; English.

PS The invention relates to the human ABC1 cholesterol transporter protein

CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is

CC a member of the ATP-binding cassette (ABC transporter) superfamily of

CC proteins, and plays a crucial role in cholesterol transport, particularly

CC intracellular cholesterol trafficking in monocytes and fibroblasts, being

CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is

CC located on chromosome 9q31, and mutations in this gene are associated

CC with two genetic HDL (high density lipoprotein) deficiency disorders,

CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases

CC are distinguishable in that TD is an autosomal recessive disorder, while

CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ('good

CC cholesterol') in the blood correlate with a high risk of cardiovascular

CC disease, particularly coronary artery disease, but also cerebrovascular

CC disease, coronary restenosis, and peripheral vascular disease.

CC Conversely, a high level of HDL has protective effects against

CC cardiovascular disease. The invention provides genetic constructs and

CC transgenic cells and non-human animals comprising human ABC1 nucleic

CC acids, and methods of gene therapy for the treatment or prevention of

CC cardiovascular disease comprising the administration of an expression

CC vector encoding ABC1 or an active fragment thereof. The invention also

CC encompasses compounds which mimic ABC1 activity, compounds which

CC stimulate ABC1 expression and methods of screening for such compounds.

CC It further relates to methods for determining whether a patient has an

CC increased risk for cardiovascular disease due to polymorphisms in the

CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat

CC or prevent cardiovascular disease, especially coronary artery disease,

CC cerebrovascular disease, coronary restenosis or peripheral vascular

CC disease. They may also be used in the treatment of diseases associated

CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick

CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.

CC The invention specifically excludes proteins with the exact amino acid

CC sequences of GenBank Accession No: CAI10005.1 and X75926, and the nucleic

CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The

CC present sequence represents a mutant human ABC1 cholesterol transporter

CC associated with an altered cholesterol level and therefore an altered

CC risk of cardiovascular disease.

CC Note: The present sequence is not shown in the specification, but is

CC derived from the native human ABC1 shown on pages 152-157.

XX

SQ Sequence 2261 AA:

Query Match 99.9%; Score 11785; DB 21; Length 2261;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2257; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACWPOLRLIMRNLTFRROTCLLEVAWPLIFLILISVRLSYPEQECRPPNKA 60

Db 1 macwpqlrlimrnlfrrotclllewawplifllilsvrlsyppqechpnpka 60

QY 61 MPSAGTLPWVGITICNANNPCFRPTTPEGAQGVGNFKNSTVARLFSDARLLLYSQKDT 120

Db 61 mpsagclpwvggjlcnannpcfrytpcpaepvgvgnfnksivarlfadarrlllysgkdt 120
Qy 121 SMKBRKRLTLQOIKKSSNLKQDPLVNETPSSGLYHNLSPKSTVDMKLRADYILH 180
Db 121 smkdmrkvrltlqglksssnlklddfivdnetisgilyhnlslpkstvdmlradylh 180
Qy 181 KVFLOGVOLHJLSCNCSKSEEMOLQDOEVESELGJLPEKELAAERLRSNMDILPIL 240
Db 181 kvflggqyjlhltslcnsgskseemigldqdvsejcgjprekilaaeavyltsmmdlkprl 240
Qy 241 RTLNSTSPSPSKELAEATKTLHSLGLTALQELFSMRKSDMRQOEVMFLTVNVSSSSSTQI 300
Db 241 rltlnstspfskelaeatkllhslgltaelgfmsrwsdmrgvmfltnvssssstqj 300
Qy 301 QOANSRIVCGHPREGGLKIKSLMNYEDNNKALFGGNTEDATFPDNTTPPCNDLKM 360
Db 301 yqavsrlvcjhpgegglkikslmnyednnkalfgngtledaeflydnstltpcndlmk 360
Qy 361 NLESPLSRITIMKALPLLVGKIYTPDTPATROVMAEVNKTFOELAFVHDLGEMWELIS 420
Db 361 nlsspslrrllwkalrpllvgklllytpdtpatrrymaevnktfqlavfhdlegmwels 420
Qy 421 PKIWTFMENSOBMDLVRLMLDSRDNDHEWEOQLDGLMTAODIVAFLAKHPEDVQSSNGS 480
Db 421 pkltwfmensqemdlvrmlldsrndhfwegjldglwtaqdivaflakhpdevqssngs 480
Qy 481 VYTWEAENETNOARTISREMECVNLKLEPIATEVWLIKSMELDERKFMAGIYPTG 540
Db 481 vyltweaenetaartlsrimecynlklepiatevwlilksmellderkfmagiyltg 540
Qy 541 ITPGSELPHHVKYKIRMDINVERTNKIKDGYMDPGRADPFEDMRVVMGFAVLODV 600
Db 541 itpgselphhvkylrmdinvertnkikdgywopspgadpfedmryvvgfaylrvlv 600
Qy 601 EQAIIIRVLTGEEKTKTVYMOQMPYCYVDIIFLRVMSRSMPLFMTLAMIYSAVILKISIV 660
Db 601 eqaillrvltgreekctgyvmqmpcyvddiflrvmrsmpflmtlawysavavlikgiv 660
Qy 661 YKKEARLEKTRIMGLDMSIIMFSWFISSLIPPLVSAQLVYILKGLNLVYSDPSVYFV 720
Db 661 ykkaarlektrimgldmsiimfswfisslpllvsaqlvylkglnlvysdpsvfv 720
Qy 721 FLSVAVVTIIOCFILISTFESRANLAACGIIYFTLPLVLYCAVMODYVGTFLKIFAS 780
Db 721 flsvavvtliiocfilistfstranlaacgiiyftlplvlycavawdyvgtflkifas 780
Qy 781 LLSVPAFGGCEYFALFEBOGIGVOMDLFESSVEDEGNLTTSISKMLFDTFLYGVMTW 840
Db 781 llsvpafiggceyfalfeegigvqwdlfeesveedgnlttsvsmmlfdtfllygvmtw 840
Qy 841 YLEAVPPOGXGIPRMVYPCPTKSYWFGESDEKSHPGSNOKRMSRICMEEPHTHLKIGVS 900
Db 841 yleavpogxgiprmvypcptsywfgesdeksphpsnqriseimeeepthlkigvs 900
Qy 901 IONLVKYNDGKAVAVDGLALNFYEGQITSPFGHNGAGKTTMTSILTGFPRTSTAVIL 960
Db 901 ionlvkyndgmkavavdglaalfyegqitsfghngagkttsmtsilgtfprtsavil 960
Qy 961 GKDIOSEKSTIKONTGVCPOHNVLFDMLTVEEHIMFYARLKLGSKHVKAEMQALDVG 1020
Db 961 gkdiosekstikontgvcpohnvlfdmaltveehimfyarlklgskhvaeemqaldvg 1020
Qy 1021 LSSSKKSTKSTOLSGGMOKSLVALAFVGSVVVILDEPTGVDVPSRGITWELLKTRQ 1080
Db 1021 lssskkstkstolsggmoksvalafvgsvvvilldeptgvdpvpsrgitwellktrq 1080
Qy 1081 GRTIILSTHMDADVLGDRIAIISHGKLCYGVSSILFLKNQLGTYTLTVLKKEDEVSSLS 1140
Db 1081 grtiilsthmdadvlgdriaiishgklcycvssilflknqlygtlytlvkkdevssls 1140
Qy 1141 SCRNSSTVSYLKKEDEVSSQSSDAGLGDHSDPILTDVSAISNLIRKHSBALVEDI 1200
Db 1141 scrnsstvsylkkedevssqssdaglgsdhesdtltdvsaisnlirkhsearlvedi 1200

Qy 1201 GHELTIVLPEAKEGAFVLEFHEIDRLSDLGISSYGISSETTLEIFLKAEEGVDAE 1260
Db 1201 gheltyvlpeaakegafvelheidrlsdlgissygissettleiflkveesgvdae 1260
Qy 1261 TSDGTLPARRRRRAFGDKOSCLRPETEDADPNDSIDIPESRENDLSGMDGKSYQVK 1320
Db 1261 tsdgtlparrrrrafgdkgscrlpfteddaadpndsidpresretallsgmdgksyqvk 1320
Qy 1321 GMLTQOQFALLMKRLTLARRSRKGFPAOYVLPVFCIALVFSILVPPFGVPSLEIQ 1380
Db 1321 gmltqqofallmkrltlarrsrkgfpavfvcialvflvppfgvpsleiq 1380
Qy 1381 PMMYNEQYTFVNSDAPEDTLEILNALITPDPEFGYRCMEGNIPDTPCOAGEEWTAP 1440
Db 1381 pmyneqytfvnsdapeditleilnalitdpdpfgyrcmeagnipdtpcogeeewtap 1440
Qy 1441 VPQTIMDLFQNGWMTWONPSPACQSSDKIKMLPVCPPGAGLPPPOKONTADILQDL 1500
Db 1441 vpqtimdlfqngwmtwnpsspacqssdkikmlpvcppgaglpoppokontadilqdl 1500
Qy 1501 TGRNISYLVKTYVOIILAKSLKNKIWNFRVGGFSLGVSNTQALPPSOEVNDAIKOMK 1560
Db 1501 tgrnisylvktyvoilakslknkiwnfrvggfslgvsntqalppsdevndaikomk 1560
Qy 1561 HLKLAQSSADRFUNSLGRFMTGIDTFRNNYKVMFNKGMHAISSFLNVLINNALIRANLQK 1620
Db 1561 hlklakssadrfunslgrfmgtdtfrnnnykvmfnkgmhaisflnvlinnaliranlqk 1620
Qy 1621 GENPSHYGIFAFNHPLMLTKOOLEVALMTYSVDVLSICVIFAMSGVPSVYVFLIOER 1680
Db 1621 genpshygifaafnhplmltkqglevalmtysvdvlsicvifamsfvpsvfvflioger 1680
Qy 1681 VSKAKHLQFISGKVPVLYLNSNFWDMCANNVAVATVLIIFICFOQKSYSSNTLVYAL 1740
Db 1681 vskakhlqfsgkvpvlylnsnfwdmcanvavatlviifcfoqksyssntlvyal 1740
Qy 1741 LLLLYGMSITPLMYPASFEVKIPSTAVVLTYSNLFINGISVATVEYLELTDNKLNIN 1800
Db 1741 llllygmsitplmypasfvekipstavyvltysnlfingisvatveyleltdnklnin 1800
Qy 1801 DIKSVLEPFPBFCRGLIDMKANQAMADALBERGEGNRPVSPMDVORNLFAVAVEG 1860
Db 1801 diksvlefpfbfcrglidmkannqamadalbergegnrvpsmdvornlfaaveg 1860
Qy 1861 VVFLITVLQYRFFIPRPVNAKLSPINDEDEVRRERORILDDGGONLILEIKELTKI 1920
Db 1861 vvflitvlqyrffiprpvnaklspindedevrrerorilddggonlileikeltki 1920
Qy 1921 YRRRRKPAVDRICVGIPEGCEFGILGVNGAGKSSFTFKMLTGDTVTYRGAFLKNKSTILSN 1980
Db 1921 yrrrrkpaavdricvgipegcefgilgvngagkssftfkmldgtvttyrgaflknkstilsn 1980
Qy 1981 IHEVHONMGVCPOFDAITELLTGREHVEFALLRGVREKEVYGVEMARIKKGLVYKEX 2040
Db 1981 ihevhomngvcpoftdaitealltgrehefallyrgvrekvgyvemaikkglvykex 2040
Qy 2041 YAGNVSGGNRKSLSTAMALJGGPPVFLDEPTTGMDKARRFLMNCALSVYKEGRSVLT 2100
Db 2041 yagnvsggnrksslstamaljggppvfldepttgmdkarrflmncalsvykegrsvlt 2100
Qy 2101 SHSMECEALCTRAIIVWNGFRCLGSVOHLKNRFGDGYTIVRIAGSNBDLRPVODFG 2160
Db 2101 shsmeecealctraimvngfrclgsvqhlknrfgdytivrriagsnbdlrpvodfg 2160
Qy 2161 LAFPGSVLKEKHRMNOLOYLPSSLSLARIFSILSOKSKRLHIEDYVSQTTIDQYVNF 2220
Db 2161 lafpgsvlkekhrmnoloylpsslsllarifsilsokskrlhiedyvsqttidqyvnf 2220
Qy 2221 AKQSDDDHKLKDLSLHKNOTVADVAVLTSFLQDEKVESYV 2261
Db 2221 akqsdddhklkdlslhknotvadvavltlsflqdekvesyv 2261

RESULT 15
 AAB38110
 AAB38110 standard; Protein; 2261 AA.
 AC
 AC
 AAB38110;
 DT 29-JAN-2001 (first entry)
 XX
 DE Human ABC1 cholesterol transporter mutant, V399A.
 XX
 XX Human ABC1 cholesterol transporter; chromosome 9q31;
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
 KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
 KW cardiovascular disease; coronary artery disease; coronary restenosis;
 KW cerebrovascular disease; peripheral vascular disease;
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
 KW prognosis; prophylaxis; drug screening; transgenic animal; mutant;
 KW mutin.
 XX
 OS Homo sapiens.
 XX
 PN WO20005318-A2.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-1B00532.
 XX
 PR 15-MAR-1999; 990S-0124702.
 PR 08-JUN-1999; 990S-0138048.
 PR 17-JUN-1999; 990S-0139600.
 PR 01-SEP-1999; 990S-0151977.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON BIORESEARCH INC.
 XX
 PI Hayden MR, Wilson AR, Pimstone SN;
 DR WPI, 2000-587528/55.
 XX
 PT New ABC1 polypeptide is useful for treating diseases associated with
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
 PT disease and cancer -
 XX
 PS Examples; Page -; 229pp; English.
 XX
 CC The invention relates to the human ABC1 cholesterol transporter protein
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of
 CC proteins, and plays a crucial role in cholesterol transport, particularly
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
 CC located on chromosome 9q31, and mutations in this gene are associated
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,
 CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
 CC are distinguishable in that TD is an autosomal recessive disorder, while
 CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
 CC cholesterol") in the blood correlate with a high risk of cardiovascular
 CC disease, particularly coronary artery disease, but also cerebrovascular
 CC disease, coronary restenosis, and peripheral vascular disease.
 CC Conversely, a high level of HDL has protective effects against
 CC cardiovascular disease. The invention provides genetic constructs and
 CC transgenic cells and non-human animals comprising human ABC1 nucleic
 CC acids, and methods of gene therapy for the treatment or prevention of
 CC cardiovascular disease comprising the administration of an expression
 CC vector encoding ABC1 or an active fragment thereof. The invention also
 CC encompasses compounds which mimic ABC1 activity, compounds which
 CC stimulate ABC1 expression and methods of screening for such compounds.
 CC It further relates to methods for determining whether a patient has an
 CC increased risk for cardiovascular disease due to polymorphisms in the
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
 CC or prevent cardiovascular disease, especially coronary artery disease,

CC cerebrovascular disease, coronary restenosis or peripheral vascular
 CC disease. They may also be used in the treatment of diseases associated
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
 CC The invention specifically excludes proteins with the exact amino acid
 CC sequences of Genbank Accession No: CAA10005.1 and X75926, and the nucleic
 CC acid with the exact sequence as Genbank Accession No: AJ012376.1. The
 CC present sequence represents a mutant human ABC1 cholesterol transporter
 CC associated with an altered cholesterol level and therefore an altered
 CC risk of cardiovascular disease.
 CC Note: The present sequence is not shown in the specification, but is
 CC derived from the native human ABC1 shown on pages 152-157.
 CC
 XX
 XX
 SQ Sequence 2261 AA;
 Query Match 99.9%; Score 11785; DB 21; Length 2261;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2257; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MACWPQLRLIMKULTRRROTCQLLEVAWPLEFILILISVRLSPYRBOHCHEPNKA 60
 DB 1 macwpqlrlllmknltfrrrtcglllevawplfiflllsvrlsypyeqhechfnka 60
 QY MPSAGTLPMWOGIICNANNPCFRRYPTRGPAAGVYGNFNKSTVARLSRDARLLYSQKPT 120
 DB 61 mpsagtlpmwvglicnannpcfrryptrgpaagvygnfnkstarlsrdarlllysqkdt 120
 QY 61 mpsagtlpmwvglicnannpcfrryptrgpaagvygnfnkstarlsrdarlllysqkdt 120
 DB 121 SMKDMRVLTLOQIKSSSNLKLDFLVNTEFSGFLYHNLSLPKSTYDKMLRADVILH 180
 DB 121 smkdmrvlrtlqgiksssnlklqdflvnetfsgflynhlslpkstvdkmrladvilh 180
 QY 181 KVFQGYOLHHTSLCNSKSEEMIQLCDQVSELGCPKPKKLAARVLRSMNDILKPIIL 240
 DB 181 kvflqgyqlhhtslcngskseemlqldqveselcglpkeklaaarvlrsmndilkipill 240
 QY 241 RTLNSTSPFPSKELAEATKTLHSLGLTAEFLSMKSMSPMRQEVNLFVNSSSSSTQI 300
 DB 241 rtlnstspfskelaetktlhlslgltaeflsmksmspmrqevnflvnssssstq 300
 QY 241 rtlnstspfskelaetktlhlslgltaeflsmksmspmrqevnflvnssssstq 300
 DB 301 YOAVSRIVCGHPBGGLIKISLWYEDNNYKALPGNGTEDEATETTYDNTTPYCNDLMK 360
 DB 301 ygavsrivcghpbgglkikslwyednnnykalpgngteedaetettydnttpycndlmk 360
 QY 361 NLESPLSRIIMAKPLVGLTLYTPDPATQVAAEVNKKPQELAVRHDLGMEELS 420
 DB 361 nlesplsrilimwkalpvlgltytpdpataqvaaevnkkpqelavrhdlgmeels 420
 QY 421 PKIWTMENSOEMDLVRLDSDHNDHFWEQULDGLDWTADIVATLAKHPEDVOSSNGS 480
 DB 421 pkltwmensqemdlvrmldsdhndhfwequldglwtadivatlakhpedvossngs 480
 QY 481 VYTWREAFNTNQAIRISFMECVNLKLEPATEVWLINSMELDRKKTWAGIVPFG 540
 DB 481 vytwreaftntnqairtsfmevcvnlklepatevwlinsmelldrkktwagivpfg 540
 QY 541 ITFGSTELPRHHVYKXIRMDIDNVERTNKIKDQWGDGPADPEEDRYVWYGPAVLODV 600
 DB 541 itfgstelprrhvykxirmdidnvertnkikdqwgdgpapdeedryvwygpaavlodv 600
 QY 601 EQAIIIVLTGTEKKTGVVMOQMPYCYVDIFLRVNSRSMPLFMTLAWTVSAVITKIV 660
 DB 601 eqaillvltgtektektgvvmoqmpcyvddiflrvmrsmpflmtlawtvsavitkiv 660
 QY 661 YEKEALKEKMRIMGIDNSTIMSPSTSLPLVASGLLVITLKGNLPRSDSVFV 720
 DB 661 yekealkekmrimgidnstimspsstslplvasglvlvltlkgnlprsdsvfv 720
 QY 721 FLISFAVVTILQCLISTLFSRANLAAAGGIIYFLYLYVLCVAMQDYVFTLKIPAS 780
 DB 721 flisfavvtllqclistlfsranlaaaggiiyfllylvlcvamqdyvftlkifas 780
 QY 781 LISPVAFGCGEYFALFEQIGVQMDNLESPVEEDGFNLTTSSMILFDFTLXGVMTW 840

```

|||||:|||||
Db 11spafgfcyefallfeegiygvwnlfeespeedgnlftsvnmldftflyawt 840
QY YTEAVFPGOYGIIPRPMYPCPKSYWFGESDEKSHPGSNOKRMEITCMEEPHTLKGVGS 900
Db 841 YTEAVFPGOYGIIPRPMYPCPKSYWFGESDEKSHPGSNOKRMEITCMEEPHTLKGVGS 900
QY YTEAVFPGOYGIIPRPMYPCPKSYWFGESDEKSHPGSNOKRMEITCMEEPHTLKGVGS 900
Db 841 YTEAVFPGOYGIIPRPMYPCPKSYWFGESDEKSHPGSNOKRMEITCMEEPHTLKGVGS 900
QY IONLVKVRDGMKVAVJGLALNFYEGQITSFGLHNGAGKTTTMSILTGLEPPTSGTAYIL 960
Db 901 IONLVKVRDGMKVAVJGLALNFYEGQITSFGLHNGAGKTTTMSILTGLEPPTSGTAYIL 960
QY IONLVKVRDGMKVAVJGLALNFYEGQITSFGLHNGAGKTTTMSILTGLEPPTSGTAYIL 960
Db 901 IONLVKVRDGMKVAVJGLALNFYEGQITSFGLHNGAGKTTTMSILTGLEPPTSGTAYIL 960
QY 961 GKDIREMSTIRONLGVCPQHNVLFDMLTVEEHTMFAARKLGSEKHVAKAMEQMALDVG 1020
Db 961 GKDIREMSTIRONLGVCPQHNVLFDMLTVEEHTMFAARKLGSEKHVAKAMEQMALDVG 1020
QY 961 GKDIREMSTIRONLGVCPQHNVLFDMLTVEEHTMFAARKLGSEKHVAKAMEQMALDVG 1020
Db 961 GKDIREMSTIRONLGVCPQHNVLFDMLTVEEHTMFAARKLGSEKHVAKAMEQMALDVG 1020
QY 1021 LPSKSKTSKTSOLSGMORUKLSVALAFVGSKVYLDEPTGVPYSPRGIMELLYKVRQ 1080
Db 1021 LPSKSKTSKTSOLSGMORUKLSVALAFVGSKVYLDEPTGVPYSPRGIMELLYKVRQ 1080
QY 1021 LPSKSKTSKTSOLSGMORUKLSVALAFVGSKVYLDEPTGVPYSPRGIMELLYKVRQ 1080
Db 1021 LPSKSKTSKTSOLSGMORUKLSVALAFVGSKVYLDEPTGVPYSPRGIMELLYKVRQ 1080
QY 1081 GRTIILSTHMDADVILGDRIAIISHGKLCVSSSLFLKNOLGTGYVLTLYKKDVESLS 1140
Db 1081 GRTIILSTHMDADVILGDRIAIISHGKLCVSSSLFLKNOLGTGYVLTLYKKDVESLS 1140
QY 1141 SCRNSSTSVYTLKEDSVSSSSDAGLSDHESPTITDVAISNLRKHVSEARLYVEDI 1200
Db 1141 SCRNSSTSVYTLKEDSVSSSSDAGLSDHESPTITDVAISNLRKHVSEARLYVEDI 1200
QY 1201 GHELYVLPYEAKEGAVELEFHEIDRLSDLGISSYGISSETTELEFLKVAEESGVAE 1260
Db 1201 GHELYVLPYEAKEGAVELEFHEIDRLSDLGISSYGISSETTELEFLKVAEESGVAE 1260
QY 1261 TSDGTLPARNRRAFADKOSCLRPTEBDADPNDSIDIPESRETDLLSGMDKGSYQV 1320
Db 1261 TSDGTLPARNRRAFADKOSCLRPTEBDADPNDSIDIPESRETDLLSGMDKGSYQV 1320
QY 1321 GMLKLOOQFVALMLMKRLIARSRKGFPAQIYLPVAFVLCIALVFSIYVPPFGKYSLEIQ 1380
Db 1321 GMLKLOOQFVALMLMKRLIARSRKGFPAQIYLPVAFVLCIALVFSIYVPPFGKYSLEIQ 1380
QY 1381 PMYNEQYTFVNSADPEDTGTLELLNALTKDFGSTRCMENPDPTRCQAGEEWTAP 1440
Db 1381 PMYNEQYTFVNSADPEDTGTLELLNALTKDFGSTRCMENPDPTRCQAGEEWTAP 1440
QY 1441 VQGTIMDLFONGNMTMONNSPACOCSSDKIKMLPVCPPGAGGLPPOROKONTADILDL 1500
Db 1441 VQGTIMDLFONGNMTMONNSPACOCSSDKIKMLPVCPPGAGGLPPOROKONTADILDL 1500
QY 1501 TGRNISDYLVKTYVOIIAKSLKNKTWVNEFRYGFSLGAVSNTQALPPSOEVNDATKOMK 1560
Db 1501 TGRNISDYLVKTYVOIIAKSLKNKTWVNEFRYGFSLGAVSNTQALPPSOEVNDATKOMK 1560
QY 1561 HLKLAOSSADRLNSLGRFMTGLDTRNNVYKWFENKKGWHAISSEFLNYINNAILRANLQK 1620
Db 1561 HLKLAOSSADRLNSLGRFMTGLDTRNNVYKWFENKKGWHAISSEFLNYINNAILRANLQK 1620
QY 1621 GENPSHYGTATFHPNLNFKOOLSEVALMTSDVLSICVIFAMSEVPASFEVLIDR 1680
Db 1621 GENPSHYGTATFHPNLNFKOOLSEVALMTSDVLSICVIFAMSEVPASFEVLIDR 1680
QY 1681 VSKAKHLOEISGVKPVLYWLSNFWDMCNVVPATLVIIIFICFOOKSYVSSTNLPLVAL 1740
Db 1681 VSKAKHLOEISGVKPVLYWLSNFWDMCNVVPATLVIIIFICFOOKSYVSSTNLPLVAL 1740
QY 1741 LLLLGWSTPLMYPASFEFKIPSTAYVYVLTSYNLFIGINGSVAPFVLELFTDNKLNNIN 1800
Db 1741 LLLLGWSTPLMYPASFEFKIPSTAYVYVLTSYNLFIGINGSVAPFVLELFTDNKLNNIN 1800
QY 1801 DILKSVFLFPHFCLGRGLDMYKNOAMADALREFGENRFVSPLSWDLVGRNLFAMAVEG 1860
Db 1801 DILKSVFLFPHFCLGRGLDMYKNOAMADALREFGENRFVSPLSWDLVGRNLFAMAVEG 1860
QY 1861 VFEFLITVLIOYRFFTRPREVNAKLSPLNDEDEVRERORIIDGGONDLEIKELTKI 1920
Db 1861 VFEFLITVLIOYRFFTRPREVNAKLSPLNDEDEVRERORIIDGGONDLEIKELTKI 1920

```

Search completed: September 15, 2002, 12:59:42
 Job time: 331 sec

```

Db 1861 vffllitvllyqrrftrpprnaklsplndedvrrergrllldgggqndlleikeltki 1920
QY 1921 YRRRRKPAVDRLICVGIPEBCEGLGVNGAKSSTFKMLTGDTVTYRGDAFLNKSJLSN 1980
Db 1921 YRRRRKPAVDRLICVGIPEBCEGLGVNGAKSSTFKMLTGDTVTYRGDAFLNKSJLSN 1980
QY 1981 IHEVHONMGCPQFQDAITELLGREGHEVFPALLRGVPEKEVGKVGEMALTKGLVYGEK 2040
Db 1981 IHEVHONMGCPQFQDAITELLGREGHEVFPALLRGVPEKEVGKVGEMALTKGLVYGEK 2040
QY 2041 YAGNYSGNRKLSTAMALIGBPVVFLEPTTGMDPKARFLMNCALSVKEGRSVLT 2100
Db 2041 YAGNYSGNRKLSTAMALIGBPVVFLEPTTGMDPKARFLMNCALSVKEGRSVLT 2100
QY 2101 SHSMECEALCTMAIMVNGREFCLGVHUKRFGDGTIYVRIKGSNPDLKPVQDFRG 2160
Db 2101 SHSMECEALCTMAIMVNGREFCLGVHUKRFGDGTIYVRIKGSNPDLKPVQDFRG 2160
QY 2161 IAPPGSVLKKEHHRNMLQYOLPSSLSLARIFSLSSKKRRLHIEDYSVSGOTTLQVFN 2220
Db 2161 IAPPGSVLKKEHHRNMLQYOLPSSLSLARIFSLSSKKRRLHIEDYSVSGOTTLQVFN 2220
QY 2221 AKDQSDDDHLKDLILHKNQTVVDVAVLTSLQDEKYESYV 2261
Db 2221 AKDQSDDDHLKDLILHKNQTVVDVAVLTSLQDEKYESYV 2261

```

Mon Sep 16 10:20:20 2002

us-09-595-526b-2.rag

Page 26

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2002, 07:48:35 ; Search time 1589.81 Seconds
(without alignments)
7347.976 Million cell updates/sec

Title: US-09-595-526b-1_COPY_291_7094

Perfect score: 6804
1 atggctgtgtgcccacgct.....gaagaatccctgtcatacgg 6804

Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*

- 1: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1980.DAT.*
- 2: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT.*
- 3: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT.*
- 4: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT.*
- 5: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1984.DAT.*
- 6: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT.*
- 7: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT.*
- 8: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1987.DAT.*
- 9: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT.*
- 10: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1989.DAT.*
- 11: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1990.DAT.*
- 12: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1991.DAT.*
- 13: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1992.DAT.*
- 14: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1993.DAT.*
- 15: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1994.DAT.*
- 16: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1995.DAT.*
- 17: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1996.DAT.*
- 18: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT.*
- 19: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT.*
- 20: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT.*
- 21: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT.*
- 22: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6804	100.0	10442	22	AAF24680
2	6804	100.0	10442	22	AAF24702
3	6802.4	100.0	10474	22	AAF24685
4	6802.4	100.0	10474	22	AAF24686
5	6802.4	100.0	10474	22	AAF24707
6	6802.4	100.0	10474	22	AAF24708
7	6796	99.9	7860	22	AAF92835
8	6792.8	99.8	7860	22	AAF83826
9	6788	99.8	7260	22	AAF21326

10	6788	99.8	7260	22	AA170315	Human ATP binding
11	6784.8	99.7	9741	22	AA506120	Human ABC1 DNA seq
12	6784.8	99.7	9854	22	AA506121	Human ABC1 DNA seq
13	6783.2	99.7	7281	22	AAK51683	Human polynucleoti
14	6762.2	99.4	7086	22	ABA09200	Human ABCA1 homolo
15	6762.2	99.4	7086	22	AAK52667	Human polynucleoti
16	6762	99.4	7864	21	AAAC69130	Human ABC1 choles
17	6760.4	99.4	7864	21	AAAC69385	Human ABC1 choles
18	6760.4	99.4	7864	21	AAAC69386	Human ABC1 choles
19	6760.4	99.4	7864	21	AAAC69389	Human ABC1 choles
20	6746	99.1	7861	21	AAAC69387	Human ABC1 choles
21	6738	99.0	7857	21	AAAC69388	Human ABC1 choles
22	6728	98.9	6880	21	AA294734	Human ATP binding
23	6728	98.9	6880	22	AA170314	Human ATP binding
24	6724.8	98.8	6880	22	AAAD21325	Human ATP binding
25	1926.8	28.3	7323	21	AA294746	ATP binding cass
26	1926.8	28.3	7784	19	AAV3392	Human stomach can
27	1922.8	28.3	5097	22	AA193913	Human CDNA sequenc
28	1922.8	28.3	5097	22	AAH18233	Human PD-ATP-bind
29	1735.8	25.5	6522	22	AA508706	Nucleotide sequenc
30	1696	24.9	6607	22	AA54812	Nucleotide sequenc
31	1531.6	22.5	5762	22	AA54792	Human secreted pro
32	1528.8	22.5	5811	22	AAAD05626	Human PD-ATP-bind
33	1465	21.5	5669	22	AA508707	Human ABCA2 transp
34	985	14.5	8040	22	AA57452	Nucleotide sequenc
35	985	14.5	8195	22	AAH75187	Human ABCA2 transp
36	953.6	14.0	3437	22	AAAD02722	Human ABCA2 transp
37	949.2	14.0	4413	23	AA583715	Nucleotide sequenc
38	949.2	12.8	2911	21	AA294751	Human ABCA2 transp
39	872.6	12.8	3635	22	AAH56389	Human ABCA2 transp
40	870.8	12.8	3635	22	AAH56389	Human ABCA2 transp
41	716.2	10.5	1556	22	AAH18606	Human ABCA2 transp
42	625.4	9.2	669	22	AAH08356	Human ABCA2 transp
43	598	8.8	2740	24	AA562249	Human ABCA2 transp
44	430.8	6.3	5994	18	AAH85474	Human ABCA2 transp
45	430.8	6.3	5994	19	AAV16307	Human ABCA2 transp

ALIGNMENTS

RESULT 1
AAF24680 standard; DNA; 10442 BP.

ID AAF24680;

AC AAF24680;

DT 20-APR-2001 (first entry)

DE Nucleotide sequence of a human ABC1 polypeptide.

XX Human; adenine triphosphate binding cassette protein 1; ABC1;

KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;

KM chromosome 9q22-9q31; heart disease; hypercholesterolemia;

KW atherosclerosis; cholesterol transport; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key

FT CDS

FT CDS

XX 18-JUN-1999; 99US-0140264.

PR 14-SEP-1999; 99US-0153872.

PR 19-NOV-1999; 99US-0166573.

QY 3841 tgccttcgcccgttcactgaagaatgctgctgcatcccaatgatctctacataagcca 3900
|||||
Db 4131 tgccttcgcccgttcactgaagaatgctgctgcatcccaatgatctctacataagcca 4190
QY 3901 gaatccagagagacagactgtcagtgaggatgagatgagcagaaggtccctacacagtgtaaa 3960
|||||
Db 4191 gaatccagagagacagactgtcagtgaggatgagatgagcagaaggtccctacacagtgtaaa 4250
QY 3961 ggttggaacttaccagacgaacaggttctgccccttctgtggaagagactgtcaattgccc 4020
|||||
Db 4251 ggttcggaacttaccagacgaacaggttctgccccttctgtggaagagactgtcaattgccc 4310
QY 4021 agacggagtggaagagattttgtctcagatgtctctcagcgtgtgtcttctgcatc 4080
|||||
Db 4311 agacggagtggaagagattttgtctcagatgtctctcagcgtgtgtcttctgcatc 4370
QY 4081 ggccttggttcaagccttgatctgtgcaaccccttggcaagtaacccagccttggaactcag 4140
|||||
Db 4371 ggccttggttcaagccttgatctgtgcaaccccttggcaagtaacccagccttggaactcag 4430
QY 4141 cccctgagttaacaacgaacagtaacacatttgcagaaatgagtgatcctctgagacacggga 4200
|||||
Db 4431 cccctgagttaacaacgaacagtaacacatttgcagaaatgagtgatcctctgagacacggga 4490
QY 4201 acccttgaaactttaaacgccttcacacaaagacccctgctcgaggacccgctgtatggaa 4260
|||||
Db 4491 acccttgaaactttaaacgccttcacacaaagacccctgctcgaggacccgctgtatggaa 4550
QY 4261 ggaacacccatcccaagacacgccttcgcaagcgaggaggagaaatgagacccctgcccga 4320
|||||
Db 4551 ggaacacccatcccaagacacgccttcgcaagcgaggaggagaaatgagacccctgcccga 4610
QY 4321 gtccccaagacataatgagaccccttcacagaatgggaactggacaatgacaaccccttca 4380
|||||
Db 4611 gtccccaagacataatgagaccccttcacagaatgggaactggacaatgacaaccccttca 4670
QY 4381 ccttgatgccaagtgtatagacgagacgaacaaatccaagaatgctgctgtgtgtccccaagg 4440
|||||
Db 4671 ccttgatgccaagtgtatagacgagacgaacaaatccaagaatgctgctgtgtgtccccaagg 4730
QY 4441 gcaagggggctgctccctcccaagaagaacaaacacactgacagatactctccagagacctg 4500
|||||
Db 4731 gcaagggggctgctccctcccaagaagaacaaacacactgacagatactctccagagacctg 4790
QY 4501 acaggaagaagaattctgagattatctgtgtgaagcgtatgtgcagatacagccaagaagc 4560
|||||
Db 4791 acaggaagaagaattctgagattatctgtgtgaagcgtatgtgcagatacagccaagaagc 4850
QY 4561 ttaagaagaagaatctggtgtaagtttagatagtgccgcttcccttggtgtgtaagt 4620
|||||
Db 4851 ttaagaagaagaatctggtgtaagtttagatagtgccgcttcccttggtgtgtaagt 4910
QY 4621 aatactcaagaacttctcctcagtgcaagaagttaatgatacgcatcaaaacaatataagaaa 4680
|||||
Db 4911 aatactcaagaacttctcctcagtgcaagaagttaatgatacgcatcaaaacaatataagaaa 4970
QY 4681 caccctaaagctggccaaggaagttctgcagatctgcagattcttcccaacagcttggagaattt 4740
|||||
Db 4971 caccctaaagctggccaaggaagttctgcagatctgcagattcttcccaacagcttggagaattt 5030
QY 4741 atgacagagctgacacacagaagaatlaatgtcaaggtgtgtgtcaataaacaagggtgcat 4800
|||||
Db 5031 atgacagagctgacacacagaagaatlaatgtcaaggtgtgtgtcaataaacaagggtgcat 5090
QY 4801 gcaatcagcttcttctgtaattgcatcaacaatgccaattctccggcgcaaccccgcaaaag 4860
|||||
Db 5091 gcaatcagcttcttctgtaattgcatcaacaatgccaattctccggcgcaaccccgcaaaag 5150
QY 4861 ggaagaacccctagacatttgaataatcagcttcaatcaatccctgaaatctcaacaag 4920
|||||
Db 5151 ggaagaacccctagacatttgaataatcagcttcaatcaatccctgaaatctcaacaag 5210
QY 4921 cagcagcttcaagagtgctctgatatgacacacatcagtgatgtctctgtgtccatctgt 4980
|||||
Db 5211 cagcagcttcaagagtgctctgatatgacacacatcagtgatgtctctgtgtccatctgt 5270
QY 4981 gtcactttgaaatgtctctgtcccgccagccttctgtctatctctgataccagaagcgg 5040
|||||
Db 5271 gtcactttgaaatgtctctgtcccgccagccttctgtctatctctgataccagaagcgg 5330
QY 5041 gtcagcaagaacaaacacactgcaatctcaatgagtgagtgaaagcctgtcatctatgctc 5100
|||||
Db 5331 gtcagcaagaacaaacacactgcaatctcaatgagtgagtgaaagcctgtcatctatgctc 5390
QY 5101 tctaatttgtctgagatgagtaatgagtggtctcccgccacactgtcatatcatc 5160
|||||
Db 5391 tctaatttgtctgagatgagtaatgagtggtctcccgccacactgtcatatcatc 5450
QY 5161 ttcactgtctccagcagaatctctatgtgtctcccaacacactgcctgtgtgtagccctt 5220
|||||
Db 5451 ttcactgtctccagcagaatctctatgtgtgtctcccaacacactgcctgtgtgtagccctt 5510
QY 5221 ctactttgtctgagatgagtgcaatgagtggtctcccgccacactgtcatatcatc 5280
|||||
Db 5511 ctactttgtctgagatgagtgcaatgagtggtctcccgccacactgtcatatcatc 5570
QY 5281 aagatcccccagcagcctatgtgtgtctcaacagcggtgaacactcttcatatgcatat 5340
|||||
Db 5571 aagatcccccagcagcctatgtgtgtgtctcaacagcggtgaacactcttcatatgcatat 5630
QY 5341 ggcagcgtgagcacccttctgtgtgagcgtgtcaacgcgaataagctgaaataatcaat 5400
|||||
Db 5631 ggcagcgtgagcacccttctgtgtgagcgtgtcaacgcgaataagctgaaataatcaat 5690
QY 5401 gatatccctgaagctccgtgtctcttgatcttccacatcttctgtctggagagaggtccatc 5460
|||||
Db 5691 gatatccctgaagctccgtgtctcttgatcttccacatcttctgtctggagagaggtccatc 5750
QY 5461 gacatggtgtaaaaacccagcgaatgagctgtatgagccttggaaggttgggagaaatcgctt 5520
|||||
Db 5751 gacatggtgtaaaaacccagcgaatgagctgtatgagccttggaaggttgggagaaatcgctt 5810
QY 5521 gtttcaacatctatcttggagcctgtgtggaagcgaacccctctgcacatgagcgtggaagg 5580
|||||
Db 5811 gtttcaacatctatcttggagcctgtgtggaagcgaacccctctgcacatgagcgtggaagg 5870
QY 5581 gtgtgtctctccatctatctgtctgcatccagtaacagattcttcaatgagcccaacact 5640
|||||
Db 5871 gtgtgtctctccatctatctgtctgcatccagtaacagattcttcaatgagcccaacact 5930
QY 5641 gtaaatgcaaaagctatctctctgaaatgtaagatgaaatgtaagcgtgggaagacag 5700
|||||
Db 5931 gtaaatgcaaaagctatctctctgaaatgtaagatgaaatgtaagcgtgggaagacag 5990
QY 5701 agaatcttctatgtgtgagggccagaaatgacatcttagaaatcaagaggttgcagaagata 5760
|||||
Db 5991 agaatcttctatgtgtgagggccagaaatgacatcttagaaatcaagaggttgcagaagata 6050
QY 5761 tatagaaggaagcgaagcgtgtgtgacagagattgtgtggaatctctcctctgtag 5820
|||||
Db 6051 tatagaaggaagcgaagcgtgtgtgacagagattgtgtggaatctctcctctgtag 6110
QY 5821 tgccttgggctccctggaggttaatggggctggaaaaatcaacttcaagaatgttaaca 5880
|||||
Db 6111 tgccttgggctccctggaggttaatggggctggaaaaatcaacttcaagaatgttaaca 6170
QY 5881 ggaatagcactgttaccgagagagatgcttctcttaacaaaatagatattatcaaac 5940
|||||
Db 6171 ggaatagcactgttaccgagagagatgcttctcttaacaaaatagatattatcaaac 6230
QY 5941 atccatgaaatgacatcaagaacatgagctacgtccctcagatttgatgcatcaagaagtg 6000
|||||
Db 6231 atccatgaaatgacatcaagaacatgagctacgtccctcagatttgatgcatcaagaagtg 6290
QY 6001 ttgactggaggaagacacgtgagttcttgccttggagagagttccagagaagaa 6060
|||||

```

Db 6291 ttgacttgagagaacacggtgagttcttgccttcttgagagagatcccgagaaga 6350
Qy 6061 gttggcaaggttggtagtgagcgaatccggaactggcctcgtagatcggagaaaa 6120
Db 6351 gttggcaaggttggtagtgagcgaatccggaactggcctcgtagatcggagaaaa 6410
Qy 6121 tatgtgttaactatagtgagagcaaaagcaagctctctacagcattgcttgatc 6180
Db 6411 tatgtgttaactatagtgagagcaaaagcaagctctctacagcattgcttgatc 6470
Qy 6181 ggcggggccctcgtgtgttcttgatgaaccaccacagcattgaccccaagcccg 6240
Db 6471 ggcggggccctcgtgtgttcttgatgaaccaccacagcattgaccccaagcccg 6530
Qy 6241 cgttcttgtagaatctgagccttaagtggttgcgaagagggagagatcagtagtcttaca 6300
Db 6531 cgttcttgtagaatctgagccttaagtggttgcgaagagggagagatcagtagtcttaca 6590
Qy 6301 tctcatagataggaagaatgtagaagctcttgcaactagatgacatcatgtagtaca 6360
Db 6591 tctcatagataggaagaatgtagaagctcttgcaactagatgacatcatgtagtaca 6650
Qy 6361 aggttcaggtgcttgagcagctgccaagccttaaaataaggttggagatgtagtaca 6420
Db 6651 aggttcaggtgcttgagcagctgccaagccttaaaataaggttggagatgtagtaca 6710
Qy 6421 atagttgtagaataagcaggtcccaaccggacctggaagcctgccaagattcttga 6480
Db 6711 atagttgtagaataagcaggtcccaaccggacctggaagcctgccaagattcttga 6770
Qy 6481 ctgtgcttcccggaaggtgttctaaaggaacccggaaatgtagtacaacagctt 6540
Db 6771 ctgtgcttcccggaaggtgttctaaaggaacccggaaatgtagtacaacagctt 6830
Qy 6541 ccatcttcattatctctctcgcgcaggaatattcagatcctctccagagcaaaaagcga 6600
Db 6831 ccatcttcattatctctctcgcgcaggaatattcagatcctctccagagcaaaaagcga 6890
Qy 6601 ctccacatagaagaactactctgttctcagacaacaccttgaccagatttgaactt 6660
Db 6891 ctccacatagaagaactactctgttctcagacaacaccttgaccagatttgaactt 6950
Qy 6661 gccaaggaacaaagtatagatgacacctaataaagacctcattacacaaaacagcaga 6720
Db 6951 gccaaggaacaaagtatagatgacacctaataaagacctcattacacaaaacagcaga 7010
Qy 6721 gtagtgagcgttgagttctacacatcttctacagagatgagaagtgaaagaagctat 6780
Db 7011 gtagtgagcgttgagttctacacatcttctacagagatgagaagtgaaagaagctat 7070
Qy 6781 gtagtgagcgttgagttctacacatcttctacagagatgagaagtgaaagaagctat 6840
Db 7071 gtagtgagcgttgagttctacacatcttctacagagatgagaagtgaaagaagctat 7094

```

RESULT 2
AAAF24702 standard; DNA: 10442 BP.

AAAF24702:
20-APR-2001 (first entry)

Nucleotide sequence of a human ABC1 polypeptide.

Human: adenosine triphosphate binding cassette protein 1; ABC1;
apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
chromosome 9q22-9q31; heart disease; hypercholesterolemia;
atherosclerosis; cholesterol transport; ss.

Homo sapiens.
Location/Qualifiers

```

FT CDS 291..7076
FT /*tag= a
FT /product= "ABC1 polypeptide"
PN WO200078971-A2.
XX 28-DEC-2000.
PD 16-JUN-2000; 2000MO-US16591.
PE 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX (CYTH-) CV THERAPEUTICS INC.
PA (UNITW) UNIV WASHINGTON.
PI Lawn RM, Wade D, Oram JF, Garvin M;
DR MPI: 2001-137811/14.
DR P-PSDB: AAB31365.
XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT polynucleotides and polypeptides, useful for treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX Claim 3; Page 117-123; 211pp; English.
PS
XX The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC membranes and utilises ATP hydrolysis to transport a wide variety of
CC substrates across the plasma membrane. ABC1 is a pivotal protein in
CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC stores. ABC1 is defective in Tangier disease, a genetic disorder
CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC useful for developing pharmaceutical agents for the treatment of heart
CC disease and other disorders associated with hypercholesterolemia and
CC atherosclerosis. The genes are useful for developing screening assays to
CC screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC are also useful as diagnostic indicators of cardiovascular disease and
CC other disorders associated with hypercholesterolemia.
XX
SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other:
Query Match 100.0%; Score 6804; DB 22; Length 10442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 atggctgtgtgcccagctgagctgtgctgtgtagaagaacctcacttcagaaga 60
Db 291 atggctgtgtgcccagctgagctgtgctgtgtagaagaacctcacttcagaaga 350
Qy 61 caaacatgcaagctgttaactggaagtgagcctgacctattatctctcgtatcgtac 120
Db 351 caaacatgcaagctgttaactggaagtgagcctgacctattatctctcgtatcgtac 410
Qy 121 tctgttgcgtgaagctaccacacctatgaacaactgaatgacatttccaataaagcc 180
Db 411 tctgttgcgtgaagctaccacacctatgaacaactgaatgacatttccaataaagcc 470
Qy 181 atgacctgcaggaacacctcttgggttcaggggattatctgtaatgccaacaacccc 240
Db 471 atgacctgcaggaacacctcttgggttcaggggattatctgtaatgccaacaacccc 530
Qy 241 tgttcggttaaccgactctcgtggaagctcccggaagtgttggaaactttaacaatcc 300
Db 531 tgttcggttaaccgactctcgtggaagctcccggaagtgttggaaactttaacaatcc 590
Qy 301 atgtgtgcgcgtctgttctcagatgctcgtgaagcttcttatacagccagaagaaccc 360

```

Db 591 atgtggctgcgcctgttctcagatgctcggagctcttcttatacagccggaagaagacc 650
Qy 361 agcttgaagacatgcgcaagttcttgaagacattacagcagatcaagaatccagctca 420
Db 651 agcttgaagacatgcgcaagttcttgaagacattacagcagatcaagaatccagctca 710
Qy 421 aacttgaagcttcaagaattctcctgtgtgagacatgaagaccttctgtgttccatctac 480
Db 711 aacttgaagcttcaagaattctcctgtgtgagacatgaagaccttctgtgttccatctac 770
Qy 481 aacctctctcccaagcttactgtgtgagacatgaagaccttctgtgttccatctac 540
Db 771 aacctctctcccaagcttactgtgtgagacatgaagaccttctgtgttccatctac 830
Qy 541 aagttattttgcaagctcagcttactgtgtgagacatgaagaccttctgtgttccatctac 600
Db 831 aagttattttgcaagctcagcttactgtgtgagacatgaagaccttctgtgttccatctac 890
Qy 601 gaagagatgattcaacttggctgacccaagaagttcttgaagcttgtgtgtccccaagaag 660
Db 891 gaagagatgattcaacttggctgacccaagaagttcttgaagcttgtgtgtccccaagaag 950
Qy 661 aacttgcctgcgacgacgagagttactgtgttccacaatggaatccctgaagccaatccctg 720
Db 951 aacttgcctgcgacgacgagagttactgtgttccacaatggaatccctgaagccaatccctg 1010
Qy 721 agaacactaaactatactctccctcccgaggaagagctgtgtgtgaagcccaaaaaa 780
Db 1011 agaacactaaactatactctccctcccgaggaagagctgtgtgtgaagcccaaaaaa 1070
Qy 781 ttgtgtcatagttcttggagactgtgcccagagctgtgttcaagcatgagaagctgtgagctgac 840
Db 1071 ttgtgtcatagttcttggagactgtgcccagagctgtgttcaagcatgagaagctgtgagctgac 1130
Qy 841 atgcgcaagagagttgttcttctgaccaaattggaagaagctccaagctccccaacaaatc 900
Db 1131 atgcgcaagagagttgttcttctgaccaaattggaagaagctccaagctccccaacaaatc 1190
Qy 901 taacagagctgtgtctcgtatgttctgtcgagcaatcccgagggaggggctgagaatccaag 960
Db 1191 taacagagctgtgtctcgtatgttctgtcgagcaatcccgagggaggggctgagaatccaag 1250
Qy 961 tctctcaactgttatgagagcaacaactacaagccctcttggagagcaatgagcactgag 1020
Db 1251 tctctcaactgttatgagagcaacaactacaagccctcttggagagcaatgagcactgag 1310
Qy 1021 gaagatgctgaaacctctatgacaactatacaactccttactgtgaatgttgaatgaag 1080
Db 1311 gaagatgctgaaacctctatgacaactatacaactccttactgtgaatgttgaatgaag 1370
Qy 1081 aatttggagttactgtctcttcccgcatatctgtgaagactctgaagccgtctgtctgt 1140
Db 1371 aatttggagttactgtctcttcccgcatatctgtgaagactctgaagccgtctgtctgt 1430
Qy 1141 gggagagatcctgttatacactgtacactctccagccacaagcgagttcatgctgaggtgagc 1200
Db 1431 gggagagatcctgttatacactgtacactctccagccacaagcgagttcatgctgaggtgagc 1490
Qy 1201 aagaccttccaggaactgtgtgttccatgactgtgaggaagcaatgttggaggaactcagc 1260
Db 1491 aagaccttccaggaactgtgtgttccatgactgtgaggaagcaatgttggaggaactcagc 1550
Qy 1261 cccaagatctgagactgtgtgttccatgactgtgaggaagcaatgttggaggaactcagc 1320
Db 1551 cccaagatctgagactgtgtgttccatgactgtgaggaagcaatgttggaggaactcagc 1610
Qy 1321 gacagcagagacatgacactcttggaggaagcaatgttggaggtctagatgtgagcagcc 1380
Db 1611 gacagcagagacatgacactcttggaggaagcaatgttggaggtctagatgtgagcagcc 1670
Qy 1381 caagacatcgtgtgtgttggcgaagcaccgaagagatgtccagtcagtaaggttct 1440
Db 1671 caagacatcgtgtgtgttggcgaagcaccgaagagatgtccagtcagtaaggttct 1730
Qy 1441 gtgtacaccttgagaggaagcttccaagagatcaaccggaatcccgacatatctgcg 1500
Db 1731 gtgtacaccttgagaggaagcttccaagagatcaaccggaatcccgacatatctgcg 1790
Qy 1501 ttcatgtgagtggttcaacctgaacaagctgaagcccatagacaagaagttctgtctatc 1560
Db 1791 ttcatgtgagtggttcaacctgaacaagctgaagcccatagacaagaagttctgtctatc 1850
Qy 1561 aacaagttccatgagctgtctgtatgagaggaagttctgtgtgttattgttcaacgga 1620
Db 1851 aacaagttccatgagctgtctgtatgagaggaagttctgtgtgttattgttcaacgga 1910
Qy 1621 attactccagcagcatgtgaagctgcccaatcatgttcaagtaacaagatccgaattgagatc 1680
Db 1911 attactccagcagcatgtgaagctgcccaatcatgttcaagtaacaagatccgaattgagatc 1970
Qy 1681 gacaaatgtggagagagacaataaataaagatgtgtactgtgtgtgtgtgtgtgtgtgt 1740
Db 1971 gacaaatgtggagagagacaataaataaagatgtgtactgtgtgtgtgtgtgtgtgtgtgt 2030
Qy 1741 gacctcttggagacatgctgt 1800
Db 2031 gacctcttggagacatgctgt 2090
Qy 1801 gagcagaggaatcatcagaggt 1860
Db 2091 gagcagaggaatcatcagaggt 2150
Qy 1861 cagatgccctatccctgttcaagttgatacacttctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1920
Db 2151 cagatgccctatccctgttcaagttgatacacttctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2210
Qy 1921 cccctcttcaatgacgt 1980
Db 2211 cccctcttcaatgacgt 2270
Qy 1981 tatagaag 2040
Db 2271 tatagaag 2330
Qy 2041 ctctgtgttgaagctgt 2100
Db 2331 ctctgtgttgaagctgt 2390
Qy 2101 gtgtgtactctgtgaagttgaagaacactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2160
Db 2391 gtgtgtactctgtgaagttgaagaacactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2450
Qy 2161 ttctgtgtcgt 2220
Db 2451 ttctgtgtcgt 2510
Qy 2221 tccagagccaactgt 2280
Db 2511 tccagagccaactgt 2570
Qy 2281 taagttcgt 2340
Db 2571 taagttcgt 2630
Qy 2341 ctgtgtgtcctgt 2400
Db 2631 ctgtgtgtcctgt 2690
Qy 2401 ggcattggaggtgagtgaggaacaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2460
Db 2691 ggcattggaggtgagtgaggaacaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2750
Qy 2461 ctcaacacttgatctccatgt 2520
Db 2751 ctcaacacttgatctccatgt 2810

QY 2521 tacattgagcgtctcttccagcgcaatgccagcccttgatattctctgc 2580
|||||
Db 2811 tacattgagcgtctcttccagcgcaatgccagcccttgatattctctgc 2870
QY 2581 accaagctctactggttgcgaggaagtgatagaagagcaaccttgatccaacag 2640
|||||
Db 2871 accaagctctactggttgcgaggaagtgatagaagagcaaccttgatccaacag 2930
QY 2641 aagaagaatgcgaatctgcatgaggaagaaacccccccttgaaagcggtgtcc 2700
|||||
Db 2931 aagaagaatgcgaatctgcatgaggaagaaacccccccttgaaagcggtgtcc 2990
QY 2701 attcgaacctgtaaaagctctacagagatggatagaagtgcgtctcgaatgcctgga 2760
|||||
Db 2991 attcgaacctgtaaaagctctacagagatggatagaagtgcgtctcgaatgcctgga 3050
QY 2761 ctgaattttatgagggcgagatcacctctctctgcgacaaatgagacggggaaagc 2820
|||||
Db 3051 ctgaattttatgagggcgagatcacctctctctgcgacaaatgagacggggaaagc 3110
QY 2821 accacatgtcaatctgaacgggtgttccccccagacctgcgggacacgctataatctg 2880
|||||
Db 3111 accacatgtcaatctgaacgggtgttccccccagacctgcgggacacgctataatctg 3170
QY 2881 ggaagaagacatctgcgtctgagatgagcaacatccgcgagaaacctggtctctccca 2940
|||||
Db 3171 ggaagaagacatctgcgtctgagatgagcaacatccgcgagaaacctggtctctccca 3230
QY 2941 cataaagtgctgtttgacatgctgactgtctgaagaacacatctggtttctatgcgcgttg 3000
|||||
Db 3231 cataaagtgctgtttgacatgctgactgtctgaagaacacatctggtttctatgcgcgttg 3290
QY 3001 aagaagcctctctgagagacacgtgagagcgagatgagcaatgagccctgagatgtgt 3060
|||||
Db 3291 aagaagcctctctgagagacacgtgagagcgagatgagcaatgagccctgagatgtgt 3350
QY 3061 ttgcatcaagcagactggaagaacaaacacacacgctgttcaggtgagatgacagagag 3120
|||||
Db 3351 ttgcatcaagcagactggaagaacaaacacacacgctgttcaggtgagatgagagagag 3410
QY 3121 ctatctgtgaccttgacctgttcgagggagatctgaatctctgagatgaaccaca 3180
|||||
Db 3411 ctatctgtgaccttgacctgttcgagggagatctgaatctctgagatgaaccaca 3470
QY 3181 gctgtgtgtgagaccttaactccgcaagggaataatggagactgctctgaataaccgaca 3240
|||||
Db 3471 gctgtgtgtgagaccttaactccgcaagggaataatggagactgctctgaataaccgaca 3530
QY 3241 ggcgcgcacatattctctcttaacacacacatgagatgagcgagactctctggggagacag 3300
|||||
Db 3531 ggcgcgcacatattctctcttaacacacacatgagatgagcgagactctctggggagacag 3590
QY 3301 attgcacatctctccatgaggaagctgtgtgtgtgagcctccctcttctgaagaac 3360
|||||
Db 3591 attgcacatctctccatgaggaagctgtgtgtgtgagcctccctcttctgaagaac 3650
QY 3361 cagctgtgagacaggtctactacccctgaccttggatcaagaagaatgtggaatccctccacag 3420
|||||
Db 3651 cagctgtgagacaggtctactacccctgaccttggatcaagaagaatgtggaatccctccacag 3710
QY 3421 tctcgcgaagaacagtaagtaagctgtgtctatctgaataaagaagagacagtttctccag 3480
|||||
Db 3711 tctcgcgaagaacagtaagtaagctgtgtctatctgaataaagaagagacagtttctccag 3770
QY 3481 agcagttctgagctgagcctgagcagacgacatgagatgagacgctgacacatgctc 3540
|||||
Db 3771 agcagttctgagctgagcctgagcagacgacatgagatgagacgctgacacatgctc 3830
QY 3541 tctgtctctccacacatcaggaagcagtgctctgaagcccgctgtgtggaagacata 3600
|||||
Db 3831 tctgtctctccacacatcaggaagcagtgctctgaagcccgctgtgtggaagacata 3890

QY 3601 gggcatgagcgtgactatgctgcatatgaagctgtcgaaggagagccttctgaa 3660
|||||
Db 3891 gggcatgagcgtgactatgctgcatatgaagctgtcgaaggagagccttctgaa 3950
QY 3661 cctcttcatgagatgagatgagacggcctctcagacccctgagcatcttctagatagacatcca 3720
|||||
Db 3951 cctcttcatgagatgagatgagacggcctctcagacccctgagcatcttctagatagacatcca 4010
QY 3721 gagaagcaccctggaagaataatctccaaagggtgcgaaagagatgggtgtgtctgag 3780
|||||
Db 4011 gagaagcaccctggaagaataatctccaaagggtgcgaaagagatgggtgtgtctgag 4070
QY 3781 accctgaatgtaaccttgccagcaagacgaacagcgagccttcgggagcaagcagagc 3840
|||||
Db 4071 accctgaatgtaaccttgccagcaagacgaacagcgagccttcgggagcaagcagagc 4130
QY 3841 tgtcttcgcccgtctacatgaatgagatgctgtctatccaaatgattcttgacatagacca 3900
|||||
Db 4131 tgtcttcgcccgtctacatgaatgagatgctgtctatccaaatgattcttgacatagacca 4190
QY 3901 gaatccagagagacagactgtgtctcagtgagatgagtgacaaagggtctctaccagtgaa 3960
|||||
Db 4191 gaatccagagagacagactgtgtctcagtgagatgagtgacaaagggtctctaccagtgaa 4250
QY 3961 ggtctgaaatcttacaacagcaagtttgtgcacctttgtgaaagagactgtctaatgtcc 4020
|||||
Db 4251 ggtctgaaatcttacaacagcaagtttgtgcacctttgtgaaagagactgtctaatgtcc 4310
QY 4021 agacagagctcggaagaagattttgtctcagatgtctgtccagactgtgtgtgtgtcatc 4080
|||||
Db 4311 agacagagctcggaagaagattttgtctcagatgtctgtgtccagactgtgtgtgtcatc 4370
QY 4081 ggcctgtgttgaagcctgt 4140
|||||
Db 4371 ggcctgt 4430
QY 4141 cctctgagtgatcaacagaaagatcaacatltgtcagaatgtatgtctctgagagacagga 4200
|||||
Db 4431 cctctgagtgatcaacagaaagatcaacatltgtcagaatgtatgtctctgagagacagga 4490
QY 4201 accctggaactcttgaagcctctcacaagaacccctgtgtgtgtgtgtgtgtgtgtgtgtgt 4260
|||||
Db 4491 accctggaactcttgaagcctctcacaagaacccctgtgtgtgtgtgtgtgtgtgtgtgtgt 4550
QY 4261 ggaaccccaatcccaagacacgcccctgcagcgagggaggaagtggaacactgtcccca 4320
|||||
Db 4551 ggaaccccaatcccaagacacgcccctgcagcgagggaggaagtggaacactgtcccca 4610
QY 4321 gttcccaagacatcatggaactctctccagaatgggaactgtgaaacatgtcagaaccccttca 4380
|||||
Db 4611 gttcccaagacatcatggaactctctccagaatgggaactgtgaaacatgtcagaaccccttca 4670
QY 4381 cctgtcatgcaagtgtagcagcgaacaaatcaagaagaatgtctcctgtgtgtgtgtgtgtgt 4440
|||||
Db 4671 cctgtcatgcaagtgtagcagcgaacaaatcaagaagaatgtctcctgtgtgtgtgtgtgtgt 4730
QY 4441 gcaagggt 4500
|||||
Db 4731 gcaagggt 4790
QY 4501 acaaggaagaacatcttctggaattatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4560
|||||
Db 4791 acaaggaagaacatcttctggaattatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4850
QY 4561 ttaagagaagaatctgt 4620
|||||
Db 4851 ttaagagaagaatctgt 4910
QY 4621 aatacgaagcactctctccagatcgaagaatgaatgaatgaatgaatgaatgaatgaatgaat 4680
|||||
Db 4911 aatacgaagcactctctccagatcgaagaatgaatgaatgaatgaatgaatgaatgaatgaat 4970
QY 4681 caactaaagctgtgcgaaggaagctgtcgaatcgaatcttctcaacagctgtggaagatct 4740

|||||
Db 4971 caccataagctgccaagagcaggttcgcagatcagatttctcaacgcgttggaagattt 5030
OY 4741 atgacagagctggaacacagaaataatgltcaagggtgltgttcaataacaagggtgcat 4800
Db 5031 atgacagagctggaacacagaaataatgltcaagggtgltgttcaataacaagggtgcat 5090
OY 4801 gcaatcagctcttcctggaatgltcatcaacaatgcattctccgggccaactcgcaaaag 4860
Db 5091 gcaatcagctcttcctggaatgltcatcaacaatgcattctccgggccaactcgcaaaag 5150
OY 4861 ggaagaaacccatagccatlatagaaattactgcttcaatccatccctgatactcaacaag 4920
Db 5151 ggaagaaacccatagccatlatagaaattactgcttcaatccatccctgatactcaacaag 5210
OY 4921 cagcagctctcagaggtggtcctgagacacacagtgatgctctgtgtccatctgt 4980
Db 5211 cagcagctctcagaggtggtcctgagacacacagtgatgctctgtgtccatctgt 5270
OY 4981 gtaatcttgcaatgctcctgctccagcagcttgctgtaattccctgtaaccagagcg 5040
Db 5271 gtaatcttgcaatgctcctgctccagcagcttgctgtaattccctgtaaccagagcg 5330
OY 5041 gtacgcaagcaaaacacacgtcagttcaatcagtgagtgaaagcctgtcactacgtc 5100
Db 5331 gtacgcaagcaaaacacacgtcagttcaatcagtgagtgaaagcctgtcactacgtc 5390
OY 5101 tctaatcttgctggaataatgcaattacgttccctggcacaactgtaattatc 5160
Db 5391 tctaatcttgctggaataatgcaattacgttccctggcacaactgtaattatc 5450
OY 5161 ttcacatgctccacagaaagatccctatgctgctccacacatcblacgtgtgtagccct 5220
Db 5451 ttcacatgctccacagaaagatccctatgctgctccacacatcblacgtgtgtagccct 5510
OY 5221 ctactttgctgtatgggtggtcaatcaacctccacatgtaaccagcctcctgtgttc 5280
Db 5511 ctactttgctgtatgggtggtcaatcaacctccacatgtaaccagcctcctgtgttc 5570
OY 5281 aagatcccccagacacagcctatgctgctcaacagcgtgaaacctctcatgtgcatat 5340
Db 5571 aagatcccccagacacagcctatgctgctcaacagcgtgaaacctctcatgtgcatat 5630
OY 5341 ggcagcgtggaacacacgttctgtgctggaagcgtgtcacagcaataagctgaataataat 5400
Db 5631 ggcagcgtggaacacacgttctgtgctggaagcgtgtgtcacagcaataagctgaataataat 5690
OY 5401 gatacctggaagctcgttctgtgcttccacacatttctgctgggagcgaggtctatc 5460
Db 5691 gatacctggaagctcgttctgtgcttccacacatttctgctgggagcgaggtctatc 5750
OY 5461 gacatggtggaataaacacaggaatgctgatagcctggaaggtttggggagaatcgctt 5520
Db 5751 gacatggtggaataaacacaggaatgctgatagcctggaaggtttggggagaatcgctt 5810
OY 5521 gtgtacacattatctgtggaactgtgtggaggaacacctctgcgcagatggcggtgaagg 5580
Db 5811 gtgtacacattatctgtggaactgtgtggaggaacacctctgcgcagatggcggtgaagg 5870
OY 5581 gtgtgttcttcctcaatctactgtctgtatccagatcagatctctcatcagcgccagcct 5640
Db 5871 gtgtgttcttcctcaatctactgtctgtatccagatcagatctctcatcagcgccagcct 5930
OY 5641 gtaaatcaaaagctatcctctgtaatgataagaatgataatgtgagcgaggaaagacag 5700
Db 5931 gtaaatcaaaagctatcctctgtaatgataagaatgataatgtgagcgaggaaagacag 5990
OY 5701 agaattcttgatggtggaagcgaggaatgacalctagaagaatcaagaggttgacgaagata 5760
Db 5991 agaattcttgatggtggaagcgaggaatgacalctagaagaatcaagaggttgacgaagata 6050
OY 5761 tatagaaggaagcgagagcctgtctgtgacaggaattgctggtgcatctccctgtgtag 5820
|||||

Db 6051 tatagaaggaagcgagagcctgtctgtgacaggaattgctggtgcatctccctgtgtag 6110
OY 5821 tgccttggtccctccctggtggttgaatggtggtctggaataatcatcaacttcaagaatttaca 5880
Db 6111 tgccttggtccctccctggtggttgaatggtggtctggaataatcatcaacttcaagaatttaca 6170
OY 5881 ggaataaccactgttaaccagagagatgcttctcttaacaaataaglatatcttacaac 5940
Db 6171 ggaataaccactgttaaccagagagatgcttctcttaacaaataaglatatcttacaac 6230
OY 5941 atccatgaagctacatcaagaatggtcactgacctgaattgtgtgctccatccagagctg 6000
Db 6231 atccatgaagctacatcaagaatggtcactgacctgaattgtgtgctccatccagagagctg 6290
OY 6001 ttgactgggaagacaacgltgagattcttctgaccttttgagagagctcccaagagaagaa 6060
Db 6291 ttgactgggaagacaacgltgagattcttctgaccttttgagagagctcccaagagaagaa 6350
OY 6061 gtgtgcaaggtgtgtgagtgagtgagcgatccgaaactgggctcgtgaaagatggaagaaa 6120
Db 6351 gtgtgcaaggtgtgtgagtgagtgagcgatccgaaactgggctcgtgaaagatggaagaaa 6410
OY 6121 tatgtgttaactaagtgagagggcaacaacgcaagctctctacagcatggtttgattc 6180
Db 6411 tatgtgtgttaactaagtgagagggcaacaacgcaagctctctacagcatggtttgattc 6470
OY 6181 ggcgggctccctgtgtgttctgagatgaacccaacagagcatggaatcccaagccgg 6240
Db 6471 ggcgggctccctgtgtgttctgagatgaacccaacagagcatggaatcccaagccgg 6530
OY 6241 cgtgtctgtggaatltgtgctccctaaggtgtgtgaagagggagatcagtagtcttaca 6300
Db 6531 cgtgtctgtggaatltgtgctccctaaggtgtgtgaagagggagatcagtagtcttaca 6590
OY 6301 tctcaatagatggaagaaatgtgaagctcttgcactagagatggaatggaatcagtgaaatgga 6360
Db 6591 tctcaatagatggaagaaatgtgaagctcttgcactagagatggaatggaatcagtgaaatgga 6650
OY 6361 aggttcaaggtgctgtggaatgttccagcatcttaaaaaataagtttgagatgttataca 6420
Db 6651 aggttcaaggtgctgtggaatgttccagcatcttaaaaaataagtttgagatgttataca 6710
OY 6421 atagttgtaagaaatagcaaggttccaaacccggaacctgaagcctgtccagagattcttga 6480
Db 6711 atagttgtaagaaatagcaaggttccaaacccggaacctgaagcctgtccagagattcttga 6770
OY 6481 ctgtgcaattccctggaaggtgttcttaaaagaaacacccggaacatgctatacaatcagctt 6540
Db 6771 ctgtgcaattccctggaaggtgttcttaaaagaaacacccggaacatgctatacaatcagctt 6830
OY 6541 ccatcttcaatctctctcgtgccaagatatcagcatcctcccaaggcgaaagacga 6600
Db 6831 ccatcttcaatctctctcgtgccaagatatcagcatcctcccaaggcgaaagacga 6890
OY 6601 ctccacaatagaagaactactcgttcttcagacaacaactlgacaagtattgtgaactt 6660
Db 6891 ctccacaatagaagaactactcgttcttcagacaacaactlgacaagtattgtgaactt 6950
OY 6661 gccaaaggacaaagtataatagacaacatgaagcctcttatcacaaaaacacagaca 6720
Db 6951 gccaaaggacaaagtataatagacaacatgaagcctcttatcacaaaaacacagaca 7010
OY 6721 gtagtgagcgtgtgcagttctccacatcttcttaacagagatgagaaggtgaagaagaagctat 6780
Db 7011 gtagtgagcgtgtgcagttctccacatcttcttaacagagatgagaaggtgaagaagaagctat 7070
OY 6781 gtaatgaagaatccgtttcatacg 6804
Db 7071 gtaatgaagaatccgtttcatacg 7094

RESULT 3
AAF24685

QY	1201	aagaccttcaggaactgagctgctgtgtctccatgacctctggaagagacgtgtggagaggaactcagc	1260
Db	1523	aagaccttcacaggaactgctgtgtctccatgacctctggaagagacgtgtggagaggaactcagc	1582
QY	1261	cccaagatctggaactcttaatgagaaacagccaaagaaatggaacctgtccgagtcgctgtg	1320
Db	1583	cccaagaaatctggaactcttaatgagaaacagccaaagaaatggaacctgtccgagtcgctgtg	1642
QY	1321	gacacagaggaacaaatgacaactctttggaacaaacaaatgtgacgtcgttaagtgtgacagcc	1380
Db	1643	gacacagaggaacaaatgacaactctttggaacaaacaaatgtgacgtcgttaagtgtgacagcc	1702
QY	1381	caagacatccgtgctgtttttggccaagaccacgaagatgtccagttccagtaatgtgtct	1440
Db	1703	caagacatccgtgctgtttttggccaagaccacgaagatgtccagttccagtaatgtgtct	1762
QY	1441	gtgtacaccttggaagagagctcttccaaagagaaactaaacagagcaatccggacatatctcgc	1500
Db	1763	gtgtacaccttggaagagagctcttccaaagagaaactaaacagagcaatccggacatatctcgc	1822
QY	1501	ttcatgagagctgtgtccaacctgaaacaaagcttaagaaaccatgtgcaagaagatctgtctatc	1560
Db	1823	ttcatgagagctgtgtccaacctgaaacaaagcttaagaaaccatgtgcaagaagatctgtctatc	1882
QY	1561	aacaaagtccatcagagcgctgcgtcgagatgagagaggaagttctcgtgctgtatgtgttccactgga	1620
Db	1883	aacaaagtccatcagagcgctgcgtcgagatgagagaggaagttctcgtgctgtatgtgttccactgga	1942
QY	1621	attactccaaagcaacatctgagctgcgcccatctatgtccaagttaaaagatccgaatggaacat	1680
Db	1943	attactccaaagcaacatctgagctgcgcccatctatgtccaagttaaaagatccgaatggaacat	2002
QY	1681	gacaaatgtgagagagagacaataaatacgaagatgagttacctctggagacctgtgtctcgaagct	1740
Db	2003	gacaaatgtgagagagagacaataaatacgaagatgagttacctctggagacctgtgtctcgaagct	2062
QY	1741	gacctccttgagagacatgagctgtacgtctctgggggggcttcgcctactcttggaagatgtgtgtg	1800
Db	2063	gacctccttgagagacatgagctgtacgtctctgggggggcttcgcctactcttggaagatgtgtgtg	2122
QY	1801	gagcagagcaatcatcagagtgctgtcagcgggacacggagaagaactgtgtctatlatgcaaa	1860
Db	2123	gagcagagcaatcatcagagtgctgtcagcgggacacggagaagaactgtgtctatlatgcaaa	2182
QY	1861	cagatgcacctataccctgttaccgtttgattgacatcttctgcgggtgagatgagccggtcaatg	1920
Db	2183	cagatgcacctataccctgttaccgtttgattgacatcttctgcgggtgagatgagccggtcaatg	2242
QY	1921	ccacctctcatgagcgtgagctcgtgattctactcaatgagctgtgacatcatcaagagccatcgtg	1980
Db	2243	ccacctctcatgagcgtgagctcgtgattctactcaatgagctgtgacatcatcaagagccatcgtg	2302
QY	1981	tatagaagaagagcagcagcgtcgtgaagaagacaaatgcgatcatatgagctcgtgaaacagcata	2040
Db	2303	tatagaagaagagcagcagcgtcgtgaagaagacaaatgcgatcatatgagctcgtgaaacagcata	2362
QY	2041	ctcgcggtttagcgtgtctcatctagtagagccctacatctctctctgttggaacgctgagcgtgcta	2100
Db	2363	ctcgcggtttagcgtgtctcatctagtagagccctacatctctctctgttggaacgctgagcgtgcta	2422
QY	2101	gtgtgtaatccctgaagttaagaacactgtcgccttaacagtgaatcccaagcgtgagttgttc	2160
Db	2423	gtgtgtaatccctgaagttaagaacactgtcgccttaacagtgaatcccaagcgtgagttgttc	2482
QY	2161	ttctcgtgcggtgtttgtctgtgtgtaacaatccctcgaagtgctctcctgtattagaacaactcttc	2220
Db	2483	ttctcgtgcggtgtttgtctgtgtgtaacaatccctcgaagtgctctcctgtattagaacaactcttc	2542
QY	2221	ttcagagacaaacctgtgcagacagcctcgtgtggggacatcatcaacttcaagcgtgtacccgccc	2280
Db	2543	ttcagagacaaacctgtgcagacagcctcgtgtggggacatcatcaacttcaagcgtgtacccgccc	2602

[illegible]

|||||
Db 3683 gcctgagggaacaggtactaccctgaccttggtccaagaagctgtgaaatcctccctcagtt 3742
QY 3421 tccctgagaagaagtagtagcaactgtgtcatcacttgaaaaagggagcaggtttctcag 3480
Db 3743 tccctgcagaanaacagtagtagcaactgtgtcatcacttgaaaaagggagcaggtttctcag 3802
QY 3481 agcagttctgagctgctgctggcgagcagcacaatgagtagcaagcttgacacatcagtgctc 3540
Db 3803 agcagttctgagctgctgctggcgagcagcacaatgagtagcaagcttgacacatcagtgctc 3862
QY 3541 tctgtatctccaaacctcaatcaggaagcagtgtgtctgaaagcccgctgtgtgagaacata 3600
Db 3863 tctgtatctccaaacctcaatcaggaagcagtgtgtctgaaagcccgctgtgtgagaacata 3922
QY 3601 gggcagtagctgacactatgtgtctgcacatatgaaagctgtcgaaggagagccttctgtgaa 3660
Db 3923 gggcagtagctgacactatgtgtctgcacatatgaaagctgtcgaaggagagccttctgtgaa 3982
QY 3661 ctcttcatgagatlgatlgaccggtctcagaacctgaggcattctagtatcgacatca 3720
Db 3983 ctcttcatgagatlgatlgaccggtctcagaacctgaggcattctagtatcgacatca 4042
QY 3721 gagaagacctggaagaataatctctcagaagtgtgcggaagagagtgagggtgagtgctag 3780
Db 4043 gagaagacctggaagaataatctctcagaagtgtgcggaagagagtgagggtgagtgctag 4102
QY 3781 acctcagatgtagctctgtccagaagaacagacagcgagccttcggggagacaaagcagagc 3840
Db 4103 acctcagatgtagctctgtccagaagaacagacagcgagccttcggggagacaaagcagagc 4162
QY 3841 tgtcttcgcccgttcaactgagaatgtagtctgtcatcaaatgattctgacataaacca 3900
Db 4163 tgtcttcgcccgttcaactgagaatgtagtctgtcatcaaatgattctgacataaacca 4222
QY 3901 gaatccgagaagaagacagactgtgtccagtggagatgagtgagcaaaagtggtccatacagtgtaa 3960
Db 4223 gaatccgagaagaagacagactgtgtccagtggagatgagtgagcaaaagtggtccatacagtgtaa 4282
QY 3961 ggtctggaacttacaacagcaacagcttgtgtgccccttctgtggaagaagactgttaattgcc 4020
Db 4283 ggtctggaacttacaacagcaacagcttgtgtgccccttctgtggaagaagactgttaattgcc 4342
QY 4021 agacgagctcggaagaagatttttgtctcagaatgtctcttcagcagctgtgtttgtctgcat 4080
Db 4343 agacgagctcggaagaagatttttgtctcagaatgtctcttcagcagctgtgtttgtctgcat 4402
QY 4081 ggccttgttccaagctgtagcccttgacaccccttggcagaagtaaccagcctgtgaacttcag 4140
Db 4403 ggccttgttccaagctgtagcccttgacaccccttggcagaagtaaccagcctgtgaacttcag 4462
QY 4141 cctctgtagtacaacggaacagtagacatltgtcagaacatgtatctctctgaagacagga 4200
Db 4463 cctctgtagtacaacggaacagtagacatltgtcagaacatgtatctctctgaagacagga 4522
QY 4201 acctgtgaccttaaacgcccctcacaagaagacctgtgtctggagaccgctataggaa 4260
Db 4523 acctgtgaccttaaacgcccctcacaagaagacctgtgtgtctggagaccgctataggaa 4582
QY 4261 ggaacccaatcccaagacagcctctgcagcgagggaggaagagtgaaacactgtcccca 4320
Db 4583 ggaacccaatcccaagacagcctctgcagcgagggaggaagagtgaaacactgtcccca 4642
QY 4321 gtccccaagacatcatgacctctctccagaaatgggaactgtggaacatgacgaaccccttca 4380
Db 4643 gtccccaagacatcatgacctctctccagaaatgggaactgtggaacatgacgaaccccttca 4702
QY 4381 cctgtatgccagtgtagcagcgacaanaatcaagaagatgtgtcctgtgtgtctccccaagg 4440
Db 4703 cctgtatgccagtgtagcagcgacaanaatcaagaagatgtgtcctgtgtgtctccccaagg 4762
QY 4441 gcaaggggggtgtgtcctctccacaagaagaacaaacactgtcagatataccttcaaggacctg 4500
|||||

Db 4763 gcaaggggggtgtgtcctctccacaagaagaacaaacactgtcagatataccttccaggacctg 4822
QY 4501 acagaagaagaacattcggattatctgtgtgaagacgtatgtgcaagatcatagccaagaagc 4560
Db 4823 acagaagaagaacattcggattatctgtgtgaagacgtatgtgcaagatcatagccaagaagc 4882
QY 4561 ttaagaagaagaatctgtgtgaatgatttagtagtagcgagcttctccctgggtgtcagtt 4620
Db 4883 ttaagaagaagaatctgtgtgaatgatttagtagtagcgagcttctccctgggtgtcagtt 4942
QY 4621 aatcactcaagcacttccctccagatccagaagttaatgtatgcataccaacaaatgaagaaa 4680
Db 4943 aatcactcaagcacttccctccagatccagaagttaatgtatgcataccaacaaatgaagaaa 5002
QY 4681 caactaaagctggccaagagacagctctccagatcgattctccaacagcttggagagatt 4740
Db 5003 caactaaagctggccaagagacagctctccagatcgattctccaacagcttggagagatt 5062
QY 4741 atgacagagctggaacacagaaataatgtcaaggtgtgttcaataacaaggctgtgcat 4800
Db 5063 atgacagagctggaacacagaaataatgtcaaggtgtgttcaataacaaggctgtgcat 5122
QY 4801 gcaatcagctcttccctgaatgtcatcaacaatgccattccccgggccaacctgcaaaag 4860
Db 5123 gcaatcagctcttccctgaatgtcatcaacaatgccattccccgggccaacctgcaaaag 5182
QY 4861 gggagagaaccttagccattatggaattactgtcttccaatcaccctgaaatccacaag 4920
Db 5183 gggagagaaccttagccattatggaattactgtcttccaatcaccctgaaatccacaag 5242
QY 4921 cagcagctctcagaagtggtctctgtagtaccacaatcagtagtagtctctgtgtcatcgt 4980
Db 5243 cagcagctctcagaagtggtctctgtagtaccacaatcagtagtagtctctgtgtcatcgt 5302
QY 4981 gtaactcttgcaatgtctctgtgtccagcagcttgtgtatcttccatccagaagcgg 5040
Db 5303 gtaactcttgcaatgtctctgtgtccagcagcttgtgtatcttccatccagaagcgg 5362
QY 5041 gtcagcaagaacaaacacctgcagttcatcatcagtgtagtgaaacctgtcatcactgtctc 5100
Db 5363 gtcagcaagaacaaacacctgcagttcatcatcagtgtagtgaaacctgtcatcactgtctc 5422
QY 5101 tctaatttgcctgtagtatgtgcaattacgtgtccctgcgcaacactgtgtcatctatc 5160
Db 5423 tctaatttgcctgtagtatgtgcaattacgtgtgtccctgcgcaacactgtgtcatctatc 5482
QY 5161 ttcatctgcttccagcagaaggtccatagtgtctccacaacatctgctgtgtaagcctt 5220
Db 5483 ttcatctgcttccagcagaaggtccatagtgtctccacaacatctgctgtgtaagcctt 5542
QY 5221 ctactttgtctgtatgtgtgtcatcatcacactcctcatgtacccaagcctcttgtgttc 5280
Db 5543 ctactttgtctgtatgtgtgtcatcatcacactcctcatgtacccaagcctcttgtgttc 5602
QY 5281 aagatccccaagcacagcctatgtgtgtctcaacaggtgaacctctctgttgcatat 5340
Db 5603 aagatccccaagcacagcctatgtgtgtctcaacaggtgaacctctctgttgcatat 5662
QY 5341 ggcagcgtgtgcacacttgtgtctggaagctgttcaacgaacataagcttgaaataatcaat 5400
Db 5663 ggcagcgtgtgcacacttgtgtctggaagctgttcaacgaacataagcttgaaataatcaat 5722
QY 5401 gatatcctgtaagttccgtgttcttgatcttccacaattttgtccttggaagaggtccatc 5460
Db 5723 gatatcctgtaagttccgtgttcttgatcttccacaattttgtccttggaagaggtccatc 5782
QY 5461 gacatgtgtgaaaaacaggaatgagctgtgtagtcccttggaagaagtttggaagaatcgtctt 5520
Db 5783 gacatgtgtgaaaaacaggaatgagctgtgtagtcccttggaagaagtttggaagaatcgtctt 5842
QY 5521 gtgtcacatatacttggagactgtgtgtggaagaaacctctgcgcatgtgcgtgtgaagg 5580
Db 5843 gtgtcacatatacttggagactgtgtgtggaagaaacctctgcgcatgtgcgtgtgaagg 5902
|||||

[illegible]

Db	3443	ctatctgctgacctgagcccttgcccttgctcgagggtgatctaaggtgtgcaattcttgatgaataccaca	3501
Qy	3181	gctgctgtgtgaaccccttactcccgccaggggaaatagvgagctgctgtcgtgaataccagaa	3240
Db	3503	gctgtgtgtgaaccccttactcccgccaggggaaatagvgagctgctgtcgtgaataccagaa	3565
Qy	3241	ggcgcgacaattattctctctacaaaccaatgtgaatagaacgcgaactcctgtggggacag	3300
Db	3563	ggcgcgacaattattctctctacaaaccaatgtgaatagaacgcgtctcctgtggggacag	3622
Qy	3301	atggccatcatctcccaatggggaagctgtgcgtgtgtggccctcccgcttctcgaagac	3366
Db	3623	atggccatcatctcccaatggggaagctgtgcgtgtgtggccctcccgcttctcgaagac	3688
Qy	3361	cagctgtgggaacagcgtactaacctgtaaccttggtcaagaagaatgtgtgaatccctcag	3420
Db	3683	cagctgtgggaacagcgtactaacctgtaaccttggttccaagaagaatgtgtgaatccctcag	3744
Qy	3421	tctctcagaanaagcagcagcagctgtgtcgaacctgtgaacctgtgaagaagagacagcttcttcag	3480
Db	3743	tctctcagaanaagcagcagcagctgtgtcgaacctgtgtcaacctgtgaagaagagacagcttcttcag	3807
Qy	3481	agcagttctgtatgtctgtgcctgtggcgagcgaacatgtagaaggtgaacagctgtgacaatcgatgc	3540
Db	3803	agcagttctgtatgtctgtgcctgtggcgagcgaacatgtagaaggtgaacagctgtgacaatcgatgc	3865
Qy	3541	tctgtctatctccaacctcatagaagaacatgtgtctgaagcccggtctgtgtgaagaata	3600
Db	3863	tctgtctatctccaacctcatagaagaacatgtgtctgtgaagcccggtctgtgtgaagaata	3922
Qy	3601	gggcatagtgcgtgaacctatgtctgtcccaatagaagcgtctaaaggaaggaacctgtga	3660
Db	3923	gggcatagtgcgtgaacctatgtctgtcccaatagaagcgtctaaaggaaggaacctgtgtga	3982
Qy	3661	ctcttctcatgagattgtgaaccggctctctcaagacctgggaatttctaagtatgtgaatcca	3720
Db	3983	ctcttctcatgagattgtgaaccggctctctcaagacctgggaatttctaagtatgtgaatcca	4042
Qy	3721	gagacgaacccctgggaagaataatctctcaaggtgtgcgaagaagatgtgggtgtgaatctga	3780
Db	4043	gagacgaacccctgggaagaataatctctcaaggtgtgcgaagaagatgtgggtgtgaatctga	4102
Qy	3781	acctcaagatgtgtacaccttgccaagacgaagaacagcgcgctctcgtgggaacagcagaagc	3840
Db	4103	acctcaagatgtgtacaccttgccaagacgaagaacagcgcgctctcgtgggaacagcagaagc	4162
Qy	3841	tgctctgcgcggcttccactctgaagatgtatgctgcgtgataccaatgattctctgacatagaacca	3900
Db	4163	tgctctgcgcggcttccactctgaagatgtatgctgcgtgataccaatgattctctgacatagaacca	4222
Qy	3901	gaatccagaagagacagactgtctcagatgtgaatgtgaatagaaggctctaccaggtga	3960
Db	4223	gaatccagaagagacagactgtctcagatgtgaatgtgaatagaaggctctaccaggtga	4282
Qy	3961	ggctgggaaccttaacagcgacagattgttggcccttgttggaagaagctctaatggcc	4020
Db	4283	ggctgggaaccttaacagcgacagattgttggcccttgttggaagaagctctaatggcc	4342
Qy	4021	agacgcgagctcggaagaagatttttgtccagatgtgtcttgccgcgcgtgtttgtctgcat	4080
Db	4343	agacgcgagctcggaagaagatttttgtctcagatgtgtcttgccgcgcgtgtttgtctgcat	4402
Qy	4081	ggccttgttgaagcctgtatcggtgcacaccttggccaagtacccagcctvggaacttcag	4140
Db	4403	ggccttgttgaagcctgtatcggtgcacaccttggccaagtacccagcctvggaacttcag	4462
Qy	4141	ccctgtgaatgtacaagaaagctgaacaattgtgtcaagaatgtgtccctgtgaagaacgtga	4200
Db	4463	ccctgtgaatgtacaagaaagctgaacaattgtgtcagcaatgtatgtcctcgtgaagaacgtga	4522
Qy	4201	acctgtgaacctttaaagcgcctcaccaaaagacctgtgctcgtgggaacccgctgtatgaa	4260
Db	4523	acctgtgaacctttaaagcgcctcaccaaaagacctgtgctcgtgggaacccgctgtatgaa	4582

QY 4261 ggaacccaatcccaagacgcccctgcccagggaggaagatggaacactgccca 4320
|||||
Db 4583 ggaacccaatcccaagacgcccctgcccagggaggaagatggaacactgccca 4642
QY 4321 gtccccagaccatcatggaactcttcaggaatggaaatggaacacttca 4380
|||||
Db 4643 gtccccagaccatcatggaactcttcaggaatggaaatggaacacttca 4702
QY 4381 cctgcacgtcgaatgtagcgcgaacaaatcaagaatgctgcctggtgtccccaagg 4440
|||||
Db 4703 cctgcacgtcgaatgtagcgcgaacaaatcaagaatgctgcctggtgtccccaagg 4762
QY 4441 gcaagggggtgcctccccaagaagaaacaaactgcagatactcctcaagactg 4500
|||||
Db 4763 gcaagggggtgcctccccaagaagaaacaaactgcagatactcctcaagactg 4822
QY 4501 acaaggaagaaacttcggaatctcgtgtgaagacgtatgtgacagatcaagccaaagc 4560
|||||
Db 4823 acaaggaagaaacttcggaatctcgtgtgaagacgtatgtgacagatcaagccaaagc 4882
QY 4561 ttaaagacacagatctcgtgtgaatgtagttagtgcggccttcccttggtgtcagt 4620
|||||
Db 4883 ttaaagacacagatctcgtgtgaatgtagttagtgcggccttcccttggtgtcagt 4942
QY 4621 aatactcaagcacttccctccgaatcaagaatgtaatgtagtcccaacaaatgaagaa 4680
|||||
Db 4943 aatactcaagcacttccctccgaatcaagaatgtaatgtagtcccaacaaatgaagaa 5002
QY 4681 caactaaagctgcgcaagagacgtctcgcagatcgtatcccaacagcttggaagatc 4740
|||||
Db 5003 caactaaagctgcgcaagagacgtctcgcagatcgtatcccaacagcttggaagatc 5062
QY 4741 atgacagagactgcgacacagaataatgtaaggtgtgtgtcaatacaagggtgtgcat 4800
|||||
Db 5063 atgacagagactgcgacacagaataatgtaaggtgtgtgtcaatacaagggtgtgcat 5122
QY 4801 gcaatcagccttccctccgaatgtaacaaatgcaacttcccgggccaaactgcgcaag 4860
|||||
Db 5123 gcaatcagccttccctccgaatgtaacaaatgcaacttcccgggccaaactgcgcaag 5182
QY 4861 ggaagagaacctagacatlaatggaatgcttcaatcatccctgaaatctcaacaa 4920
|||||
Db 5183 ggaagagaacctagacatlaatggaatgcttcaatcatccctgaaatctcaacaa 5242
QY 4921 cagcagctctcaagaggtgtgctctgaatgaacacatcagtgatgtccttggtccatctgt 4980
|||||
Db 5243 cagcagctctcaagaggtgtgctctgaatgaacacatcagtgatgtccttggtccatctgt 5302
QY 4981 gtcaatttggaatgcttccctccgaagcgttctgctatctcgtatcccaagagcgg 5040
|||||
Db 5303 gtcaatttggaatgcttccctccgaagcgttctgctatctcgtatcccaagagcgg 5362
QY 5041 gtcaagaaagaaacacactgcagttcatcagtggaatggaactgtcatctactgctc 5100
|||||
Db 5363 gtcaagaaagaaacacactgcagttcatcagtggaatggaactgtcatctactgctc 5422
QY 5101 tctaatttgctggatagtggaatgaatggttctcctgcgaacactggtcatatcatc 5160
|||||
Db 5423 tctaatttgctggatagtggaatgaatggttctcctgcgaacactggtcatatcatc 5482
QY 5161 ttcatctgctccagcagaagtccatagtggtccccaacaaatgcgcgtgtgtagccctt 5220
|||||
Db 5483 ttcatctgctccagcagaagtccatagtggtccccaacaaatgcgcgtgtgtagccctt 5542
QY 5221 ctactttgtcgtatggtgtgtcaatcaacacactcatatgtaacagcctcttggttc 5280
|||||
Db 5543 ctactttgtcgtatggtgtgtcaatcaacacactcatatgtaacagcctcttggttc 5602
QY 5281 aagatcccaagacagcctatggtgtgtcaacagcgtgaacactcttaattggaat 5340
|||||
Db 5603 aagatcccaagacagcctatggtgtgtcaacagcgtgaacactcttaattggaat 5662

QY 5341 ggcagcgtggccacacttgtgtcgtgagctgttcaacccaataagctgaatatacat 5400
|||||
Db 5663 ggcagcgtggccacacttgtgtcgtgagctgttcaacccaataagctgaatatacat 5722
QY 5401 gatatcccaagctcgtgtgtcgtatcttccacaatttgcctggaacgaaggctcatc 5460
|||||
Db 5723 gatatcccaagctcgtgtgtcgtatcttccacaatttgcctggaacgaaggctcatc 5782
QY 5461 gacatgtgtgaaacacagacgaatgctgtagtccctcggaagagtttggggaatccgctt 5520
|||||
Db 5783 gacatgtgtgaaacacagacgaatgctgtagtccctcggaagagtttggggaatccgctt 5842
QY 5521 ggtacacatatactctggagactgtgtggagcaaacctcttcgcaatgycgtgaagg 5580
|||||
Db 5843 ggtacacatatactctggagactgtgtggagcaaacctcttcgcaatgycgtgaagg 5902
QY 5581 ggtgtgtcttccatctactgtgttctgaatccagtaacagatctcctcaatcagccagact 5640
|||||
Db 5903 ggtgtgtcttccatctactgtgttctgaatccagtaacagatctcctcaatcagccagact 5962
QY 5641 gtaaatgcaaaactatccctccctgaatgtagatgtagatgtgtgagcgggaagacag 5700
|||||
Db 5963 gtaaatgcaaaactatccctccctgaatgtagatgtagatgtgtgagcgggaagacag 6022
QY 5701 agaattctgtatggtgtgagccagaaatgacatcttaagaatcaagagttgacgaagata 5760
|||||
Db 6023 agaattctgtatggtgtgagccagaaatgacatcttaagaatcaagagttgacgaagata 6082
QY 5761 tataagaagaagcgaagacgtcgtgtgacagatcttcgtgtgagatctccctcgtgtgag 5820
|||||
Db 6083 tataagaagaagcgaagacgtcgtgtgacagatcttcgtgtgagatctccctcgtgtgag 6142
QY 5821 tgccttggtcctcctggaggttaatggtggcgtggaataatcaacacttcaagaatgtaaca 5880
|||||
Db 6143 tgccttggtcctcctggaggttaatggtggcgtggaataatcaacacttcaagaatgtaaca 6202
QY 5881 ggaatatacacgtgttaacgaagagatgcttcccttaacaaatagatcttatcaaac 5940
|||||
Db 6203 ggaatatacacgtgttaacgaagagatgcttcccttaacaaatagatcttatcaaac 6262
QY 5941 atccatgaatgtaatgaacagatggggtacttgcctcagtttgtagtccatcaacagctg 6000
|||||
Db 6263 atccatgaatgtaatgaacagatggggtacttgcctcagtttgtagtccatcaacagctg 6322
QY 6001 ttgactgggaagaaacacgtggaatcttgcctttagaagagatcccaagagaagaa 6060
|||||
Db 6323 ttgactgggaagaaacacgtggaatcttgcctttagaagagatcccaagagaagaa 6382
QY 6061 gttgcgaaggtgtgtgagtggtgcgacttcggaactggtgcctgtgaagtatggaagaaaa 6120
|||||
Db 6383 gttgcgaaggtgtgtgagtggtgcgacttcggaactggtgcctgtgaagtatggaagaaaa 6442
QY 6121 tatgctggttaactatgttgaggaacaaacgaacgtctctcaacagatggtcttgatc 6180
|||||
Db 6443 tatgctggttaactatgttgaggaacaaacgaacgtctctcaacagatggtcttgatc 6502
QY 6181 ggcgggctcctcgtgtgtgttcttgaatgaacccaacacagagcatggaatcccaagccgg 6240
|||||
Db 6503 ggcgggctcctcgtgtgtgttcttgaatgaacccaacacagagcatggaatcccaagccgg 6562
QY 6241 cgggtcttctgtggaatgtgcctcaaatgtgttcaagagagggagatcaatagtgcttaaa 6300
|||||
Db 6563 cgggtcttctgtggaatgtgcctcaaatgtgttcaagagagggagatcaatagtgcttaaa 6622
QY 6301 tctcaatagtagtgaagaatgtgaagctcttctgacataggaatggaatcaatggttcaatgga 6360
|||||
Db 6623 tctcaatagtagtgaagaatgtgaagctcttctgacataggaatggaatcaatggttcaatgga 6682
QY 6361 aggttcaggtccttgcgaggtgtccagacatcaaaaaataggttgcgagatggttataca 6420
|||||
Db 6683 aggttcaggtccttgcgaggtgtccagacatcaaaaaataggttgcgagatggttataca 6742
QY 6421 atagttgtaagataagcaggttccaaacccgagactgtgaagcctgttcaagatcttcttga 6480

PS Claim 27, Page 144-150; 211pp; English.
xx
CC The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC ATP hydrolysis to transport a wide variety of substrates across the
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC Tangier disease, a genetic disorder characterised by abnormal
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC 9q22-q31. The ABC1 genes and proteins are useful for developing
CC pharmaceutical agents for the treatment of heart disease and other
CC disorders associated with hypercholesterolemia and atherosclerosis. The
CC genes are useful for developing screening assays to screen for compounds
CC that regulate the expression of genes associated with cholesterol
CC transport. The genes and proteins are also useful for are also useful
CC as diagnostic indicators of cardiovascular disease and other disorders
CC associated with hypercholesterolemia.
xx
SQ Sequence 10474 BP; 2306 A; 2305 C; 2416 G; 2843 T; 4 other;

Query Match	100.0%	Score 6802.4	DB 22	Length 10474
Best Local Similarity	100.0%	Pred. No. 0		
Matches 6803	Conservative 0	Mismatches 1	Indels 0	Gaps 0

[illegible]

QY 721 agaacactaactctacatctccctcccgagcaagagctggtgaagccacaaaaca 780
|||||
Db 1043 agaacactaactctacatctccctcccgagcaagagctggtgaagccacaaaaca 1102
QY 781 ttgcgtacatagctctgggactctggcccaagagcttcaacatagaagctggaattac 840
|||||
Db 1103 ttgcgtacatagctctgggactctggcccaagagcttcaacatagaagctggaattac 1162
QY 841 atgcgaacagagagtgatgtttctgaaccaatgtgaacagctccagctcccaacalc 900
|||||
Db 1163 atgcgaacagagagtgatgtttctgaaccaatgtgaacagctccagctcccaacalc 1222
QY 901 taccagagctgtctcgtatgttcgcgggcatcccgagggaggggctgtaagataag 960
|||||
Db 1223 taccagagctgtctcgtatgttcgcgggcatcccgagggaggggctgtaagataag 1282
QY 961 tctctcaactgglatagagacaacaactacaagccctcttgagagcaatgcaactgag 1020
|||||
Db 1283 tctctcaactgglatagagacaacaactacaagccctcttgagagcaatgcaactgag 1342
QY 1021 gaagatgctgaaacctctctatacgaacctctactctactgaattgataag 1080
|||||
Db 1343 gaagatgctgaaacctctctatacgaacctctactctactgaattgataag 1402
QY 1081 aatttgagctagctcctctcccgcatctctgaaagctctgaagcgtctgctgt 1140
|||||
Db 1403 aatttgagctagctcctctcccgcatctctgaaagctctgaagcgtctgctgt 1462
QY 1141 ggggaatccctgtalatacactctgaacctccagccacaagcaggtcaatgctgagtgaac 1200
|||||
Db 1463 ggggaatccctgtalatacactctgaacctccagccacaagcaggtcaatgctgagtgaac 1522
QY 1201 aagaacctccaggaacctgctgtgttccatgtatctgaaagcagctgaggagaaactcaac 1260
|||||
Db 1523 aagaacctccaggaacctgctgtgttccatgtatctgaaagcagctgaggagaaactcaac 1582
QY 1261 cccaagatctggaacctctctatgagaaacagccaagaatgagacctctcccgatgctgtg 1320
|||||
Db 1583 cccaagatctggaacctctctatgagaaacagccaagaatgagacctctcccgatgctgtg 1642
QY 1321 gacagcagggacaatgacaacttttggaacagcagcttgatgagcttaagattgagaccc 1380
|||||
Db 1643 gacagcagggacaatgacaacttttggaacagcagcttgatgagcttaagattgagaccc 1702
QY 1381 caagacatcgtgctgtttttggccaagcaccaggaagatgctcaagctcaatgtgtct 1440
|||||
Db 1703 caagacatcgtgctgtttttggccaagcaccaggaagatgctcaagctcaatgtgtct 1762
QY 1441 gtgtacacctgagagagaagcttccaacgagactaaccaagcaatcccgaccatctcgc 1500
|||||
Db 1763 gtgtacacctgagagagaagcttccaacgagactaaccaagcaatcccgaccatctcgc 1822
QY 1501 ttcatgagatgtgttcaacctgaaacagctagaacccaatagcaacagaagctctgctcacc 1560
|||||
Db 1823 ttcatgagatgtgttcaacctgaaacagctagaacccaatagcaacagaagctctgctcacc 1882
QY 1561 aacaagtctcatgagctgtctgagatgaggaagttcttggtctgtattgttctcactgga 1620
|||||
Db 1883 aacaagtctcatgagctgtctgagatgaggaagttcttggtctgtattgttctcactgga 1942
QY 1621 attactccaagcagcatttgagctgtcccatcatgctcaagatacagaatccgaatgagcat 1680
|||||
Db 1943 attactccaagcagcatttgagctgtcccatcatgctcaagatacagaatgagcat 2002
QY 1681 gacaatgtgagagagacaataaataatcaagatggttactggaacctggtctctcagact 1740
|||||
Db 2003 gacaatgtgagagagacaataaataatcaagatggttactggaacctggtctctcagact 2062
QY 1741 gacctctttagagacatgctgctgctggtggtggtctgctcactctgcaagatgtgtg 1800
|||||
Db 2063 gacctctttagagacatgctgctgctggtggtggtctgctcactctgcaagatgtgtg 2122

QY 1801 gacgagcaatcatcaggtgtctgacgggcaacgagagaanaactggtgtctatagcaaa 1860
|||||
Db 2123 gacgagcaatcatcaggtgtgtgacgggcaacgagagaanaactggtgtctatagcaaa 2182
QY 1861 cagatgccctatccctgttactgctgatacattctctcggtgtgatagacggtcaat 1920
|||||
Db 2183 cagatgccctatccctgttactgctgatacattctctcggtgtgatagacggtcaat 2242
QY 1921 cccctcttcatgagcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1980
|||||
Db 2243 cccctcttcatgagcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 2302
QY 1981 tatgagaagagagcagctgtaaaagacatgctggaatcaltggtggtcgtgacaacagata 2040
|||||
Db 2303 tatgagaagagagcagctgtaaaagacatgctggaatcaltggtggtcgtgacaacagata 2362
QY 2041 cctctggtttagctgttcaatagacctcaatctcctctctctgtgaaagctggtcgtcta 2100
|||||
Db 2363 cctctggtttagctgttcaatagacctcaatctcctctctctgtgaaagctggtcgtcta 2422
QY 2101 gtgtgcatccctgaaagttaagaaacctgtgcccctacagtgatcccaagctgtgttctgtc 2160
|||||
Db 2423 gtgtgcatccctgaaagttaagaaacctgtgcccctacagtgatcccaagctgtgttctgtc 2482
QY 2161 ttctgtctcgt 2220
|||||
Db 2483 ttctgtctcgt 2542
QY 2221 tccagagcaaaccttgagcagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2280
|||||
Db 2543 tccagagcaaaccttgagcagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2602
QY 2281 taagctcgt 2340
|||||
Db 2603 taagctcgt 2662
QY 2341 ctgtcgtctcctgt 2400
|||||
Db 2663 ctgtcgtctcctgt 2722
QY 2401 ggcattgagatgagctgtggaacacctgttttgaagcttccctgtggaagagagcttcaat 2460
|||||
Db 2723 ggcattgagatgagctgtggaacacctgttttgaagcttccctgtggaagagagcttcaat 2782
QY 2461 ctccacctctgactctcatgatagtctgtttgaacacctctctctatgggtgatagcctgg 2520
|||||
Db 2783 ctccacctctgactctcatgatagtctgtttgaacacctctctctatgggtgatagcctgg 2842
QY 2521 tacattgagctgtgtcttccagcagctagcgaatttcccaagcctgtglatctcctgtc 2580
|||||
Db 2843 tacattgagctgtgtcttccagcagctagcgaatttcccaagcctgtglatctcctgtc 2902
QY 2581 accaagctcctactgt 2640
|||||
Db 2903 accaagctcctactgt 2962
QY 2641 aagagaaatgtcaagaatctgcaatgaggaagaaacccaaccttgaagctgtgctgtcc 3022
|||||
Db 2963 aagagaaatgtcaagaatctgcaatgaggaagaaacccaaccttgaagctgtgctgtcc 3082
QY 2701 attcgaacctgtgtaaaagtctaccagagatggaatgaaagtgtgctgtcagatgcctgga 2760
|||||
Db 3023 attcgaacctgtgtaaaagtctaccagagatggaatgaaagtgtgctgtcagatgcctgga 3082
QY 2761 ctgaatttttaagagggccaagatacctcctctcctgtgggccaacatgagagcggaagagcg 2820
|||||
Db 3083 ctgaatttttaagagggccaagatacctcctcctcctgtgggccaacatgagagcggaagagcg 3142
QY 2821 accacatgttcaatccttacacgggtgttcccccagacctcgggacacggcctacatcctg 2880
|||||
Db 3143 accacatgttcaatccttacacgggtgttcccccagacctcgggacacggcctacatcctg 3202
QY 2881 ggaataagacatcgtctgtgagatgagacacatccggcagaacctgtgggtgtgtgtccag 2940

Db	3203	ggaaaaagacattcgcgtctgagatgagacaccatcccgagagacctggggtctctcccaag	3265
QY	2941	cataacgctgctgtttggaatgctgactgctcgaaagacaacatctggttctatgcccgttgc	3000
Db	3263	cataaagctgctgtttggaatgctgactgctcgaaagacaacatctggttctatgcccgttgc	3322
QY	3001	aaaaggctctcgaaagacaacgctgaaagcggagatgagatgagatgacctgagatttgtt	3060
Db	3323	aaaaggctctcgaaagacaacgctgaaagcggagatgagatgagatgacctgagatttgtt	3380
QY	3061	ttgccaataagcaagctgaaaaagcaaaacaagccagctgttcaggtggaatgcaagaagaag	3120
Db	3383	ttgccaataagcaagctgaaaaagcaaaacaagccagctgttcaggtggaatgcaagaagaag	3442
QY	3121	ctatctgtgacctgagacctgtgttcggggggtctaaagttgtaattcttgatgaaccaca	3180
Db	3443	ctatctgtgacctgagacctgtgttcggggggtctaaagttgtaattcttgatgaaccaca	3502
QY	3181	gctgtgtgagaccttactcccgagagggaatactggagatgtgtctgtcgataaccgaca	3240
Db	3503	gctgtgtgagaccttactcccgagagggaatactggagatgtgtctgtcgataaccgaca	3566
QY	3241	ggccgacacattatctctctcaacacacatgatatgaagcggagtccttgagggaacag	3300
Db	3563	ggccgacacattatctctctcaacacacatgatatgaagcggagtccttgagggaacag	3622
QY	3301	attgcaatcatctcccatgagaaagctgtgtgtgtgacctccctctgtcttgtaagac	3360
Db	3623	attgcaatcatctcccatgagaaagctgtgtgtgtgacctccctctgtcttgtaagac	3682
QY	3361	cagctgggaaacagctactactcctgagacctgtgtcaagaaagatgtgaaatctcctcag	3420
Db	3683	cagctgggaaacagctactactcctgagacctgtgtcaagaaagatgtgaaatctcctcag	3742
QY	3421	tccttcanaaaacagtaagtaagacatgtgtctactccttaaaaagagagacagttttctag	3480
Db	3743	tccttcanaaaacagtaagtaagacatgtgtctactccttaaaaagagagacagttttctag	3802
QY	3481	agcagcttctgactgctgagcctggcgagcgacatgaaagatgaaacgctgacatctgaatgc	3540
Db	3803	agcagcttctgactgctgagcctggcgagcgacatgaaagatgaaacgctgacatctgaatgc	3862
QY	3541	tcgtgtatctcaaaccccatcaagaaagacatgtgtctgaagcccgctggttgaaacaata	3600
Db	3863	tcgtgtatctcaaaccccatcaagaaagacatgtgtctgaagcccgctggttgaaacaata	3922
QY	3601	gggcaatgagctgacactatgtgtgtgccaataagacgtgacaaagagggagcctttgaa	3660
Db	3923	gggcaatgagctgacactatgtgtgtgccaataagacgtgacaaagagggagcctttgaa	3982
QY	3661	ctctttcaatgagattgattgagccggtctctcaagacctgagaccttcaattatgagcatcca	3720
Db	3983	ctctttcaatgagattgattgagccggtctctcaagacctgagaccttcaattatgagcatcca	4042
QY	3721	gagaagacacctgagaaagaaataatctctcaagatgtgcgaagagatgtgggttgatgctag	3780
Db	4043	gagaagacacctgagaaagaaataatctctcaagatgtgcgaagagatgtgggttgatgctag	4102
QY	3781	acctcaagatgtgtactcttgccagcaagaagaacaaagcgggaccttcgggacaagaagac	3840
Db	4103	acctcaagatgtgtactcttcggcaagaagaagaacaaagcgggaccttcgggacaagaagac	4162
QY	3841	tgcttcgcccgggttcaacttgaaagatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	3900
Db	4163	tgcttcgcccgggttcaacttgaaagatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	4222
QY	3901	gaatccagagagacagctgtgtctcagctggagatggaatgagcaaaaggtctctaccaggtgaa	3960
Db	4223	gaatccagagagacagctgtgtctcagctggagatggaatgagcaaaaggtctctaccaggtgaa	4282
QY	3961	ggctggaaacttaacagcaaacgcttctgtgaccttctgtgaaagagactgtctaattgccc	4020

Dh	4283	ggctggaaccttaacagcaacagcttgctgccccttttggaagaagatgtaattgac	43432
Qy	4021	agaacgagctcggaaagagattttttgtccagatgtctctgcagctgtgtttgtcgaat	40800
Dh	4343	agaacgagctcggaaagagattttttgtccagatgtctctgcagctgtgtttgtcgaat	44020
Qy	4081	ggcctgtgttcacgcgcatctgtgcacaccttggcaagtaaccacgcttgaaacttaag	41400
Dh	4403	ggccttggtgttcagcctcgatctgtgcacaccttggcaagtaaccacgcttgaaacttaag	44620
Qy	4141	cccttgatgtatacaacgaaagtaacattgttgaagaaatgtctctcgtgaagacgysga	42000
Dh	4463	cccttgatgtatacaacgaaagtaacattgttgaagaaatgtctctcgtgaagacgysga	45222
Qy	4201	accctggagacactttaaagccgctctacccaagacccttgcttcggagaccgcgtgtgaa	42600
Dh	4523	accctggagacactttaaagccgctctacccaagacccttgcttcggagaccgcgtgtgaa	45822
Qy	4261	ggaaaccccaatcccaagacaacgcccctgcagacgagggagaaagatgtgaacccatcccca	43200
Dh	4583	ggaaaccccaatcccaagacaacgcccctgcagacgagggagaaagatgtgaacccatcccca	46422
Qy	4321	gttcccgaagaccatcatatgatccctcttcagaaatgggaactgtgacaatgcagaaccttca	43800
Dh	4643	gttcccgaagaccatcatatgatccctcttcagaaatgggaactgtgacaatgcagaaccttca	47020
Qy	4381	ccctgaatccagctgttaacagacgaaataacaaagaatgtctcctgtgtgtcccccaggg	44400
Dh	4703	ccctgaatccagctgttaacagacgaaataacaaagaatgtctcctgtgtgtcccccaggg	47622
Qy	4441	gcaaggggggctgtcctcctccacaagaagaaacaaacaaactgcagatactcttcaagacctg	45000
Dh	4763	gcaaggggggctgtcctcctccacaagaagaaacaaacaaactgcagatactcttcaagacctg	48222
Qy	4501	acaaggaagaagaacatttgagttatctctgtgaaagacgtatgtcacataatagccaaaagc	45600
Dh	4823	acaaggaagaagaacatttgagttatctctgtgaaagacgtatgtcacataatagccaaaagc	48822
Qy	4561	ttaaagaaacaaagatcttggtgaaatgtgaaatgtgaaatgtgaaatgtgaaatgtgaaat	46200
Dh	4883	ttaaagaaacaaagatcttggtgaaatgtgaaatgtgaaatgtgaaatgtgaaatgtgaaat	49422
Qy	4621	aatctcaagacacttctctccgagtcgaagatgaatgatgtgcataaaacaatgaagaaga	46800
Dh	4943	aatctcaagacacttctctccgagtcgaagatgaatgatgtgcataaaacaatgaagaaga	50022
Qy	4681	cacctaaagctgtgcgaagagacagttctgtcagatctgaattctctcaacagatttggaagattt	47400
Dh	5003	cacctaaagctgtgcgaagagacagttctgtcagatctgaattctctcaacagatttggaagattt	50622
Qy	4741	atgacaggaactgtgacacacagaataatgttcaagtgtagtggttcaataacaaagggcttgcat	48000
Dh	5063	atgacaggaactgtgacacacagaataatgttcaagtgtagtggttcaataacaaagggcttgcat	51222
Qy	4801	gcaatcagcctcttctcgtgaatgttcaatcaacaatgtccattctccggggccaacctgtcaaaag	48600
Dh	5123	gcaatcagcctcttctcgtgaatgttcaatcaacaatgtccattctccggggccaacctgtcaaaag	51822
Qy	4861	ggagagaaacctagcatattgaattgaattactgtcttcaatcatccctgtaatctcaacag	49200
Dh	5183	ggagagaaacctagcatattgaattgaattactgtcttcaatcatccctgtaatctcaacag	52422
Qy	4921	cagagagctctcgaagtggtgtcgtatgagaccacataatgtagatgtctctgttccatctgt	49800
Dh	5243	cagagagctctcgaagtggtgtcgtatgagaccacataatgtagatgtctctgttccatctgt	53022
Qy	4981	gtcaactcttgcaatgtctccttgcgccagacagcttctgtcgtatcttccgtatcccaagagcgg	50400
Dh	5303	gtcaactcttgcaatgtctccttgcgccagacagcttctgtcgtatcttccgtatcccaagagcgg	53622
Qy	5041	gtcagcaagaacaaacacactgtcagttcatcagtgtagatgtgaagcctgtlcatctactgtctc	51000
Dh	5363	gtcagcaagaacaaacacactgtcagttcatcagtgtagatgtgaagcctgtlcatctactgtctc	54222

QY 5101 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5160
 DB 5423 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5482
 QY 5161 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5220
 DB 5483 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5542
 QY 5221 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5280
 DB 5543 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5602
 QY 5281 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5340
 DB 5603 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5662
 QY 5341 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5400
 DB 5663 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5722
 QY 5401 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5460
 DB 5723 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5782
 QY 5461 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5520
 DB 5783 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5842
 QY 5521 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5580
 DB 5843 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5902
 QY 5581 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5640
 DB 5903 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5962
 QY 5641 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5700
 DB 5963 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6022
 QY 5701 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5760
 DB 6023 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6082
 QY 5761 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5820
 DB 6083 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6142
 QY 5821 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5880
 DB 6143 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6202
 QY 5881 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 5940
 DB 6203 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6262
 QY 5941 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6000
 DB 6263 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6322
 QY 6001 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6060
 DB 6323 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6382
 QY 6061 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6120
 DB 6383 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6442
 QY 6121 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6180
 DB 6443 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6502

QY 6181 ggcgggctctctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6240
 DB 6503 ggcgggctctctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6562
 QY 6241 ggcgggctctctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6300
 DB 6563 ggcgggctctctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6622
 QY 6301 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6360
 DB 6623 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6682
 QY 6361 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6420
 DB 6683 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6742
 QY 6421 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6480
 DB 6743 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6802
 QY 6481 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6540
 DB 6803 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6862
 QY 6541 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6600
 DB 6863 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6922
 QY 6601 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6660
 DB 6923 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6982
 QY 6661 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6720
 DB 6983 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 7042
 QY 6721 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6780
 DB 7043 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 7102
 QY 6781 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 6840
 DB 7103 tctaatcttctgctggatatagtgcaatagctgtccctgcacacatgtgcatatcatc 7126

RESULT 6
 AAF24708
 ID AAF24708 standard; DNA; 10474 BP.
 XX
 AC AAF24708;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
 XX
 KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
 KW apolipoprotein-mediated mobilization; cholesterol; Tangier disease;
 KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
 KW atherosclerosis; cholesterol transport; ss.
 KW
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 323..7108
 FT /tag= a
 FT /product= "defective ABC1 polypeptide"
 XX
 XX
 PN W0200078971-A2.
 XX
 PD 28-DEC-2000.
 XX
 PF 16-JUN-2000; 2000M0-US16591.
 XX

QY	1561	aacaagtccatgagctgctgtagatgaggaattctggtctgtgtatgttgaatgga	1620
Db	1883	aacaagttccatgagctgctgtagatgaggaattctggtctgtgtatgttgaatgga	1942
QY	1621	attactccagagcagatgagctgtgcccatagtcacaatccaaatccagatgagact	1680
Db	1943	attactccagagcagatgagctgtgcccatagtcacaatccaaatccagatgagact	2002
QY	1681	gacaaatgtgagagagacaataaatacaagatggtatctggtgagccctgtctcagact	1740
Db	2003	gacaaatgtgagagagacaataaatacaagatggtatctggtgagccctgtctcagact	2062
QY	1741	gacccctttagagacatgctgtagctgtggtggtggtctgctacttgcagatgtgtg	1800
Db	2063	gacccctttagagacatgctgtagctgtggtggtggtctgctacttgcagatgtgtg	2122
QY	1801	gagcagagcaatcatcagaggtgtctgacggtgacccgagaaagaaactggtctatatgcaa	1860
Db	2123	gagcagagcaatcatcagaggtgtctgacggtgacccgagaaagaaactggtctatatgcaa	2182
QY	1861	cagatgcccataccctgttagctgtgtagacatcttctgctggtgtgtagagccgttcaatg	1920
Db	2183	cagatgcccataccctgttagctgtgtagacatcttctgctggtgtgtagagccgttcaatg	2242
QY	1921	ccctcttcatgacgtctgctgctggtatctactcaatgctgtgtatcatcaaggtcactgtg	1980
Db	2243	ccctcttcatgacgtctgctgctggtatctactcaatgctgtgtatcatcaaggtcactgtg	2302
QY	1981	tatgaaagagagcagcgtctgaaagagacacatgacgatcatggtcgtctgacacacagcata	2040
Db	2303	tatgaaagagagcagcgtctgaaagagacacatgacgatcatggtcgtctgacacacagcata	2362
QY	2041	ctctggtttagctgtgttcatatgtagcctcatctcctctctgtgtagcgtgtgctgtcta	2100
Db	2363	ctctggtttagctgtgttcatatgtagcctcatctcctctctgtgtagcgtgtgctgtcta	2422
QY	2101	gtgtgtatctcctgaagttaagaaacccgtctgacctacagatgacacacagcgtgtgtgttc	2160
Db	2423	gtgtgtatctcctgaagttaagaaacccgtctgacctacagatgacacacagcgtgtgtgttc	2482
QY	2161	ttccctgtccgtgtgtctgtgtgtacacatccctgacgtgtctctctgtatgacacactcttc	2220
Db	2483	ttccctgtccgtgtgtctgtgtgtacacatccctgacgtgtctctctgtatgacacactcttc	2542
QY	2221	tccagagccaacctgtgacagcgtgtgtgtgtgtgtatcatctacttcaagctgttgaactgcc	2280
Db	2543	tccagagccaacctgtgacagcgtgtgtgtgtgtgtatcatctacttcaagctgttgaactgcc	2602
QY	2281	taagctctgt	2340
Db	2603	taagctctgt	2662
QY	2341	ctgt	2400
Db	2663	ctgt	2722
QY	2401	gtgcatgtgagatgagtgaggaacaacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2460
Db	2723	gtgcatgtgagatgagtgaggaacaacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2782
QY	2461	ctaacacattcgtatccatagatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2520
Db	2783	ctaacacattcgtatccatagatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2842
QY	2521	tacattgaggt	2580
Db	2843	tacattgaggt	2902
QY	2581	accaagttcctactgt	2640
Db	2903	accaagttcctactgt	2962

QY	2641	aagagaatgtccagaataatctgcatgagaggaagaaacccacattgaagctgggtgtcc	2700
Db	2963	aagagaatgtccagaataatctgcatgagaggaagaaacccacattgaagctgggtgtcc	3022
QY	2701	attcagaacctgtgttaaaagtctacacagatgtggtatgaggtgtgtgtgtgtgtgtgtgt	2760
Db	3023	attcagaacctgtgttaaaagtctacacagatgtggtatgaggtgtgtgtgtgtgtgtgtgt	3082
QY	2761	ctggaattttatgagggccagatcactctctctctgtgtgtgtgtgtgtgtgtgtgtgtgt	2820
Db	3083	ctggaattttatgagggccagatcactctctctctgtgtgtgtgtgtgtgtgtgtgtgtgt	3142
QY	2821	accacacatgtcaatccctgagacgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2880
Db	3143	accacacatgtcaatccctgagacgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	3202
QY	2881	ggaagaagacatctgctctgtgagatgagacacatccggcagaagacctgtgtgtgtgtgtgt	2940
Db	3203	ggaagaagacatctgctctgtgagatgagacacatccggcagaagacctgtgtgtgtgtgtgt	3262
QY	2941	cataagctgt	3000
Db	3263	cataagctgt	3322
QY	3001	aaaggtctctctgtgagagcagtgtaagcgagatgtgagacagatgtgtgtgtgtgtgtgt	3060
Db	3323	aaaggtctctctgtgagagcagtgtaagcgagatgtgagacagatgtgtgtgtgtgtgtgt	3382
QY	3061	ttgcatcaagcaagctgtgaaagcaaaacagcagctgttcaaggtgtgtgtgtgtgtgtgtgt	3120
Db	3383	ttgcatcaagcaagctgtgaaagcaaaacagcagctgttcaaggtgtgtgtgtgtgtgtgtgt	3442
QY	3121	ctatctgt	3180
Db	3443	ctatctgt	3502
QY	3181	gtctgt	3240
Db	3503	gtctgt	3562
QY	3241	ggcgcagccattatctctctcaacacacatgtgataagcgagcgtctgtgtgtgtgtgtgtgt	3300
Db	3563	ggcgcagccattatctctctcaacacacatgtgataagcgagcgtctgtgtgtgtgtgtgtgt	3622
QY	3301	attgcatcatctcccatgt	3360
Db	3623	attgcatcatctcccatgt	3682
QY	3361	cagctgt	3420
Db	3683	cagctgt	3742
QY	3421	tcctgtcaagaacagtagtagacacgtgtgtcatatccctgtgtgtgtgtgtgtgtgtgtgt	3480
Db	3743	tcctgtcaagaacagtagtagacacgtgtgtcatatccctgtgtgtgtgtgtgtgtgtgtgt	3802
QY	3481	agcagttctgtatgt	3540
Db	3803	agcagttctgtatgt	3862
QY	3541	tctgtcatctccacatccatcaagaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	3600
Db	3863	tctgtcatctccacatccatcaagaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	3922
QY	3601	gggcatgt	3660
Db	3923	gggcatgt	3982
QY	3661	ctcttcatgagatgtatgacgggtctcacaagacctgtgtgtgtgtgtgtgtgtgtgtgtgt	3720
Db	3983	ctcttcatgagatgtatgacgggtctcacaagacctgtgtgtgtgtgtgtgtgtgtgtgtgt	4042
QY	3721	gagacagccctgtgagaataatctctcacaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	3780

Db 4043 ggaagcccttgaaagaatattcctccaagtgagccgaagagatggggtgagtctcgag 4102
QY 3781 acctcaatgtacctgacagcaagaacgaagcgagcccttgagggaacaagcgaagc 3840
Db 4103 acctcagatgtacacctgacagcaagaacgaagcgagcccttgagggaacaagcgaagc 4162
QY 3841 tctcttcgcccgttacctgaagatgtagtctgtctgaatccaatgattctgacatagaacca 3900
Db 4163 tgtcttcgcccgttacctgaagatgtagtctgtctgaatccaatgattctgacatagaacca 4222
QY 3901 gaattccagagagacagactgtgcagtgaggatgtagtggaaaagcgccctacaagcgtaaa 3960
Db 4223 gaattccagagagacagactgtgcagtgaggatgtagtggaaaagcgccctacaagcgtaaa 4282
QY 3961 ggcctggaacttaccagacacagattgtgagccctttgtggaagaagactgtcaattgac 4020
Db 4283 ggcctggaacttaccagacacagattgtgagccctttgtggaagaagactgtcaattgac 4342
QY 4021 agacggagctgggaagaatttttctgacagattgtcttcagcgtgtgttctgacatt 4080
Db 4343 agacggagctgggaagaatttttctgacagattgtcttcagcgtgtgttctgacatt 4402
QY 4081 ggcctgtgttccagccttgatcgttgccaccccttggcaagtaaccagccttggaacttga 4140
Db 4403 ggcctgtgttccagccttgatcgttgccaccccttggcaagtaaccagccttggaacttga 4462
QY 4141 cccctgagatgacaaagaaacgatacatttgcagcaatgagtctccatgaggaacggga 4200
Db 4463 cccctgagatgacaaagaaacgatacatttgcagcaatgagtctccatgaggaacggga 4522
QY 4201 acccttgaaactcttaaacgcgccttccacaagaaccccttgcttggaacccgcgtatgga 4260
Db 4523 acccttgaaactcttaaacgcgccttccacaagaaccccttgcttggaacccgcgtatgga 4582
QY 4261 ggaagaccacatccacagacacgccttgccagcgagggaggaagatgagccactgccc 4320
Db 4583 ggaagaccacatccacagacacgccttgccagcgagggaggaagatgagccactgccc 4642
QY 4321 gtccccaagaccatctgagacactcttccagaaatggagacatggaacatggaaccccttca 4380
Db 4643 gtccccaagaccatctgagacactcttccagaaatggagacatggaacatggaaccccttca 4702
QY 4381 cctgacatgcagtgtagcagcgacaaatccaagaagatgctgcctgcgtgtgtccccaagg 4440
Db 4703 cctgacatgcagtgtagcagcgacaaatccaagaagatgctgcctgcgtgtgtccccaagg 4762
QY 4441 gcaagggggctgctcctccacaagaagaaacacacatgacagataccttcaagaactg 4500
Db 4763 gcaagggggctgctcctccacaagaagaaacacacatgacagataccttcaagaactg 4822
QY 4501 acaggaagaacatctcgatatactgtggaagacgtatgtgacagatatacgaagaagc 4560
Db 4823 acaggaagaacatctcgatatactgtggaagacgtatgtgacagatatacgaagaagc 4882
QY 4561 ttaagaagaacagatctgggtgaaatgagtttaagtaatggcggtcttccctgggtgacgt 4620
Db 4883 ttaagaagaacagatctgggtgaaatgagtttaagtaatggcggtcttccctgggtgacgt 4942
QY 4621 aatctccaagcactcctcccgagtcagaagaatttaatgtagcatataaacaatgagaaga 4680
Db 4943 aatctccaagcactcctcccgagtcagaagaatttaatgtagcatataaacaatgagaaga 5002
QY 4681 caactaaagctggccaagagacagttctgacagatcatttccaacagcttgggaagatt 4740
Db 5003 caactaaagctggccaagagacagttctgacagatcatttccaacagcttgggaagatt 5062
QY 4741 atgacagagactgggaacacagaataatgtagcaggtgtgttccaataacaagggtgcgat 4800
Db 5063 atgacagagactgggaacacagaataatgtagcaggtgtgttccaataacaagggtgcgat 5122
QY 4801 gcaatcagactcttctctaagtatacaaatgcattctccgggccaacttcgaag 4860
Db 5123 gcaatcagactcttctctaagtatacaaatgcattctccgggccaacttcgaag 5182
QY 4861 ggaagaaacccctagacatataggaattactgtcttccaatatacctccctgaatccaag 4920
Db 5183 ggaagaaacccctagacatataggaattactgtcttccaatatacctccctgaatccaag 5242
QY 4921 cagcagcctcagaggtgtgcctctgataagcaccatcagtgagatgtctctgttccatcgt 4980
Db 5243 cagcagcctcagaggtgtgcctctgataagcaccatcagtgagatgtctctgttccatcgt 5302
QY 4981 gtacatttgaagatgtccttcgtccagcagccttgcgtatctcctgaatccagagcg 5040
Db 5303 gtacatttgaagatgtccttcgtccagcagccttgcgtatctcctgaatccagagcg 5362
QY 5041 gtccagcaagcaaaaacacctgcagttacatcagtggaatgagcctgtcactactggtc 5100
Db 5363 gtccagcaagcaaaaacacctgcagttacatcagtggaatgagcctgtcactactggtc 5422
QY 5101 tctaatttgcctggagatgtagcaatgaagtgtagccctgcacacatggtcaatatac 5160
Db 5423 tctaatttgcctggagatgtagcaatgaagtgtagccctgcacacatggtcaatatac 5482
QY 5161 ttcatctgtccacagcaagaatcccatgagtgctccccaacatcgccctgtgtagccct 5220
Db 5483 ttcatctgtccacagcaagaatcccatgagtgctccccaacatcgccctgtgtagccct 5542
QY 5221 ctacttctgtgtagtggtgtagcaatcaacacttcaatgtagccagcctcttgtgttc 5280
Db 5543 ctacttctgtgtagtggtgtagcaatcaacacttcaatgtagccagcctcttgtgttc 5602
QY 5281 aagatccccaagcagacatagtggtgtccacagcgtagaaccttctcatatgacat 5340
Db 5603 aagatccccaagcagacatagtggtgtccacagcgtagaaccttctcatatgacat 5662
QY 5341 ggcagcgttgagcacccttgtagtctgtagaagctgtccacgaacataagctgaaataatcaat 5400
Db 5663 ggcagcgttgagcacccttgtagtctgtagaagctgtgttcaacgaacataagctgaaataatcaat 5722
QY 5401 gatatcctggaatcgtgttcttgaatcttccacacatttgccttggaagagggctcact 5460
Db 5723 gatatcctggaatcgtgttcttgaatcttccacacatttgccttggaagagggctcact 5782
QY 5461 gacatgtgaaacacagcgaagtgatgacatgacatgacatgacatgacatgacatgacat 5520
Db 5783 gacatgtgaaacacagcgaagtgatgacatgacatgacatgacatgacatgacatgacat 5642
QY 5521 ggttcaacatlatcttggagcttggtaggaagaaacctcttcgcacatgagcgtggaagg 5580
Db 5843 ggttcaacatlatcttggagcttggtaggaagaaacctcttcgcacatgagcgtggaagg 5902
QY 5581 gtggtgttcttccatctactgtttctgatacagatatttcaatccagggccagact 5640
Db 5903 gtggtgttcttccatctactgtttctgatacagatatttcaatccagggccagact 5962
QY 5641 gtaatgcaagcatalctcccttgaatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaat 5700
Db 5963 gtaatgcaagcatalctcccttgaatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaat 6022
QY 5701 agaatcttgaatgtaggaagcagaatgacatcttgaagaatcaaggaatgtagcagaagata 5760
Db 6023 agaatcttgaatgtaggaagcagaatgacatcttgaagaatcaaggaatgtagcagaagata 6082
QY 5761 tatagaaggaagcgaagcctgtcgttgaagagatttgggtgggaatttccctcgttgag 5820
Db 6083 tatagaaggaagcgaagcctgtcgttgaagagatttgggtgggaatttccctcgttgag 6142
QY 5821 tgccttggcctctggaggttaaagtgagcgtggaataatcaacttcaagaatgtagtaaa 5880
Db 6143 tgccttggcctctggaggttaaagtgagcgtggaataatcaacttcaagaatgtagtaaa 6202
QY 5881 ggaagataccactgttaccagagagatgcttcccttaacaaaatagtagtcttatacaaac 5940
Db 6203 ggaagataccactgttaccagagagatgcttcccttaacaaaatagtagtcttatacaaac 6262

QY 5941 atccatgaagatcatcagaacatgggtactgacctcagtttgatgacatcacagagctg 6000
 |||||||
 Db 6263 atccatgaagatcatcagaacatgggtactgacctcagtttgatgacatcacagagctg 6322
 QY 6001 ttgacttgagagagacacagtgagttcttctgaccttttgagagagagttcccaagaagaa 6060
 |||||||
 Db 6323 ttgacttgagagagacacagtgagttcttctgaccttttgagagagagttcccaagaagaa 6382
 QY 6061 gttgcaagagttggtgagtgagcgaatcgcgaacatgggcccgtggaagtatgagaa 6120
 |||||||
 Db 6383 gttgcaagagttggtgagtgagcgaatcgcgaacatgggcccgtggaagtatgagaa 6442
 QY 6121 tatgtctgtaactatagtgagagcaacaacagcagctctctacagcagtgctttatc 6180
 |||||||
 Db 6443 tatgtctgtaactatagtgagagcaacaacagcagctctctacagcagtgctttatc 6502
 QY 6181 gggcgagccctggtgtgttctgagatgaacccacagcagtgatcccaagcccg 6240
 |||||||
 Db 6503 gggcgagccctggtgtgttctgagatgaacccacagcagtgatcccaagcccg 6562
 QY 6241 cgttcttgagagatgagtcctcagagtggttgcagagagggagagatcagtagtgcttaca 6300
 |||||||
 Db 6563 cgttcttgagagatgagtcctcagagtggttgcagagagggagagatcagtagtgcttaca 6622
 QY 6301 tctcatagatgagagatgagtgagccttctgactagagatgagcagatgagtgatgga 6360
 |||||||
 Db 6623 tctcatagatgagagatgagtgagccttctgactagagatgagcagatgagtgatgga 6682
 QY 6361 aggttcaagtgagccttgagcagtgctccagcactcaaaaataggttgagagatgagtgatgga 6420
 |||||||
 Db 6683 aggttcaagtgagccttgagcagtgctccagcactcaaaaataggttgagagatgagtgatgga 6742
 QY 6421 atagttgtagaagatagcagagtgctccaccccgagcctggaagcctgagagatgagtgatgga 6480
 |||||||
 Db 6743 atagttgtagaagatagcagagtgctccaccccgagcctggaagcctgagagatgagtgatgga 6802
 QY 6481 ctggcagcttctcgagagtggttctcaaaaagagaacacccggaacatgctcaataacagctt 6540
 |||||||
 Db 6803 ctggcagcttctcgagagtggttctcaaaaagagaacacccggaacatgctcaataacagctt 6862
 QY 6541 ccatctcatatctctctcgtgcagagatattcagcatctctccacagagcaaaaagcga 6600
 |||||||
 Db 6863 ccatctcatatctctctcgtgcagagatattcagcatctctccacagagcaaaaagcga 6922
 QY 6601 ctccacatagaagactactgttcttcagacaacacttgacacagatatttgactt 6660
 |||||||
 Db 6923 ctccacatagaagactactgttcttcagacaacacttgacacagatatttgactt 6982
 QY 6661 gccaaagacacaaagtatgagtgacacttaaaaagacctctcatattacacaaaacagagaa 6720
 |||||||
 Db 6983 gccaaagacacaaagtatgagtgacacttaaaaagacctctcatattacacaaaacagagaa 7042
 QY 6721 gtagtgagcgttgaggttccacatcttcttcacagatgagagaaagtgaagaagctat 6780
 |||||||
 Db 7043 gtagtgagcgttgaggttccacatcttcttcacagatgagagaaagtgaagaagctat 7102
 QY 6781 gtagtgagcgttgaggttccacag 6804
 |||||||
 Db 7103 gtagtgagcgttgaggttccacag 7126

RESULT 7
 AAF92835
 ID AAF92835 standard; DNA: 7860 BP.
 XX
 AC AAF92835;
 XX
 XX 17-MAY-2001 (first entry)
 DT
 DE Human ABC1 cDNA.
 XX
 KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ss.

XX OS Homo sapiens.
 XX PN WO200115676-A2.
 XX
 XX 08-MAR-2001.
 XX
 XX 01-SEP-2000; 2000WO-1B01492.
 XX
 XX 01-SEP-1999; 99US-0151977.
 XX 15-MAR-2000; 2000US-0526193.
 XX 23-JUN-2000; 2000US-0213958.
 XX
 XX (UNVR-) UNIV BRITISH COLUMBIA.
 XX (XENO-) XENON GENETICS INC.
 XX
 XX Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM.
 XX WPL; 2001-244356/25.
 XX
 XX Treating a lower than normal high density lipoprotein-cholesterol
 XX (HDL-C) level, a higher than normal triglyceride level, or a
 XX cardiovascular disease, by administering a compound that modulates LXR-
 XX or RXR-mediated transcriptional activity -
 XX
 XX Disclosure; Fig 2; 317pp; English.
 XX
 XX The present invention relates to a method for treating a patient
 XX diagnosed as having a lower than normal high density
 XX lipoprotein-cholesterol (HDL-C) level, a higher than normal
 XX triglyceride level, or a cardiovascular disease, involving
 XX administering a compound that modulates LXR- or RXR-mediated
 XX transcriptional activity or ABC1 expression or activity.
 XX The LXR gene product may be used in an assay to identify
 XX compounds useful for the treatment of a disease or condition selected a
 XX lower than normal HDL cholesterol level, a higher than normal
 XX triglyceride level, and a cardiovascular disease.
 XX
 XX Sequence 7860 BP; 2014 A; 1860 C; 2008 G; 1978 T; 0 other:
 XX
 XX Query Match 99.9%; Score 6796; DB 22; Length 7860;
 XX Best Local Similarity 99.9%; Pred. No. 0;
 XX Matches 6799; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 atggtctgttgcgtcagctgagtgagtgctgctgtgtggaagaacctcacttcagaagaaga 60
 |||||||
 Db 75 atggtctgttgcgtcagctgagtgagtgctgctgtgtggaagaacctcacttcagaagaaga 134
 QY 61 caaacatgtcagctgttactcgtggaagtgctggtccttattatcttctgtatcctgagc 120
 |||||||
 Db 135 caaacatgtcagctgttactcgtggaagtgctggtccttattatcttctgtatcctgagc 194
 QY 121 tctgttcgtgagctacccacccctatgaaacaatgagtgccatttccaaataaagcc 180
 |||||||
 Db 195 tctgttcgtgagctacccacccctatgaaacaatgagtgccatttccaaataaagcc 254
 QY 181 atgcccctcgaagaacacttcttggttcaggggattatctgttaatgcaacaacccc 240
 |||||||
 Db 255 atgcccctcgaagaacacttcttggttcaggggattatctgttaatgcaacaacccc 314
 QY 241 tgttccgttacccgactctctgggaagctcccgaggttggttgaaacttaacaatcc 300
 |||||||
 Db 315 tgttccgttacccgactctctgggaagctcccgaggttggttgaaacttaacaatcc 374
 QY 301 atgtgctcgcgttctcagatgctcagaggtcttcttatacagcagaagaagacc 360
 |||||||
 Db 375 atgtgctcgcgttctcagatgctcagaggtcttcttatacagcagaagaagacc 434
 QY 361 agcatgaagacatgagcagaagttctgagaacattcagcagatcagaagaatccagcttca 420
 |||||||
 Db 435 agcatgaagacatgagcagaagttctgagaacattcagcagatcagaagaatccagcttca 494

QY	421	aacttgaagcttcaagattctctctgtgttgacaatgaaacctctctctgttccctataaac	480
Db	495	aacttgaagcttcaagattctctctgtgttgacaatgaaacctctctctgttccctataaac	554
QY	481	aaactctctcccaaaagtctactctgttgacaagaatgctggaaggtgtgtatcttccaa	540
Db	555	aaactctctcccaaaagtctactctgttgacaagaatgctggaaggtgtgtatcttccaa	614
QY	541	aaggtatcttttgcaggcttaccagttacatttgacaagctctgttgacaatgataataca	600
Db	615	aaggtatcttttgcaggcttaccagttacatttgacaagctctgttgacaatgataataca	674
QY	601	gaagagatgtattcaactctgtgtgacaagaagtcttcaagcttttggccctaccagaagg	660
Db	675	gaagagatgtattcaactctgtgtgacaagaagtcttcaagcttttggccctaccagaagg	734
QY	661	aaactgtctgcagcagcagagacttacttcttccacaatgagacacctggaagccaactcgg	720
Db	735	aaactgtctgcagcagcagagacttacttcttccacaatgagacacctggaagccaactcgg	794
QY	721	agaacaactaaactacacttcccttcccgagccaagagctgtgtgacaagccaanaaca	780
Db	795	agaacaactaaactacacttcccttcccgagccaagagctgtgtgacaagccaanaaca	854
QY	781	ttgtctgcatagtcttctgtgagactctgtgccaagagctgttctcagcattgagaactgtgaatgac	840
Db	855	ttgtctgcatagtcttctgtgagactctgtgccaagagctgttctcagcattgagaatgac	914
QY	841	atgagcagcaggagggtgatgttctctgaccaaagttagacaagctccagctctctccaccaatc	900
Db	915	atgagcagcaggagggtgatgttctctgaccaaagttagacaagctccagctctctccaccaatc	974
QY	901	taccaggtctgtctcgtcatgtctgttgaggacatcccgaggaaggagggtgcttgaaatcaag	960
Db	975	taccaggtctgtctcgtcatgtctgttgaggacatcccgaggaaggagggtgcttgaaatcaag	1034
QY	961	tcttcccaactctgttatgtagagacaactacaaagccctcttggaggacaatgagcaatgag	1020
Db	1035	tcttcccaactctgttatgtagagacaactacaaagccctcttggaggacaatgagcaatgag	1094
QY	1021	gaagatgtctgaaactctctatagacaactctacaactcccttaacgtgcaatgtatgttgaag	1080
Db	1095	gaagatgtctgaaactctctatagacaactctacaactcccttaacgtgcaatgtatgttgaag	1154
QY	1061	aatttggagctctagttccctcttcccgcatatctgtgaaagctctgaaagcgcgtctgctgt	1144
Db	1155	aatttggagctctagttccctcttcccgcatatctgtgaaagctctgaaagcgcgtctgctgt	1214
QY	1141	gggaagatctcgtgtatacccttgaaactcccgacccaaggaagctgaatgtgttgaaagtgaac	1200
Db	1215	gggaagatctcgtgtatacccttgaaactcccgacccaaggaagctgaatgtgttgaaagtgaac	1274
QY	1201	aagaccttccaggaactgtgctgtgttccatgacatctggaagacatgtggagagaaactcgc	1260
Db	1275	aagaccttccaggaactgtgctgtgttccatgacatctggaagacatgtggagagaaactcgc	1334
QY	1261	cccgaagatctcggaactctcatgaggagaacccaagaaatgagactgttcccgatctgtgtg	1320
Db	1335	cccgaagatctcggaactctcatgaggagaacccaagaaatgagactgttcccgatctgtgtg	1394
QY	1321	gacagcagggacaatgacaactcttttggagacagcagatttgacatgctgtatgtagacaac	1380
Db	1395	gacagcagggacaatgacaactcttttggagacagcagatttgacatgctgtatgtagacaac	1454
QY	1381	caagaacatctgttcgcttttttggccaagacccaagggatgtccagatccaatgaatgtctc	1440
Db	1455	caagaacatctgttcgcttttttggccaagacccaagggatgtccagatccaatgaatgtctc	1514
QY	1441	gtgtacacctgtgagagaagcttcttcaacgagacttaacccaagcaatccggacaatatctgc	1500
Db	1515	gtgtacacctgtgagagaagcttcttcaacgagacttaacccaagcaatccggacaatatctgc	1574
QY	1501	tctcatgagtggttcatcaacttgacaacagctagaacccaatagacaagaagatctgtgtcaac	1560

Db	1575	ttcatgtggtgtgtcaacctgtgacaagcttgaaacctatgacaacagaagtctggtctaac	1634
QY	1561	aacaaatccatggaagctgtctgtatgaaagaagaagttctggctgtgatatgtgttcaatctga	1620
Db	1635	aacaagaatccatggaagctgtctgtatgaaagaagaagttctggctgtgatatgtgttcaatctga	1694
QY	1621	attaccctgaagcagaagattgagctgtccccaatcatgttcaagtaacaaagttccgaatgtgaatt	1688
Db	1695	attaccctgaagcagaagattgagctgtccccaatcatgttcaagtaacaaagttccgaatgtgaatt	1754
QY	1681	gacaatgtgtgaaagagacaacaataaatacaagaatgtgtgtactgtggaacctgtctctgagact	1740
Db	1755	gacaatgtgtgaaagagacaacaataaatacaagaatgtgtgtactgtggaacctgtctctgagact	1814
QY	1741	gaaccttttgaaagaaatgtgcgttaagttctgtgggtggcttcgacctactgtcagaatgtgtgtg	1800
Db	1815	gaaccttttgaaagaaatgtgcgttaagttctgtgggtggcttcgacctactgtcagaatgtgtgtg	1874
QY	1801	gaacagagcaatcatcagaagtgctgaacgggcaaccgaagaagaagaactgtgttctatgtga	1866
Db	1875	gaacagagcaatcatcagaagtgctgaacgggcaaccgaagaagaagaactgtgttctatgtga	1934
QY	1861	cgagatgcccataccctgtttagcgtttgatgatactcttctgtgggtgtgtatgagccggtcaatg	1920
Db	1935	cgagatgcccataccctgtttagcgtttgatgatactcttctgtgggtgtgtatgagccggtcaatg	1994
QY	1921	cccctcttcataagacgtgtgccttggaatttactcaagtggtcgtgtatcatcaagaagcactgtg	1960
Db	1995	cccctcttcataagacgtgtgccttggaatttactcaagtggtcgtgtatcatcaagaagcactgtg	2054
QY	1981	latgtgaagtgaaagcagcgtgtgaagaagacaatgcggatcatatgtgctgtgacaacaagcata	2040
Db	2055	latgtgaagtgaaagcagcgtgtgaagaagacaatgcggatcatatgtgctgtgacaacaagcata	2114
QY	2041	ctcttggttttagcgtgttcatatagtgaagctctaatctctctctctgtgtgaagcgtgtgcctgta	2100
Db	2115	ctcttggttttagcgtgttcatatagtgaagctctaatctctctctctgtgtgaagcgtgtgcctgta	2174
QY	2101	gtgtgcatcccggaagtttagaagaacctgtctccctaaagtgaatcccaagcgtgtgtttgttc	2160
Db	2175	gtgtgcatcccggaagtttagaagaacctgtctccctaaagtgaatcccaagcgtgtgtttgttc	2234
QY	2161	ttccctgtccgtgtttgtctgtgtgtgaacaatccctgtcagttgtcttcgtatagaacaacttcc	2220
Db	2235	ttccctgtccgtgtttgtctgtgtgtgaacaatccctgtcagttgtcttcgtatagaacaacttcc	2294
QY	2221	ttccaaagaacaacctgtgacagacgtctgtgtggggatcatatattactatagcgttgaattgtcc	2280
Db	2295	ttccaaagaacaacctgtgacagacgtctgtgtggggatcatatattactatagcgttgaattgtcc	2354
QY	2281	taagtcctgtgtgtgtgacatgtgcagaactacgtgtgtgtgttcaacctaaatcttcgtatgc	2340
Db	2355	taagtcctgtgtgtgtgacatgtgcagaactacgtgtgtgtgttcaacctaaatcttcgtatgc	2414
QY	2341	ctgcgtgtctctgtgtggttttgggttttggtctgtgtgtgtactttgtccctttttgagaagcag	2400
Db	2415	ctgcgtgtctctgtgtggttttgggttttgggtctgtgtgtgtactttgtccctttttgagaagcag	2474
QY	2401	ggcatctggagtgacgtgtgtgtgacaacaacctgttttgagaatctctgtgtgaagaagaatgtgtcaat	2460
Db	2475	ggcatctggagtgacgtgtgtgtgacaacaacctgttttgagaatctctgtgtgaagaagaatgtgtcaat	2534
QY	2461	ctcaacaacttcgatctccatagatagtcgttttgacaaccttcctctataggtgtgatacctgtg	2520
Db	2535	ctcaacaacttcgatctccatagatagtcgttttgacaaccttcctctataggtgtgatacctgtg	2594
QY	2521	tacaatgaagcgtgtcttcttcagaagcagaatccgaatctcccaagccctgtattttctctgc	2580
Db	2595	tacaatgaagcgtgtcttcttcagaagcagaatccgaatctcccaagccctgtattttctctgc	2654
QY	2581	accaaagttcctactgtgtttgtgcgaagaagtgtatgaagaagcacaacctgtttccaacaa	2640

Db 2655 accaagtcctactggtttgagcgaagaaatgataagaaagacacccctggttcccaacag 2714
QY 2641 aagagaatgtcaagaatctgcatgtgaggaagaaacccacacttgaaagctgggctgtcc 2700
Db 2715 aaggaataatacagaatctgtcagtagaggaagaaacccacacttgaaagctgggctgtcc 2774
QY 2701 attcgaacacctgtaaaagttacccagaatgagatgaaagtgtgctgtcgaatggcctggca 2760
Db 2775 attcgaacacctgtaaaagttacccagaatgagatgaaagtgtgctgtcgaatggcctggca 2834
QY 2761 ctgaattttttgagggccagatcacccctctctctggccaacatggaaggggaaagag 2820
Db 2835 ctgaattttttgagggccagatcacccctctctctggccaacatggaaggggaaagag 2894
QY 2821 accaccatgtcaactctgacccgggtgtgttcccccagacctgggacccgctacatctg 2880
Db 2895 accaccatgtcaactctgacccgggtgtgttcccccagacctgggacccgctacatctg 2954
QY 2881 ggaataagacatctgctctgagatgagacacatcccgccagaaacctgggggtctgtccca 2940
Db 2955 ggaataagacatctgctctgagatgagacacatcccgccagaaacctgggggtctgtccca 3014
QY 2941 cctaaagtgctgtttgacatgtgacatgctgcgaagaacacatctgttctatgcccgttg 3000
Db 3015 cctaaagtgctgtttgacatgtgacatgctgcgaagaacacatctgttctatgcccgttg 3074
QY 3001 aaaaaggctctctgagaagacagtgagaagcggaatgagacagatggccctggatgttggc 3060
Db 3075 aaaaaggctctctgagaagacagtgagaagcggaatgagacagatggccctggatgttggc 3134
QY 3061 ttggcctcagaagaagctgaaagaacaaacaaacagcgttcaaggtggaatcagaagaag 3120
Db 3135 ttggcctcagaagaagctgaaagaacaaacaaacagcgttcaaggtggaatcagaagaag 3194
QY 3121 ctatctgtgacctggtgctgtgcggggagatcctaaggttgcatactctgagatgaaccca 3160
Db 3195 ctatctgtgacctggtgctgtgcggggagatcctaaggttgcatactctgagatgaaccca 3254
QY 3181 gctggtgtggaaccttactcccccaggggaataatggaagctgtgcttcaataaccca 3240
Db 3255 gctggtgtggaaccttactcccccaggggaataatggaagctgtgcttcaataaccca 3314
QY 3241 ggcgcgaacatlatctctctctacacacacacacatgataagcggaagcttccggggagac 3300
Db 3315 ggcgcgaacatlatctctctctacacacacacacatgataagcggaagcttccggggagac 3374
QY 3301 attgcaatcatctccatgaggaagctgtgctgtgtgagcttccctccctgtttctgaagac 3360
Db 3375 attgcaatcatctccatgaggaagctgtgctgtgtgagcttccctccctgtttctgaagac 3434
QY 3361 caagctgggaacagagctactacacccgacctgtgtcaagaagaatgtggaatccctccctc 3420
Db 3435 caagctgggaacagagctactacacccgacctgtgtcaagaagaatgtggaatccctccctc 3494
QY 3421 tctctgcaagaacagtagacatgtgtcatcatccctgtaaaaaaggaagacagtggttctca 3480
Db 3495 tctctgcaagaacagtagacatgtgtcatcatccctgtaaaaaaggaagacagtggttctca 3554
QY 3481 agcaagttctgaatgtgctgtggcagcgacacatgataagatgacagctgtgacatctgtc 3540
Db 3555 agcaagttctgaatgtgctgtggcagcgacacatgataagatgacagctgtgacatctgtc 3614
QY 3541 tctgtctatctcccaacctcaggaagacatgtgtctgaagcccggtgtgtgtaagaacata 3600
Db 3615 tctgtctatctcccaacctcaggaagacatgtgtgtctgaagcccggtgtgtgtaagaacata 3674
QY 3601 gggaatgagctgacatgtgtctgacatataagaaagtgttaagaagggagccttgttgaa 3660
Db 3675 gggaatgagctgacatgtgtctgacatataagaaagtgttaagaagggagccttgttgaa 3734
QY 3661 cctcttcaatgagatgtatgacccggtctctcagacctgggacatctctgttatgtgacatcta 3720
Db 3735 cctcttcaatgagatgtatgacccggtctctcagacctgggacatctctgttatgtgacatcta 3794

QY 3721 gagaagacccctggaagaataatactctcaaggtggccgaagaagatgggggtgagatgtcgag 3780
Db 3795 gagaagacccctggaagaataatactctcaaggtggccgaagaagatgggggtgagatgtcgag 3854
QY 3781 acctcagaatgttacctgtgccaagacgaacacagcggggctctcgggggaacagacagac 3840
Db 3855 acctcagaatgttacctgtgccaagacgaacacagcggggctctcgggggaacagacagac 3914
QY 3841 tgtcttgcgccgttccactggaagatgagatgtgtatctcaatgatcttgacatagaccca 3900
Db 3915 tgtcttgcgccgttccactggaagatgagatgtgtatctcaatgatcttgacatagaccca 3974
QY 3901 gaatccagagacacagatctgctcagtgagatgagatgcaaaaggttccatccaggtgaa 3960
Db 3975 gaatccagagacacagatctgctcagtgagatgagatgcaaaaggttccatccaggtgaa 4034
QY 3961 ggtctgaaacttacaacagcaacagttgtggccctctgtgtggaagagacgtcaattggc 4020
Db 4035 ggtctgaaacttacaacagcaacagttgtggccctctgtgtggaagagacgtcaattggc 4094
QY 4021 aagcggagtcggaaagagatgtttgtcagaatgtctctgcagctgtgtctgcat 4080
Db 4095 aagcggagtcggaaagagatgtttgtcagaatgtctctgcagctgtgtctgcat 4154
QY 4081 ggcctgtgttcaagcctgacgtgccaaccttggccaagtaccccaagctggaaactcag 4140
Db 4155 ggcctgtgttcaagcctgacgtgccaaccttggccaagtaccccaagctggaaactcag 4214
QY 4141 cccctgagatcacacgaacagtaacatcttgcagcaatgtgtgtctctgaagaacggga 4200
Db 4215 cccctgagatcacacgaacagtaacatcttgcagcaatgtgtgtctctgaagaacggga 4274
QY 4201 accttgaaactcttaaacgcctctccacaaagacccctgtcttcgggaacccgtgtatgaa 4260
Db 4275 accttgaaactcttaaacgcctctccacaaagacccctgtcttcgggaacccgtgtatgaa 4334
QY 4261 ggaaccccaatcccaagacacgccttgcagcgaggggggaaggttgaaacacgtgccca 4320
Db 4335 ggaaccccaatcccaagacacgccttgcagcgaggggggaaggttgaaacacgtgccca 4394
QY 4321 gttccccaacacatcatgagaccttcccaagaaatgggaactggaacatcagaacacctca 4380
Db 4395 gttccccaacacatcatgagaccttcccaagaaatgggaactggaacatcagaacacctca 4454
QY 4381 cctgcatctgcagtgtagcagcgacaaaatcaagaagatgtgctgtgtgttccccaggg 4440
Db 4455 cctgcatctgcagtgtagcagcgacaaaatcaagaagatgtgctgtgtgttccccaggg 4514
QY 4441 gcaagggggctgctccctcccaacaaagaaacaaacacatgcagatatactctcaggaactg 4500
Db 4515 gcaagggggctgctccctcccaacaaagaaacaaacacatgcagatatactctcaggaactg 4574
QY 4501 acaggaagaaacatcttcggaatctctggtgaagacgatatgtcatatcatagcaaaagc 4560
Db 4575 acaggaagaaacatcttcggaatctctggtgaagacgatatgtcatatcatagcaaaagc 4634
QY 4561 ttaagaacacagatctgtggtgaatgagtttagttatgctgcttccctgggtgtcagc 4620
Db 4635 ttaagaacacagatctgtggtgaatgagtttagttatgctgcttccctgggtgtcagc 4694
QY 4621 aatactaaagcacttccctccgagatcaagaatgataagatgacatcaaaatgaaagaa 4680
Db 4695 aatactaaagcacttccctccgagatcaagaatgataagatgacatcaaaatgaaagaa 4754
QY 4681 caactaaagctggccaaggaacgttctgcagatcgaatctctcaacagcttggaaagatt 4740
Db 4755 caactaaagctggccaaggaacgttctgcagatcgaatctctcaacagcttggaaagatt 4814
QY 4741 atgacagagactggaacacagaaatlaatgtcaaggtgtgttcaatacaagagctggcat 4800
Db 4815 atgacagagactggaacacagaaatlaatgtcaaggtgtgttcaatacaagagctggcat 4874

QY	4801	gaatcgcgtctttccgaaatgtaacaaatgcacatcccgcccaactgcaaaag	4860
Db	4875	gcaatcagctcttctcgaatgtaatacaaatgcattccctccggccaactgcaaaag	4934
QY	4861	ggagaaagccctacgaactatgatgaatctaacgtcttcaataatccccgaatctcaaaag	4920
Db	4935	ggagagaacctagccaattatgatgaattacgtcttcaataatccccgaatctcaaaag	4994
QY	4921	cagcagctctcagaagtgtgctctgaatgaaccaatcagttgatatgtcctgtgtccatgtc	4980
Db	4995	cagaagcctctcagaggtgtgctctgatataccaacatcagttgatgtgctgtgtccatgtc	5054
QY	4981	gtcactttgaaatgtctcttcgtcccgcaagctgttgtattccgtacccagagagcg	5040
Db	5055	gtcactttgaaatgtctcttcgtcccgcaagctgttgtattccgtacccagagagcg	5114
QY	5041	gtcagcaagcaaaacacctgtcagttcatcagtgtgagttgaagcctgtcactatcgtctc	5100
Db	5115	gtcagcaagcaaaacacctgtcagttcatcagtgtgagttgaagcctgtcactatcgtctc	5174
QY	5101	tcraattttctcggagatagtccaattagttgtccctgtcccaactgtcattatcacc	5160
Db	5175	tcraattttctcggagatagtccaattagttgtccctgtcccaactgtcattatcacc	5234
QY	5161	ttcaatctgtctccagcaagaatccctatgtgtccctcccaacatctgcctgtgcagccct	5220
Db	5235	ttcaatctgtctccagcaagaatccctatgtgtccctcccaacatctgcctgtgcagccct	5294
QY	5221	ctcaactttgtctgaatgagtggtgtaataccaacccctcatatgccagcctcttggtctc	5280
Db	5295	ctcaactttgtctgaatgagtggtgtaataccaacccctcatatgccagcctcttggtctc	5354
QY	5281	aagatccccaagcaacgaactatgtgtgtgtccacaagcgtgaacctctcaattgtgcattat	5340
Db	5355	aagatccccaagcaacgaactatgtgtgtgtccacaagcgtgaacctctcaattgtgcattat	5414
QY	5341	ggagaggtgtgcacccctttgtcgtcgagcgtgttcaaccgacaataaagctgataataat	5400
Db	5415	ggagaggtgtgcacccctttgtcgtcgagcgtgttcaaccgacaataaagctgataataat	5474
QY	5401	gatatccctgaagtcgtgtctctgtatctccccaattttgtcctgtgagagaggtccatc	5460
Db	5475	gatatccctgaagtcgtgtctctgtatctccccaattttgtcctgtgagagaggtccatc	5534
QY	5461	gaatgtgtgtaaaaaacagggccaatgtgctatgtccctgtgaaaggtttggggagaatcgctt	5520
Db	5535	gaatgtgtgtaaaaaacagggccaatgtgctatgtccctgtgaaaggtttggggagaatcgctt	5594
QY	5521	gtctccaccaattactgtgggaactgtgtgtgagagcaaaacctttgcacatggccgttgaaagg	5580
Db	5595	gtctccaccaattactgtgggaactgtgtgtgagagcaaaacctttgcacatggccgttgaaagg	5654
QY	5581	gtgtgtgtcttcccatctaacgtgtctctgatccaagtaacgaattcttcaagggcccaagact	5640
Db	5655	gtgtgtgtcttcccatctaacgtgtctctgatccaagtaacgaattcttcaagggcccaagact	5714
QY	5641	gttaaatgtcaaaagctatctctcctctgtaatgtatgaatgtgaagcgtgagcggaagacag	5700
Db	5715	gttaaatgtcaaaagctatctctcctctgtaatgtatgaatgtgaagcgtgagcggaagacag	5774
QY	5701	agaattcttgatgtgtgagggccaagaatgacactatagaatctaaagaggttgaacgaagta	5760
Db	5775	agaattcttgatgtgtgagggccaagaatgacactatagaatctaaagaggttgaacgaagta	5834
QY	5761	tataaagaagaaacggaacgctgtgtttacaggaatttcgtgtgggcatctccctcgtgtgag	5820
Db	5835	tataaagaagaaacggaacgctgtgtttacaggaatttcgtgtgggcatctccctcgtgtgag	5894
QY	5821	tgctttgtggctctcgtggagttaatgtgggctgtgaaatcatcaacttcaagagtttlaaa	5880
Db	5895	tgctttgtggctctcgtggagttaatgtgggctgtgaaatcatcaacttcaagagtttlaaa	5954
QY	5881	ggagataccactggttaacagagggagatgtcttcccttcaacaaaataglatatcttacaac	5940

D	5955	gagagataacacccgttatacccgagggagatgcttctcttaacaaaatagtattatcaaac	6014
Q	5941	atccatgaagtatatacgaagaacatgggctactgcccatagtttgatagtcatcaacagctg	6000
D	6015	atccatgaagtatatacgaagaacatgggctactgcccatagtttgatagtcatcaacagctg	6074
Q	6001	ttacgtggagaggaacacgctggaggttcttgcccttttgagagagatcccaagaagaa	6060
D	6075	ttgactgggagaggaacacgctggaggttcttgcccttttgagagagatcccaagaagaa	6134
Q	6061	gttcgcaaggtttgtgtagtgggacgtatccgaaaactggccctcgtgagatgtgagaagaa	6120
D	6135	gttcgcaaggtttgtgtagtgggacgtatccgaaaactggccctcgtgagatgtgagaagaa	6194
Q	6121	tatgctggtgaactataagtggagggacacaacacgaaagctctctacagccatggtcttgatc	6180
D	6195	tatgctggtgaactataagtggagggacacaacacgaaagctctctacagccatggtcttgatc	6254
Q	6181	ggcgggctcctctgtgtgtttctctgatagaacccacacagccatgagatcccaagccgg	6240
D	6255	ggcgggctcctcgtgtgtttctctgatagaacccacacagccatgagatcccaagccgg	6314
Q	6241	cggttctctgttggaattgtgtgcccctaagtgtgtcaagagagggagatcagtagtgctta	6300
D	6315	cggttctctgttggaattgtgtgcccctaagtgtgtcaagagagggagatcagtagtgctta	6374
Q	6301	tctcagtagtatgagaagaatgtgtagagcctcttgacacagagatgtgcaatcatgtcaatgga	6360
D	6375	tctcagtagtatgagaagaatgtgtagagcctcttgacacagagatgtgcaatcatgtcaatgga	6434
Q	6361	aggttcacggtgctccttgagcaatgtgtccagcatctaaaaataagtttggagatggtataca	6420
D	6435	aggttcacggtgctccttgagcaatgtgtgtccagcatctaaaaataagtttggagatggtataca	6494
Q	6421	atagtttgacgaatagacagaggtcccaacccgacctgaagccgtgtccagagattcttggga	6480
D	6495	atagtttgacgaatagacagaggtcccaacccgacctgaagccgtgtccagagattcttggga	6554
Q	6481	cttgcatttctctggaagtgttcttaaaagagaacacccggaacatgtctacaataccagctt	6540
D	6555	cttgcatttctctggaagtgttcttaaaagagaacacccggaacatgtctacaataccagctt	6614
Q	6541	ccatcttcataatctctctcggccagagatattcaagatcctctcccaagagaaaagcga	6600
D	6615	ccatcttcataatctctctcggccagagatattcaagatcctctcccaagagaaaagcga	6674
Q	6601	ctccacatagaagaactactctgtttcttcagacaacacttgacaagaatattgtgaactt	6660
D	6675	ctccacatagaagaactactctgtttcttcagacaacacttgacaagaatattgtgaactt	6734
Q	6661	gccaaaggacaaagtgtatgtgacccattaaagaacctctatcacgaaaacccagaca	6720
D	6735	gccaaaggacaaagtgtatgtgacccattaaagaacctctctatcacgaaaacccagaca	6794
Q	6721	gtatgtgacgtttgcagttctcacactttttctacagatggaagaagtgaagaagaactat	6780
D	6795	gtatgtgacgtttgcagttctcacactttttctacagatggaagaagtgaagaagaactat	6854
Q	6781	gtatgaagaatccgtttcatagc	6804
D	6855	gtatgaagaatccgtttcatagc	6878
RESULT	8		
AAF83826			
ID	AAF83826	standard; DNA; 7860 BP.	
XX			
AC	AAF83826;		
XX			
DT	06-AUG-2001	(first entry)	
DE	Human ABC1 nucleotide sequence.		

RESULT	8
AAF83826	
ID	AAF83826 standard; DNA; 7860 BP
XX	
XX	
AC	AAF83826;
XX	
DT	06-AUG-2001 (first entry)
DE	Human ABC1 nucleotide sequence.

QY	1321	gacagcagggacaaatgacacattcttgggaaacagcaattgagcttgagttcagatctggacacgc	1380
Db	1395	gacagcagggacaaatgacacattcttgggaaacagcaattgagcttgagttcagatctggacacgc	1454
QY	1381	caaaacatctgaggttttttggccaagcaaccaggagatgctccagttccagtaagtgttct	1440
Db	1455	caagacatctgaggttttttggccaagcaaccaggagatgctccagttccagtaagtgttct	1514
QY	1441	gtgtacacctggagagaaagctttcaacgagaaactaacaggaatcccgagacatactccgc	1500
Db	1515	gtgtacacctggagagaaagctttcaacgagaaactaacaggaatcccgagacatactccgc	1574
QY	1501	ttcaatgagatgtgtcaacacctgaaacagctagaaccataagaaagaaagtctgctatc	1560
Db	1575	ttcaatgagatgtgtcaacacctgaaacagctagaaccataagaaagaaagtctgctatc	1634
QY	1561	aacaaatccatgtgagctgtctgtgaatgagaggaagttctctggctgtgtatgtgttaactgga	1620
Db	1635	aacaaatccatgtgagctgtctgtgaatgagaggaagttctctggctgtgtatgtgttaactgga	1694
QY	1621	attaccacaagcagcatctgagctgtcccatcatgtctcaagtaagtaaacagatccgaatggaact	1680
Db	1695	attaccacaagcagcatctgagctgtcccatcatgtctcaagtaagtaaacagatccgaatggaact	1754
QY	1681	gacaaatgtgagagagacaaataaataalcaagatgtgactcggagacccctgtgtcccgagct	1740
Db	1755	gacaaatgtgagagagacaaataaataalcaagatgtgactcggagacccctgtgtgtcccgagct	1814
QY	1741	gacccctttgagagacatgtgagctgtctgtgggggagctctgcctactctgcaagatgtgtgt	1800
Db	1815	gacccctttgagagacatgtgagctgtctgtgggggagctctgcctactctgcaagatgtgtgt	1874
QY	1801	gagcagagcaatctcaagaggtgtctgtgacggagccagagagaanaaactgtgtgtctatgtcaa	1860
Db	1875	gagcagagcaatctcaagaggtgtctgtgacggagccagagagaanaaactgtgtgtctatgtcaa	1934
QY	1861	caagatgccatctccctgttaccgttctgtatgacatcttctctgaggtgtgatgagccggtcaatg	1920
Db	1935	caagatgccatctccctgttaccgttctgtatgacatcttctctgaggtgtgatgagccggtcaatg	1994
QY	1921	cccccttcaatgacgtctgagccttgagattactcaagtgtgctgtgacatcaaggagcatgtgt	1980
Db	1995	cccccttcaatgacgtctgagccttgagattactcaagtgtgctgtgacatcaaggagcatgtgt	2054
QY	1981	tatgaaagaagagcagagcgtctgaaagaagacatgtcgagataatgtggcctgtgacaacagcata	2040
Db	2055	tatgaaagaagagcagagcgtctgaaagaagacatgtcgagataatgtggcctgtgacaacagcata	2114
QY	2041	ctctgtttagcgtgtcatatgaatcctcatctccctctctcttctgttgagcgctgtgcgtcta	2100
Db	2115	ctctgtttagcgtgtcatatgaatcctcatctccctctctctcttctgttgagcgctgtgcgtcta	2174
QY	2101	gtgtgtatccctgaagttaagaaacctgtctgcctcagatgtatccagcgtgtgtgttctgtc	2160
Db	2175	gtgtgtatccctgaagttaagaaacctgtctgcctcagatgtatccagcgtgtgtgttctgtc	2234
QY	2161	ttccctgtccgttttgtctgtgttgacaatccctgtcagctgtgttccctgttttgacaacaccttc	2220
Db	2235	ttccctgtccgttttgtctgtgttgacaatccctgtcagctgtgttccctgttttgacaacaccttc	2294
QY	2221	tccaaagacaaacctgtgcagcagctgtgtggggacatcatctactctacgcgtgtacacgtgcc	2280
Db	2295	tccaaagacaaacctgtgcagcagctgtgtggggacatcatctactctacgcgtgtacacgtgcc	2354
QY	2281	tacgtccgtgtgtgtgcagatgtgagagactacgtgtgggtctcaacactcaagaactctgcgtagc	2340
Db	2355	tacgtccgtgtgtgtgcagatgtgagagactacgtgtgggtctcaacactcaagaactctgcgtagc	2414
QY	2341	ctgagctctccctgtgcttctgt	2400
Db	2415	ctgagctctccctgtgcttctgt	2474
QY	2401	ggcatctgagatgtgcagtgtgagacaacctgttctgaagatccctgtgtgaggaagatgtgttcaat	2460

Db	2475	ggcatctgagatgtgcagtgtgagacaacctgttctgaagatccctgtgtgaggaagatgtgttcaat	2534
QY	2461	ctcaacacttcagatctccatgatatgtctgttgacaacctctctatagtgtgtatgtacctgtg	2520
Db	2535	ctcaacacttcagatctccatgatatgtctgttgacaacctctctatagtgtgtatgtacctgtg	2594
QY	2521	tacatitgagctgtcttccagggccagtacgaattcccaaggccctgtatcttctctgc	2580
Db	2595	tacatitgagctgtcttccagggccagtacgaattcccaaggccctgtatcttctctgc	2654
QY	2581	accaaatccctacgtgtgttgctgtgaggaagtgtatgtatgagaagaagccaacctgtgtccaacag	2640
Db	2655	accaaatccctacgtgtgttgctgtgaggaagtgtatgtatgagaagaagccaacctgtgtccaacag	2714
QY	2641	aaggaatgtcagaacatctcatatgtgaggaagaacccaacctgtgaagctgtgggtgtcc	2700
Db	2715	aaggaatgtcagaacatctcatatgtgaggaagaacccaacctgtgaagctgtgggtgtcc	2774
QY	2701	attcaagaacctgtgtaaagtctctacagatatgtgaagtgtgctgtctgaatgtgcctgtgca	2760
Db	2775	attcaagaacctgtgtaaagtctctacagatatgtgaagtgtgctgtctgaatgtgcctgtgtgca	2834
QY	2761	ctgaattttatgagggccagatccaacctctctctctctgtggccaacatgtgagggaggaagc	2820
Db	2835	ctgaattttatgagggccagatccaacctctctctctctgtggccaacatgtgagggaggaagc	2894
QY	2821	accacaatgtcaatccctgacccgggtgtgtcccccagcctctgggcaacgcctcaatctgt	2880
Db	2895	accacaatgtcaatccctgacccgggtgtgtcccccagcctctgggcaacgcctcaatctgt	2954
QY	2881	ggaagaagacatctgcctctgagatgagagacacatccggagaaacctgtgggtgtcttccacag	2940
Db	2955	ggaagaagacatctgcctctgagatgagagacacatccggagaaacctgtgggtgtcttccacag	3014
QY	2941	cataacgtgtctgtttgacalgtctgacatgtctgaaagaacacactctgtgtctatagtcccgctg	3000
Db	3015	cataacgtgtgtctgtttgacalgtctgacatgtctgaaagaacacactctgtgtctatagtcccgctg	3074
QY	3001	aaagggtctctctgagaaagccgtggaaggcggaaatgtgaggaatgtgcccgtgattgtgt	3060
Db	3075	aaagggtctctctgagaaagccgtggaaggcggaaatgtgaggaatgtgcccgtgattgtgt	3134
QY	3061	tgtccatcaagcaagctgtgaanaagcaaaacaaagccaagctgtctcaagtgtgaatgtcgaagaag	3120
Db	3135	tgtccatcaagcaagctgtgaanaagcaaaacaaagccaagctgtctcaagtgtgaatgtcgaagaag	3194
QY	3121	ctatctgtgtgacctgt	3180
Db	3195	ctatctgtgtgacctgt	3254
QY	3181	gtctgtgtgtgaccttaaccctcccgaa	

Dh 3555 agcaatctcgaatcgtcgccctggcgagccatagagatgacagctgacacatcatgctc 3614
Qy 3541 tctgcatctccaacatccatccaggaagcatgtctgaagcccgctggttgaaacata 3600
Dh 3615 tctgcatctccaacatccatccaggaagcatgtctgaagcccgctggttgaaacata 3674
Qy 3601 gggcatgagctacacatgtctgcatatgaagctgctaaaggagggagcccttgaggaa 3660
Dh 3675 gggcatgagctacacatgtctgcatatgaagctgctaaaggagggagcccttgaggaa 3734
Qy 3661 ctcttcgatgagatgagacggcgctccagaacccgggcatcttcaatgataagcatcca 3720
Dh 3735 ctcttcgatgagatgagacggcgctccagaacccgggcatcttcaatgataagcatcca 3794
Qy 3721 gaagagacccctgaaagaataatctccacaaagtgcgcgaagagagtggtgtagtctgag 3780
Dh 3795 gaagagacccctgaaagaataatctccacaaagtgcgcgaagagagtggtgtagtctgag 3854
Qy 3781 acctcagatgtgtaaccttgccagcaagacgaacagcggtccctcggggacaagcagagc 3840
Dh 3855 acctcagatgtgtaaccttgccagcaagacgaacagcggtccctcggggacaagcagagc 3914
Qy 3841 tgtcttcgcccgttcaactgaagatgagtctgtgtatccaaatgattcttgacataagacca 3900
Dh 3915 tgtcttcgcccgttcaactgaagatgagtctgtgtatccaaatgattcttgacataagacca 3974
Qy 3901 gaatccagagagacagactgtcagtggaatgagatgagcaaaaggtccatacaggtgaa 3960
Dh 3975 gaatccagagagacagactgtcagtggaatgagatgagcaaaaggtccatacaggtgaa 4034
Qy 3961 ggcctggaacttacaacgaacagatgtgtgcccctttgttgaaagagactgctaattgccc 4020
Dh 4035 ggcctggaacttacaacgaacagatgtgtgcccctttgttgaaagagactgctaattgccc 4094
Qy 4021 agacggagatcggaagagattttgttcagagatgtcttcagcagtgctgtcttcgcat 4080
Dh 4095 agacggagatcggaagagattttgttcagagatgtcttcagcagtgctgtcttcgcat 4154
Qy 4081 ggccttggtgtcagcgtgacgtgtgcccaccccttggaagtaaccagccttggaactcag 4140
Dh 4155 ggccttggtgtcagcgtgacgtgtgcccaccccttggaagtaaccagccttggaactcag 4214
Qy 4141 ccctggaatgtaacaggaacagtaacattgtgtacgaatgagtctcttgaggaacaggaa 4200
Dh 4215 ccctggaatgtaacaggaacagtaacattgtgtacgaatgagtctcttgaggaacaggaa 4274
Qy 4201 accttgaactcttaaacgcgcctccacaaagacccttggtctcggaacccgtgtatggaa 4260
Dh 4275 accttgaactcttaaacgcgcctccacaaagacccttggtctcggaacccgtgtatggaa 4334
Qy 4261 ggaacacccatcccaagacagccctgcaggaaggaggaagagatggacacatgcgccaa 4320
Dh 4335 ggaacacccatcccaagacagccctgcaggaaggaggaagagatggacacatgcgccaa 4394
Qy 4321 gttcccccagacatcatgagactcttccagaatgggaactgggaactggaacacccctta 4380
Dh 4395 gttcccccagacatcatgagactcttccagaatgggaactgggaactggaacacccctta 4454
Qy 4381 cctggaatgcaagtgtaagcagcgacaataatcaagaagatgctgctgtgtgtccccaagg 4440
Dh 4455 cctggaatgcaagtgtaagcagcgacaataatcaagaagatgctgctgtgtgtccccaagg 4514
Qy 4441 gcaagggggcgtgcctccccaagaagaaacaaacacatcagatctccttcagagactg 4500
Dh 4515 gcaagggggcgtgcctccccaagaagaaacaaacacatcagatctccttcagagactg 4574
Qy 4501 acaaggaagaaacattcagattatctgtgtagagcgtatgtgcagatcatagccaagaagc 4560
Dh 4575 acaaggaagaaacattcagattatctgtgtagagcgtatgtgcagatcatagccaagaagc 4634
Qy 4561 ttaagaagaacagatcgtggtgtagatgattagatgtagggcggtcttcccggtgtcag 4620
Dh 4635 ttaagaagaacagatcgtggtgtagatgattagatgtagggcggtcttcccggtgtcag 4694

Qy 4621 aatactcaagacatctcccccagatcaagaagttaatgtagtccatcaacaataagaagaa 4680
Dh 4695 aatactcaagacatctcccccagatcaagaagttaatgtagtccatcaacaataagaagaa 4754
Qy 4681 cccctaaagcttgccaagaagacagctcttcagatcagatcttcccaacagcttggagaatt 4740
Dh 4755 caccataagcttggccaagaagacagctcttcagatcagatcttcccaacagcttggagaatt 4814
Qy 4741 atgacagacttgacacccaagaataatgtcaagggtgtgttcaataacaagagctgtgat 4800
Dh 4815 atgacagacttgacacccaagaataatgtcaagggtgtgttcaataacaagagctgtgat 4874
Qy 4801 gcaatacactcttctcgtgaatgtcatcaaaatgtccattcccgggccaacactgcaaaag 4860
Dh 4875 gcaatacactcttctcgtgaatgtcatcaaaatgtccattcccgggccaacactgcaaaag 4934
Qy 4861 ggaagaaacccctagccattatggaattactgtcttcaatcaatcccttgatccacaag 4920
Dh 4935 ggaagaaacccctagccattatggaattactgtcttcaatcaatcccttgatccacaag 4994
Qy 4921 cagcagctcctcagaagtggtctgtgacccacataagtgatgtctctgttcatctgt 4980
Dh 4995 cagcagctcctcagaagtggtctgtgacccacataagtgatgtctctgttcatctgt 5054
Qy 4981 gtacacttgcaatgtctcttcgtccagccagcttgtctgtatcttcgatccaagagcgg 5040
Dh 5055 gtacacttgcaatgtctcttcgtccagccagcttgtctgtatcttcgatccaagagcgg 5114
Qy 5041 gtcagcaagaacaaacacccctgcagttcatcatcagtggagtgaaagccgtcatctcgtctc 5100
Dh 5115 gtcagcaagaacaaacacccctgcagttcatcatcagtggagtgaaagccgtcatctcgtctc 5174
Qy 5101 tctaaattgtctgggataatgtgcaattacgttgtcccgccaagctgttcaattcaatc 5160
Dh 5175 tctaaattgtctgggataatgtgcaattacgttgtcccgccaagctgttcaattcaatc 5234
Qy 5161 ttcactgcttccagaggaagctcatalgtgtctccccaacaaatctgctgtgtaagccctt 5220
Dh 5235 ttcactgcttccagaggaagctcatalgtgtctccccaacaaatctgctgtgtaagccctt 5294
Qy 5221 ctactttgtcgtatggtgtgtcaatcaacacccctcatgtacacacaccccttggcttc 5280
Dh 5295 ctactttgtcgtatggtgtgtcaatcaacacccctcatgtacacacaccccttggcttc 5354
Qy 5281 aagatcccccagcaagcctctgtgtgtcaccagcgtgaaccttctcatcttgcatlaat 5340
Dh 5355 aagatcccccagcaagcctctgtgtgtcaccagcgtgaaccttctcatcttgcatlaat 5414
Qy 5341 ggcagcgtgagcaaccttgtgtgtgagcgtgtcaacgacaataagctgaaatcaat 5400
Dh 5415 ggcagcgtgagcaaccttgtgtgtgagcgtgtcaacgacaataagctgaaatcaat 5474
Qy 5401 gatatactgaagtcctgtgtcttcatcttccacatcttggccttggaagaggtccatc 5460
Dh 5475 gatatactgaagtcctgtgtcttcatcttccacatcttggccttggaagaggtccatc 5534
Qy 5461 gacatggtgaaacaaacagcagatgctgtagcccttggaagaggttggggaatcgcctt 5520
Dh 5535 gacatggtgaaacaaacagcagatgctgtagcccttggaagaggttggggaatcgcctt 5594
Qy 5521 ggttcacatatacttgagactgtgtgtgtgagcgaacactcttcgcacatggcgtggaagg 5580
Dh 5595 ggttcacatatacttgagactgtgtgtgtgagcgaacactcttcgcacatggcgtggaagg 5654
Qy 5581 gttggtctcttcctaatatctgattcttcatccagtagacagatcttcatcaagcccaagct 5640
Dh 5655 gttggtctcttcctaatatctgattcttcatccagtagacagatcttcatcaagcccaagct 5714
Qy 5641 gtaaatgcaaaactatctcctctgaatgataagaatgaaatgtgagggcggaagacag 5700
Dh 5715 gtaaatgcaaaactatctcctctgaatgataagaatgaaatgtgagggcggaagacag 5774

```

QY 5701 agaattcttgaatggtgagcccaaatgacattctagaatcaagagattgacgaagata 5760
DB 5775 agaattcttgaatggtgagcccaaatgacattctagaatcaagagattgacgaagata 5834
QY 5761 tatagaaggaagcggaagcctgtctgtgaagaatttcgttggcattctcctgtgtgag 5820
DB 5835 tatagaaggaagcggaagcctgtctgtgaagaatttcgttggcattctcctgtgtgag 5894
QY 5821 tgccttggcctcctgggaattgaatgggctgggaataatcatcaattccaagaattaca 5880
DB 5895 tgccttggcctcctgggaattgaatgggctgggaataatcatcaattccaagaattaca 5954
QY 5881 ggagataccactgttaccagaagagatgcttcttcaacaaataaglaattcataaac 5940
DB 5955 ggagataccactgttaccagaagagatgcttcttcaacaaataaglaattcataaac 6014
QY 5941 atccataagtaactcagcaacatgggtactgcccctcagtttaagtcacacagagctg 6000
DB 6015 atccataagtaactcagcaacatgggtactgcccctcagtttaagtcacacagagctg 6074
QY 6001 ttgacttggagagaacacgctgagatcttcttcccttggagagagctcccaagaagaa 6060
DB 6075 ttgacttggagagaacacgctgagatcttcttcccttggagagagctcccaagaagaa 6134
QY 6061 gttggcaaggttgggtgagtgccgattcggaaacttggcctcgttgaagatggagaana 6120
DB 6135 gttggcaaggttgggtgagtgccgattcggaaacttggcctcgttgaagatggagaana 6194
QY 6121 tatgctgttaactatagttgaagcaacaaacgaagctctcctacacacatgcttgatc 6180
DB 6195 tatgctgttaactatagttgaagcaacaaacgaagctctcctacacacatgcttgatc 6254
QY 6181 ggcgggctcctctgtggttcttctgaaacccacacagagatgattcccaagcccg 6240
DB 6255 ggcgggctcctctgtggttcttctgaaacccacacagagatgattcccaagcccg 6314
QY 6241 cggcttcttgggaattgttcctcctcctcctcctcctcctcctcctcctcctcctcct 6300
DB 6315 cggcttcttgggaattgttcctcctcctcctcctcctcctcctcctcctcctcctcct 6374
QY 6301 tctcatagatagtggaagatgtagagctcttgcactagatgtagcaatctgttcaatgga 6360
DB 6375 tctcatagatagtggaagatgtagagctcttgcactagatgtagcaatctgttcaatgga 6434
QY 6361 aggttcaggttgccttggcagtggttccaagatcttaaaataaggttggagatgttataca 6420
DB 6435 aggttcaggttgccttggcagtggttccaagatcttaaaataaggttggagatgttataca 6494
QY 6421 atagttgtagaataagcaaggttccaaccccggaagcctgttcacagattctttgga 6480
DB 6495 atagttgtagaataagcaaggttccaaccccggaagcctgttcacagattctttgga 6554
QY 6481 cttgcaattctctggaagtggttctaaagaagaacccggaacatgctacaatcacagctt 6540
DB 6555 cttgcaattctctggaagtggttctaaagaagaacccggaacatgctacaatcacagctt 6614
QY 6541 ccatcttaatactctctgcccagagatcttcagcaatccctccccaagcgaagcga 6600
DB 6615 ccatcttaatactctctgcccagagatcttcagcaatccctccccaagcgaagcga 6674
QY 6601 ctccacatagaagactactctgttctcagacaacacttgcacaaagtgttgaactt 6660
DB 6675 ctccacatagaagactactctgttctcagacaacacttgcacaaagtgttgaactt 6734
QY 6661 gccaaagccaaagtgtgagatgagcaacttaaaagacttccattacaacaaacagaga 6720
DB 6735 gccaaagccaaagtgtgagatgagcaacttaaaagacttccattacaacaaacagaga 6794
QY 6721 gtagtgcagcttgcagttctcacatctttctacagatgagaagtgaaagaaagctat 6780
DB 6795 gtagtgcagcttgcagttctcacatctttctacagatgagaagtgaaagaaagctat 6854
QY 6781 gtagtgcagcttgcagttctcacatctttctacagatgagaagtgaaagaaagctat 6804

```

```

DB 6855 gtagtgcagcttgcagttctcacatctttctacagatgagaagtgaaagaaagctat 6878
RESULT 9
AADD21326
ID AADD21326 standard; DNA: 7260 BP.
XX
XX AADD21326;
XX
XX 28-JAN-2002 (first entry)
XX
XX Human ATP binding cassette transporter 1 (ABCI) gene.
XX
XX Human, ATP binding cassette transporter 1; ABC1; coronary heart disease;
XX dermatological; atherosclerosis; cardiovascular; inflammatory disease;
XX psoriasis; lipid disorder; antibacterial; septic shock; gene therapy;
XX immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 321..7106
XX FT /*tag= a
XX FT /product= "Human ABC1 protein"
XX
XX EP1136552-A1.
XX
XX 26-SEP-2001.
XX
XX 20-MAR-2000; 2000EP-0105820.
XX
XX 20-MAR-2000; 2000EP-0105820.
XX
XX (FARB ) BAYER AG.
XX
XX Schmitz G, Bodzioch M;
XX
XX WPI: 2001-640386/74.
XX
XX P-PSDB; AAE13022.
XX
XX New adenosine triphosphate binding cassette transporter-1 gene
XX polymorphisms, useful for diagnosing and treating lipid disorders,
XX cardiovascular diseases and inflammatory diseases
XX
XX Example 1; Fig 1; 48pp; English.
XX
XX The invention relates to four common polymorphisms in the gene encoding
XX ATP-binding cassette transporter-1 (ABCI). ABC1 is associated with
XX decreased ApoA-I mediated efflux of cholesterol. The polymorphisms in
XX ABC1 directly affects cellular lipid homeostasis, which is a key factor
XX in the atherogenic processes. The ABC1 polymorphisms are useful for
XX diagnosing and treating lipid disorders, cardiovascular diseases
XX (coronary heart disease, atherosclerosis) and inflammatory diseases
XX (psoriasis, lupus erythematosus). The identification of ABC1 as a
XX transporter for interleukin-1beta (IL-1beta) identifies this gene as
XX a candidate for treatment of inflammatory diseases including rheumatoid
XX arthritis and septic shock. The present sequence is human ABC1 gene.
XX
XX Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other.
XX
Query Match 99.8%; Score 6788; DB 22; Length 7260;
Best local Similarity 99.9%; Pred. No. 0;
Matches 6794; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 atggtctgttggcctcagctgaggtgtgctgtgtggaagaaactcaattcagaagaaga 60
DB 321 atggtctgttggcctcagctgaggtgtgctgtgtggaagaaactcaattcagaagaaga 380
QY 61 caaactgtcagctgttaactggaagtggccttgcctcattatcttcgactgtc 120
DB 381 caaactgtcagctgttaactggaagtggccttgcctcattatcttcgactgtc 440

```


121 tctgttcgctgagctaacccactatgaacaacatgatccatttccaaataaagcc 180
|||||
441 tctgttcgctgagctaacccactatgaacaacatgatccatttccaaataaagcc 500
|||||
181 atgccccttgaggaacaacttcttgggttcaagggtattatctgttaatgcacaacccc 240
|||||
501 atgccccttgaggaacaacttcttgggttcaagggtattatctgttaatgcacaacccc 560
|||||
241 tgtttccgttaccgacccctctggggaagctcccggaattgtttgnaaactttaacaaatcc 300
561 tgtttccgttaccgacccctctggggaagctcccggaattgtttgnaaactttaacaaatcc 620
|||||
301 attgtgtctgcgctgttctcagatgtctcgagagctcttcttatacagccagaagacacc 360
621 attgtgtctgcgctgttctcagatgtctcgagagctcttcttatacagccagaagacacc 680
|||||
361 agcatgaaggacatgctgcgaagaattcttgagaacattacagcagatccaagaataccagctca 420
681 agcatgaaggacatgctgcgaagaattcttgagaacattacagcagatccaagaataccagctca 740
|||||
421 aacttgaaagcttcaagatttccgtgtgacaatgaacactctctctgggttccctatccac 480
|||||
741 aacttgaaagcttcaagatttccgtgtgacaatgaacactctctctgggttccctatccac 800
|||||
481 aacctctctcccaaaagtactatgtgacaagaatgctgagagctgatatcttccac 540
801 aacctctctcccaaaagtactatgtgacaagaatgctgagagctgatatcttccac 860
|||||
541 aaggatattttgcaaggctcaccagttacatttgacaagtctgttcaatggtatcaaatca 600
861 aaggatattttgcaaggctcaccagttacatttgacaagtctgttcaatggtatcaaatca 920
|||||
601 gaagagatgattcaacttctgtgacaagaagaatttctgagcttctgtgacctcaacaaggag 660
921 gaagagatgattcaacttctgtgacaagaagaatttctgagcttctgtgacctcaacaaggag 980
|||||
661 aaactgtctgcagcagcagagagtaacttcttccaaactgagcatctcttaagccaaatctgc 720
981 aaactgtctgcagcagcagagagtaacttcttccaaactgagcatctcttaagccaaatctgc 1040
|||||
721 agaacactaaactctacatctccctccctcccgagcaagagctgtgctgaagccacaanaa 780
1041 agaacactaaactctacatctccctccctcccgagcaagagctgtgctgaagccacaanaa 1100
|||||
781 ttgctgcataagctcttgagagctctgcccagagagctgttcaagcatgaagaagctgagtgac 840
1101 ttgctgcataagctcttgagagctctgcccagagagctgttcaagcatgaagaagctgagtgac 1160
|||||
841 atgcgagcagagagtgatgttcttctgaccaaagtgaacagctcagctctccccaacaaatc 900
1161 atgcgagcagagagtgatgttcttctgaccaaagtgaacagctcagctctccccaacaaatc 1220
|||||
901 taccagagctgtgctcgtattgttctgcgggcatcccgagggaggggctggaagatacaag 960
1221 taccagagctgtgctcgtattgttctgcgggcatcccgagggaggggctggaagatacaag 1280
|||||
961 tctctcaactgtgatgaggaacaacatacaaaagcccttcttgaggagcaatgacatgag 1020
1281 tctctcaactgtgatgaggaacaacatacaaaagcccttcttgaggagcaatgacatgag 1340
|||||
1021 gaagatgctgaacactctctatgacaactctacaactccttactgacatgatttgtagag 1080
1341 gaagatgctgaacactctctatgacaactctacaactccttactgacatgatttgtagag 1400
|||||
1081 aatttgagctatgactccttctccgcatatcttggaagcctctgaagccgtgtcgtt 1140
1401 aatttgagctatgactccttctccgcatatcttggaagcctctgaagccgtgtcgtt 1460
|||||
1141 gggaagatctctgtatatcaacttgacaactccagccaagagcaggttcaatgctgagtgaa 1200
1461 gggaagatctctgtatatcaacttgacaactccagccaagagcaggttcaatgctgagtgaa 1520

1201 aagacctccaggaactgctgttctcatgatcttggaagcactgttggaggaactcagc 1260
1521 aagacctccaggaactgctgttctcatgatcttggaagcactgttggaggaactcagc 1580
|||||
1261 cccaagatctgagaccttcatgagagaacagccaagaatgagacctgttccggatgctgtt 1320
1581 cccaagatctgagaccttcatgagagaacagccaagaatgagacctgttccggatgctgtt 1640
|||||
1321 gacagcagggacaatgacacacttcttggaacagcagtttgatgttgatttgagaagcc 1380
1641 gacagcagggacaatgacacacttcttggaacagcagtttgatgttgatttgagaagcc 1700
|||||
1381 cagaacatctgtggcgttttcttgccaagaccagagagatgtccagttccaataatgttcc 1440
1701 cagaacatctgtggcgttttcttgccaagaccagagagatgtccagttccaataatgttcc 1760
|||||
1441 ggttacccttgagagaagacttccaagagacttaacaggaatcccgaccataatctgc 1500
1761 ggttacccttgagagaagacttccaagagacttccaaggaatcccgaccataatctgc 1820
|||||
1501 ttcatgagatgtgtcaacctgaacacttaagaacccaatagaagaagaatctgcttcatc 1560
1821 ttcatgagatgtgtcaacctgaacacttaagaacccaatagaagaagaatctgcttcatc 1880
|||||
1561 aacaagttcatgagcctgtctgatatgaggaagtctctggctgttatgtgttcaatgta 1620
1881 aacaagttcatgagcctgtctgatatgaggaagtctctggctgttatgtgttcaatgta 1940
|||||
1621 atthactccaagagatctgagcctgccatcatgttcaagtccaagatccgaatggaatc 1680
1941 atthactccaagagatctgagcctgccatcatgttcaagtccaagatccgaatggaatc 2000
|||||
1681 gccaagtgtgagaagaacaataaatacaagaatggtgtacttgagccctgtgctccagct 1740
2001 gccaagtgtgagaagaacaataaatacaagaatggtgtacttgagccctgtgctccagct 2060
|||||
1741 gaccttctgagagacatgctgctgacgtcttgagggggtctgcctactcttgcaagatgtgt 1800
2061 gaccttctgagagacatgctgctgacgtcttgagggggtctgcctactcttgcaagatgtgt 2120
|||||
1801 gacagcagcatcatcatcaggtgtctgacgggacacgggaagaagaactggtgtatatgcaa 1860
2121 gacagcagcatcatcatcaggtgtctgacgggacacgggaagaagaactggtgtatatgcaa 2180
|||||
1861 cagatgccatccctgttactgtatgacacatcttctgcgggtgatatgagccgttcaatg 1920
2181 cagatgccatccctgttactgtatgacacatcttctgcgggtgatatgagccgttcaatg 2240
|||||
1921 cccctcttaatacgtctgagccttgatcttaactcagtggtctgtagatcatcaaggacatgt 1980
2241 cccctcttaatacgtctgagccttgatcttaactcagtggtctgtagatcatcaaggacatgt 2300
|||||
1981 tatgagaagagagcagagcttgaaagagacatgagcatatgagcctggaacaagacata 2040
2301 tatgagaagagagcagagcttgaaagagacatgagcatatgagcctggaacaagacata 2360
|||||
2041 cctcgtgtttagcgtgttcatatgaactcattcctctctgtgagcgtgagcgtccta 2100
2361 cctcgtgtttagcgtgttcatatgaactcattcctctctgtgagcgtgagcgtccta 2420
|||||
2101 gtgtgatacctctgaagttagaanaacctgctgccttaagtgatcccgagctgtgttttct 2160
2421 gtgtgatacctctgaagttagaanaacctgctgccttaagtgatcccgagctgtgttttct 2480
|||||
2161 ttccgtgcgtgttctgtgtgtgtagacaatccctgaatgcttccctgattagacacactctc 2220
2481 ttccgtgcgtgttctgtgtgtgtagacaatccctgaatgcttccctgattagacacactctc 2540
|||||
2221 tccagagccaactcgtgagcagcctgttgaggagcatcatctactcaagctgtgaactgcc 2280
2541 tccagagccaactcgtgagcagcctgttgaggagcatcatctactcaagctgtgaactgcc 2600
|||||
2281 taagtctgtgtgtgtgtagcagagcactagtggtgttcaactcaagatcttctgctagc 2340

QY 4501 acaggaagaacatttcgatatctctgtaagacgtaattgacagatcatagccaaagc 4560
|||||
Db 4821 acaggaagaacatttcgatatctctgtaagacgtaattgacagatcatagccaaagc 4880
QY 4561 ttaagaagaacatttcgatatctctgtaagacgtaattgacagatcatagccaaagc 4620
|||||
Db 4881 ttaagaagaacatttcgatatctctgtaagacgtaattgacagatcatagccaaagc 4940
QY 4621 aatctacagacatttcgatatctctgtaagacgtaattgacagatcatagccaaagc 4680
|||||
Db 4941 aatctacagacatttcgatatctctgtaagacgtaattgacagatcatagccaaagc 5000
QY 4681 caactaaagctgagcaagacgattctgcaagctgattctcaaacagcttggaagattc 4740
5001 caactaaagctgagcaagacgattctgcaagctgattctcaaacagcttggaagattc 5060
QY 4741 atgacagacatttcgatatctctgtaagacgtaattgacagatcatagccaaagc 4800
|||||
Db 5061 atgacagacatttcgatatctctgtaagacgtaattgacagatcatagccaaagc 5120
QY 4801 gcaatcagacttcctgatatctctgtaagacgtaattgacagatcatagccaaagc 4860
5121 gcaatcagacttcctgatatctctgtaagacgtaattgacagatcatagccaaagc 5180
QY 4861 ggaagaaacctagacacattatggaattactgcttcaacatccctgtaattcaacaa 4920
5181 ggaagaaacctagacacattatggaattactgcttcaacatccctgtaattcaacaa 5240
QY 4921 caagacatttcgatatctctgtaagacgtaattgacagatcatagccaaagc 4980
5241 caagacatttcgatatctctgtaagacgtaattgacagatcatagccaaagc 5300
QY 4981 gtcatcttgcaattgctcctcgctccagcagcttgctgattctccgtaacagagcg 5040
5301 gtcatcttgcaattgctcctcgctccagcagcttgctgattctccgtaacagagcg 5360
Db 5041 gtagcaagaacaaacacacgctgacatcagatgagtgagtgagcttcaactgctgc 5100
5361 gtagcaagaacaaacacacgctgacatcagatgagtgagtgagcttcaactgctgc 5420
QY 5101 tccaatttctgctgatatgtaatactgtaattgctcctgcaacacacacacacacac 5160
5421 tccaatttctgctgatatgtaatactgtaattgctcctgcaacacacacacacacac 5480
QY 5161 ttcactgcttcagcaagaagctcctatgctcctccacacacacacacacacacac 5220
5481 ttcactgcttcagcaagaagctcctatgctcctccacacacacacacacacacac 5540
QY 5221 ctactcttgctgatatgtaatactgtaattgctcctgcaacacacacacacacacac 5280
5541 ctactcttgctgatatgtaatactgtaattgctcctgcaacacacacacacacacac 5600
Db 5281 aagatcccgagcaagac 5340
5601 aagatcccgagcaagac 5660
QY 5341 ggcagcgctgagcaac 5400
5661 ggcagcgctgagcaac 5720
QY 5401 gatactcctgagtcgctgctgctgctgctgctgctgctgctgctgctgctgctgct 5460
5721 gatactcctgagtcgctgctgctgctgctgctgctgctgctgctgctgctgctgct 5780
Db 5461 gatactcctgagtcgctgctgctgctgctgctgctgctgctgctgctgctgctgct 5520
5781 gatactcctgagtcgctgctgctgctgctgctgctgctgctgctgctgctgctgct 5840
QY 5521 gctgac 5580
5841 gctgac 5900

QY 5581 gtggtcttctcctcattactgttctgatactcagatcatagcttccacagccacacac 5640
|||||
Db 5901 gtggtcttctcctcattactgttctgatactcagatcatagcttccacagccacacac 5960
QY 5641 gtaagtcaagac 5700
5961 gtaagtcaagac 6020
QY 5701 agaattctgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtc 5760
6021 agaattctgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgag 6080
Db 6081 taaagaaagac 6140
QY 5761 taaagaaagac 5820
6081 taaagaaagac 6140
QY 5821 tgccttgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtc 5880
6141 tgccttgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtc 6200
Db 5881 ggaagaaacctgatacag 5940
6201 ggaagaaacctgatacag 6260
QY 5941 atccatgagac 6000
6261 atccatgagac 6320
Db 6001 ttgacttgagagagac 6060
6321 ttgacttgagagagac 6380
QY 6061 gttgcaagagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgag 6120
6381 gttgcaagagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgag 6440
Db 6121 tatgcttgatactatgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgag 6180
6441 tatgcttgatactatgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgag 6500
QY 6181 ggcgagtcctcctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6240
6501 ggcgagtcctcctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6560
Db 6241 cggcttctgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgag 6300
6561 cggcttctgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgag 6620
QY 6301 tctcatagatag 6360
6621 tctcatagatag 6680
Db 6361 aagtcagtcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6420
6681 aagtcagtcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 6740
QY 6421 atagtcgatacag 6480
6741 atagtcgatacag 6800
Db 6481 ctgcaattcctcgag 6860
6801 ctgcaattcctcgag 6920
QY 6541 ccatctcatatcttctcctgagagagagagagagagagagagagagagagagagagag 6600
6861 ccatctcatatcttctcctgagagagagagagagagagagagagagagagagagagag 6920
Db 6601 ctccacataag 6660
6921 ctccacataag 6980
QY 6661 gccaagac 6720

Dd	6981	gccaaaggaccaaagtgaatgataagaccacttaagaacctctcattacaacaaaacagaca	7040
Oy	6721	gtagtggaacgttgcgaattcccaactctttcttcagatgagaagaagtgaagaagcat	6780
Dd	7041	gtacgtgacgtcttgacgtcttcacactcttccttacagatgagaagaagtgaagaagcat	7100
Oy	6781	gtatgaagaatccctcttcataacgg	6804
Dd	7101	gtatgaagaatccctcttcataacgg	7124
 RESULT_10 AAI70315			
ID	AAI70315	standard; cDNA; 7260 BP.	
AC	AAI70315;		
DT	07-JAN-2002	(first entry)	
XX			
XX	Human ATP binding cassette transporter 1 (ABCI) cDNA.		
KW	ATP binding cassette transporter 1; ABC1; human; lipid disorder;		
KW	cholesterol; cardiovascular disease; inflammatory disease;		
KW	antiinflammatory; antilipemic; antipsoriatic; dermatological;		
KW	Tangier disease; coronary heart disease; diagnosis; gene therapy;		
KX	polymorphism; ss.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	CDS	321..7106	
FT		/**tag= a	
FT	CDS	501..7106	
FT		/**tag= b	
FT	variation	/note= "alternative open reading frame of AAI70314"	
FT	variation	replace(976,A)	
FT		/**tag= c	
FT	variation	replace(1516,C)	
FT		/**tag= d	
FT	variation	replace(2969,G)	
FT		/**tag= e	
FT	variation	replace(3836,C)	
FT		/**tag= f	
PN	EP1136554-A1.		
PD	26-SEP-2001.		
PF	24-MAR-2000; 2000EP-0106401.		
PR	24-MAR-2000; 2000EP-0106401.		
PA	(FARB) BAYER AG.		
PI	Schmitz G, Bodzioch M;		
DR	WPI: 2001-640389/74.		
DR	P-PSDB; AAM50228.		
PT	New adenosine triphosphate binding cassette transporter gene		
PT	cardiovascular diseases and treating lipid disorders,		
PS	Disclosure; Page 26-28; 41pp; English.		
CC	The present sequence is that of cDNA encoding the human adenosine		
CC	triphosphate (ATP) binding cassette transporter 1 (ABCI) protein		
CC	(see AAM50227). The sequence includes an extended open reading		
CC	frame (ORF) to that provided by the sequence in AAI70314, using		
CC	an alternative ATG codon as initiation codon and thereby adding an		
CC	extra 40 N-terminal amino acids to the encoded ABC1 protein (see		
CC	AAM50228). The invention provides 4 common polymorphisms in the		

CC ABCL1 gene. These were identified by sequencing the ABCL1 gene in
CC different Tangier kindreds. In the variant genes (numbering as in
CC AA170314), G is changed to A at position 596, T is changed to C at
CC position 1136, A is changed to G at position 289 or G is changed
CC to C at position 3456, or any combination of these. All of these
CC polymorphisms alter the amino acid sequence of ABCL1 and therefore
CC may affect its function. The 2 most common polymorphisms (G596A)
CC and A2589G) are both associated with a decreased *in vitro* ApoA-I
CC mediated efflux of cholesterol from mononuclear phagocytes, a
CC feature typical of Tangier disease. 3 of the variants (G596A,
CC A2589G and G3456C) are significantly increased in a population of
CC men having low high density lipoprotein-cholesterol levels and
CC established coronary heart disease (CHD) relative to CHD-free
CC control subjects. The use of the provided ABCL1 polymorphisms for
CC the diagnosis and treatment of lipid disorders, cardiovascular
CC diseases, and inflammatory diseases (e.g., psoriasis, lupus
CC erythematosus) is claimed. Modulation of ABCL1 transcripts or
CC proteins by antisense or ribozyme technology or RNA decoys is also
CC claimed.
XX
50 Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;

Query Match	99.8%	Score 6788;	DB 22;	Length 7260;
Best Local Similarity	99.98%	Pred. No. 0;		
Matches 6794; Conservative	0;	Mismatches 10;	Indels 0;	Gaps 0;

QY	1	agagctgtttggccctcaagcttaagtgatgctgtgtgtagaagaactcaacttcttgaagaaga	60
Db	321	atggtctgtgtggccccaagctgaggtgtcgtgctgtgtagaagaaccacacttccagaagaaga	380
QY	61	caaaacatgtcaagctgttaactgtgaagatgtgctgtgctctatattactctctgacctgac	120
Db	381	caaaacatgtcaagctgttactactgaaagtgtgctgtgctctattactctctgacctgac	440
QY	121	tcgttccggtctgagcttaccacccctatgaanaaatatgaagcattttccaataaacc	180
Db	441	tcgttccggtctgagcttaccacccctatgaanaaatatgaagcattttccaataaacc	500
QY	181	atgtccctctgcagaagaacacttcccttggtgttcacagggtatctgtaaatgcacaacccc	240
Db	501	atgtccctctgcagaagaacacttcccttggtgttcacagggtatctgtaaatgcacaacccc	560
QY	241	tgttttcggttaccccaagctccctgtggagagctcccggaattgttgaaacttaacaatccc	300
Db	561	tgttttcggttaccccaagctccctgtggagagctcccggaattgttgaaacttaacaatccc	620
QY	301	atgtgtgctcgcgcctgtttctcaagatgtctcggaaagctctctttatacagccagaagaacc	360
Db	621	atgtgtgctcgcgcctgtttctcaagatgtctcggaaagctctctttatacagccagaagaacc	680
QY	361	agcatatgaagacatctgcgaagaagctctctagaacaattcaagaagtcgaagaatccagctca	420
Db	681	agcatatgaagacatctgcgaagaagctctctagaacaattcaagaagtcgaagaatccagctca	740
QY	421	aaacttgaagcttcaagatlttccctgtgtgtagacaatgaaaccttctctgtgttccatatacc	480
Db	741	aaacttgaagcttcaagatlttccctgtgtgtagacaatgaaaccttctctgtgttccatatacc	800
QY	481	aaacctctctctcccaaaatctctacgtgtgtagacaagaatctgaagctgcgaatgtcaattccac	540
Db	801	aaacctctctctcccaaaatctctacgtgtgtagacaagaatctgaagctgcgaatgtcaattccac	860
QY	541	aaggtattttttgcaagagctaccaggtatcaactttgacaagaatctgtgtcaatgtgatacaaatca	600
Db	861	aaggtattttttgcaagagctaccaggtatcaactttgacaagaatctgtgtcaatgtgatacaaatca	920
QY	601	gaagagatgatattcaaatctgtgtgacccaagaagcttctcgaacttgtgtgctctcccaagaag	660
Db	921	gaagagatgatattcaaatctgtgtgacccaagaagcttctcgaacttgtgtgctctcccaagaag	980
QY	661	aaactgtgctgcagagcagagctgatactcgtttccacaatgacatccctgaagcgaactctgt	720

Db	981	aaatcgtgcagcagagcgagtaacttcgtccaaacttgacatcctcgtgaagccaactctg	1040
Qy	721	agaacactaaactctacatcctccctcccgagcaagagctctgctgaagccacaanaaca	780
Db	1041	agaacactaaactctacatcctccctcccgagcaagagctctgctgaagccacaanaaaa	1100
Qy	781	ttctcgtacatagtcttggagctctggccaggaagctcttcagctctggaagctctgattgac	840
Db	1101	ttcgtcgtacatagtcttggagctcttggccaggaagctcttcagctctggaagctctgattgac	1160
Qy	841	atgagcagagaggtgatagtcttccttgacaaatgtgacaaagctctccacccaataatc	900
Db	1161	atgagcagagaggtgatagtcttccttgacaaatgtgacaaagctctccacccaataatc	1220
Qy	901	taccagagctgtctctcgtattgtcttcgctgggcatcccgagagaggggctggaattcaag	960
Db	1221	taccagagctgtctctcgtattgtcttcgctgggcatcccgagagaggggctggaattcaag	1280
Qy	961	tctctcaactcgtatagagacaacaactacaagaagccctctcttgagagcaatctgacctgg	1020
Db	1281	tctctcaactcgtatagagacaacaactacaagaagccctctcttgagagcaatctgacctgg	1340
Qy	1021	gaagatgctgaaaaactctctatgacaactctacactcttaactgcaatgtattgataag	1080
Db	1341	gaagatgctgaaaaactctctatgacaactctacactcttaactgcaatgtattgataag	1400
Qy	1081	aatttgagatcgtactcctctctcccgatctatctctgaaagctctggaagccgcctcgtt	1140
Db	1401	aatttgagatcgtactcctctctcccgatctatctctgaaagctctggaagccgcctcgtt	1460
Qy	1141	gggaagatccctgtaatacaactcgacaactccagccacaagaagcagatcgtcgtatgaaac	1200
Db	1461	gggaagatccctgtaatacaactcgacaactccagccacaagaagcagatcgtcgtatgaaac	1520
Qy	1201	aagacactccaggaactcgtcgtgttcacatgactcgtggaagcagatgtagggagaaactaagc	1260
Db	1521	aagacactccaggaactcgtcgtgttcacatgactcgtggaagcagatgtagggagaaactaagc	1580
Qy	1261	cccaagatcctggaactctcatgagaaacagccagaagaatggaactctgctccgattcgtttg	1320
Db	1581	cccaagatcctggaactctcatgagaaacagccagaagaatggaactctgctccgattcgtttg	1640
Qy	1321	gacagcagggagaactgacccaacttttgggaacagcagttggatgcttgaatttgacagcc	1380
Db	1641	gacagcagggagaactgacccaacttttgggaacagcagttggatgcttgaatttgacagcc	1700
Qy	1381	caaagcactcctgggagcttttttggccaaagcaccagagagatgctccatccagtaatgagttc	1440
Db	1701	caaagcactcctgggagcttttttggccaaagcaccagagagatgctccatccagtaatgagttc	1760
Qy	1441	ggtctacactctggagagaagaagctcttcaacgagactaaacagggcaatcccgacaatalctgc	1500
Db	1761	ggtctacactctggagagaagaagctcttcaacgagactaaacagggcaatcccgacaatalctgc	1820
Qy	1501	ttcatgagagctgtgtcaactcgtgaaanaagctctagaagcccatagcaagaagagctctggctaac	1560
Db	1821	ttcatgagagctgtgtgtcaactcgtgaaanaagctctagaagcccatagcaagaagagctctggctaac	1880
Qy	1561	aaacaagctccaatgagagctgctgtaacgaaagaaattctctggagctgtgatatgttcaactgta	1620
Db	1881	aaacaagctccaatgagagctgctgtaacgaaagaaattctctggagctgtgatatgttcaactgta	1940
Qy	1621	attactccaagcagagattgagctgcccactcatgtaagaataaagaatccgaattgacaatt	1680
Db	1941	attactccaagcagagattgagctgcccactcatgtaagaataaagaatccgaattgacaatt	2000
Qy	1681	gacaatgctgaaagagacaataaatacaagatctgggtactgtaggaacctgtgtctcogaagct	1740
Db	2001	gacaatgctgaaagagacaataaatacaagatctgggtactgtaggaacctgtgtctcogaagct	2060
Qy	1741	gacccctttgagagacatgctcggttaagctctgggggggcttcgctcaacttgaagaatgtgtg	1800
Db	2061	gacccctttgagagacatgctcggttaagctctgggggggcttcgctcaacttgaagaatgtgtg	2120

QY	1801	gagcagagcaacatcatcagaggctgcctgacccggagccagagaaacacggtgltctatctatgcaa	1860
Db	2121	gagcagagcaacatcatcagagggtgcctgcagccagccagagaaacatcgtgtctatctatgcaa	2180
QY	1861	cagatgcgccatcatcccggttaagcttgaatgaacatctcttcgacggagtgatgagacccgtcaatg	1920
Db	2181	cagatgcgccatcatcccggttaacgtatgcatgcatctcttcgacggagtgatgagacccgtcaatg	2240
QY	1921	ccccccttcacagccgctgcgctctgagatcttaacgtatgcgtctgacatcaaggacatcgtg	1980
Db	2241	cccccttcacagccgctgcgctctgagatcttaacgtatgcgtctgacatcaaggacatcgtg	2300
QY	1961	tatgagaagagagcagcagccgtgaaagagacacagcagatcatgagggccctgcgacacagcata	2040
Db	2301	tatgagaagagagcagcagccgtgaaagagacacacagcagatcatgagggccctgcgacacagcata	2360
QY	2041	ctctgcgtttacgctgcgttcatctatgaatcaaccatctccctctctcttgagaaagcgtctgcgtcta	2100
Db	2361	ctctgcgtttacgctgcgttcatctatgaatgaatccatctccctctcttgagaaagcgtctgcgtcta	2420
QY	2101	gtgcgtacatccatgaagttagagaaacctgcctgcctcaccgtatccaccgctgcgtggtttgttc	2160
Db	2421	gtgcgtacatccatgaagttagagaaacctgcctgcctcaccgtatccaccgctgcgtggtttgttc	2480
QY	2161	ttccctgcctgcgtggtttgcgtgtgcgaacatcccgacagctgcctctgcgtatgaacacatcttc	2220
Db	2481	ttccctgcctgcgtggtttgcgtgtgcgaacatcccgacagctgcctctgcgtatgaacacatcttc	2540
QY	2221	tcccaagaccaaacccgagcagacgctctgtgggggagatcatcatctacacgctgtacacgtccc	2280
Db	2541	tcccaagaccaaacccgagcagacgctctgtgggggagatcatcatctacatccgctgtacacgtccc	2600
QY	2281	tacgtctcgtgtgtgcgcagtcgagagcactacgtgcgtgcacatcccaacatcttcgctgacg	2340
Db	2601	tacgtctcgtgtgtgcgcagtcgagagcactacgtgcgtgcacatcccaacatcttcgctgacg	2660
QY	2341	cagcgcgtcccccgcgtgcctttgcgtcttcgcgtgcagatcatcttgcaccttttgagagagcag	2400
Db	2661	cagcgcgtcccccgcgtgcctttgcgtcttcgcgtgcagatcatcttgcaccttttgagagagcag	2720
QY	2401	ggcattgcagtgacgtgagagcaaacctgttgagagctcctgcgtgcagagagatgagtttcaat	2460
Db	2721	ggcattgcagtgacgtgagagcaaacctgttgagagctcctgcgtgcagagagatgagtttcaat	2780
QY	2461	ctcaccaactctgacatctcatcagatgcgttttgacaacctccctctataaggggtgataccctg	2520
Db	2781	ctcaccaactctgacatctcatcagatgcgttttgacaacctccctctataaggggtgataccctg	2840
QY	2521	tacattgcagctgcctctctccagccagctacggaattcccaagccctgcgtattctcctgc	2580
Db	2841	tacattgcagctgcctctctccagcccaatcaggaattcccaagccctgcgtattctcctgc	2900
QY	2581	accaaatctactatggttttgaggagaaagtgatgagaaagccacacccgtgttccaacag	2640
Db	2901	accaaatctactatggttttgaggagaaagtgatgagaaagccacacccgtgttccaacag	2960
QY	2641	aagagagatgtcagaaatctgcatactgagagagaaacccaaccacttgaagcttggcgtgtcc	2700
Db	2961	aagagagatctcagaaatctgcatactgagagagaaacccaaccacttgaagcttggcgtgtcc	3020
QY	2701	attcgaaacctgttaaaagttctaccgagatgaggatgaagttgcctctgcatactgcctgcga	2760
Db	3021	attcgaaacctgttaaaagttctaccgagatgaggatgaagttgcctctgcatactgcctgcga	3080
QY	2761	ctgaatttttaagagagccagatcacacccctctctctgcgcacaaatgagcgggagaaagc	2820
Db	3081	ctgaatttttaagagagccagatcacacccctctctctgcgcacaaatgagcgggagaaagc	3140
QY	2821	accacacatgtcaactcctgcacgggtgttctcccccagccctgcggacccgctacatactctg	2880
Db	3141	accacacatgtcaactcctgcacgggtgttctcccccagccctgcggacccgctacatactctg	3200

QY	2881	ggaagaagacattcgctctggaatagaagaacatcccggaagaaacttggggtctgtcccaag	294
Db	3201	ggaaaaagacattcgctctcgaaatagaacacatcccggaagaaacttggggtctgtcccaag	3260
QY	2941	catlaacgtgtctgttttgacaatgtctacgtctctgaaagacaacatctcgtctctacgtccgttg	3000
Db	3261	catlaacgtgtctgttttgacaatgtctacgtctctgaaagacaacatctcgtctctacgtccgttg	3320
QY	3001	aaaagggtctctcggaagaacagttgaagcgggaatgtagagcagatgtgccccttgaaatgttgt	3060
Db	3321	aaaagggtctctcggaagaacagttgaagcgggaatgtagagcagatgtgccccttgaaatgttgt	3380
QY	3061	ttgccaatcaagaacagctgtgaagaagcaaaacacagccagctgtccagttgaaatgtgagaagaag	3120
Db	3381	ttgccaatcaagaacagctgtgaagaagcaaaacacagccagctgtccagttgaaatgtgagaagaag	3440
QY	3121	ctatctgtggtgccttggcctttgttcgggggtgtctaaaggtgtcatctctgaaatgaaccaca	3180
Db	3441	ctatctgtggtgccttggcctttgttcgggggtgtctaaaggtgtcatctctgaaatgaaccaca	3500
QY	3181	gtctgtgtgtgaacaccttaactcccgcaaggagataatggagactgctgtctgaataacccaaga	3240
Db	3501	gtctgtgtgtgaacaccttaactcccgcaaggagataatggagactgctgtctgaataacccaaga	3560
QY	3241	ggccgcacacattatctctcttaacacacacatgtatgaagcggacgtccctgggggaacag	3300
Db	3561	ggccgcacacattatctctctcttaacacacacatgtatgaagcggacgtccctgggggaacag	3620
QY	3301	attgcatcatctcccatctgggaagcctgtgtgtgtgtgtccctccctcttcttgaaagac	3360
Db	3621	attgcatcatctcccatctgggaagcctgtgtgtgtgtgtccctccctcttcttgaaagac	3680
QY	3361	cagctcgggaaagaagctactactacgcagaccttggatcaagaagaatgtgaaatcctccctcagt	3420
Db	3681	cagctcgggaaagaagctactactacgcagaccttggatcaagaagaatgtgaaatcctccctcagt	3740
QY	3421	tcctgtcagaaacagttagtaagcactgtgtcaactcctaagaaagagagaaagtttcttcag	3480
Db	3741	tcctgtcagaaacagttagtaagcactgtgtcaactcctaagaaagagagaaagtttcttcag	3800
QY	3481	agcagcttctgtatgtctgtgcctgggcagcgcacatgaagatgtacacgcgtgacatcgatgttc	3540
Db	3801	agcagcttctgtatgtctgtgcctgggcagcgcacatgaagatgtacacgcgtgacatcgatgttc	3860
QY	3541	tcctctatctccaacccctcatcagagaagcattgtctcgaagcccggtctgtgtgaagacata	3600
Db	3861	tcctctatctccaacccctcatcagagaagcattgtctcgaagcccggtctgtgtgaagacata	3920
QY	3601	gggcagatgagctgaacctatgtgtctgtccataatgaagctgtcaatgaagagagagcctttgtgaa	3660
Db	3921	gggcagatgagctgaacctatgtgtctgtccataatgaagctgtcaatgaagagagagcctttgtgaa	3980
QY	3661	ctcttcttaagaatttgatgaacgggtctctaaagccctgggcatttctagttaatgtcatctca	3720
Db	3981	ctcttcttaagaatttgatgaacgggtctctaaagccctgggcatttctagttaatgtcatctca	4040
QY	3721	gagaacgcccctgtgaagaataatattcctccaagcgtgtgcgcgaagagatgtgggtgtgaatcgtgag	3780
Db	4041	gagaacgcccctgtgaagaataatattcctccaagcgtgtgcgcgaagagatgtgggtgtgaatcgtgag	4100
QY	3781	acctccagatgtatcctcttgcacgaagaacgaacacagcgggtccttcggggaacagcagac	3840
Db	4101	acctccagatgtatcctcttgcacgaagaacgaacacagcgggtccttcggggaacagcagac	4160
QY	3841	tgctctgcggcgttcaactgtgaagatgatcgtgtgtgtccaagtgtctctgcatatagaacca	3900
Db	4161	tgctctgcggcgttcaactgtgaagatgatcgtgtgtgtccaagtgtctctgcatatagaacca	4220
QY	3901	gaatccagagagacagactgtgtctcagtgaggatgtatgtgtgccaagggtctctccagcgtgaa	3960
Db	4221	gaatccagagagacagactgtgtctcagtgaggatgtatgtgtgtgccaagggtctctccagcgtgaa	4280
QY	3961	ggctgtgaacttaacacagcaacagtttgtgtgccccttttgttgaaagagactgtctaattgcc	4020

Db	4281	gctcggaaacttacacagcaagctctggtgcccctctctggaagagactgtcaattgccc	43400
QY	4021	agaagagtcggaaagagattttttgtcctaagctctgtctgcacagctgtgtttctgcacat	40800
Db	4341	agacgagtcgcgaagagattttttgtcctaagctgtctgtcagctgtgtttgtctgcacat	44000
QY	4081	ggccttggtttacagctgatatgtgtccacccctttggcagaatcacccgcgcctgtgaattcag	41400
Db	4401	ggccttggtttacagctgatatgtgtccacccctttggcagaatcacccgcgcctgtgaattcag	44600
QY	4141	cccttgagttacaaagaaacagtaacacattttgcagcaatgatctctcttagagaaacggga	42000
Db	4461	cccttgagttacaaagaaacagtaacacattttgcagcaatgatctctcttagagaaacggga	45200
QY	4201	acccttggaacttttaacgcccctacccaagaacctgtgcttcggagacctgtatggaa	42600
Db	4521	acccttggaacttttaacgcccctacccaagaacctgtgcttcggagacctgtatggaa	45800
QY	4261	ggaagaccacatcccagacagccctgcacagcgagggaggaagaagatgagacactgccca	43200
Db	4581	ggaagaccacatcccagacagccctgcacagcgagggaggaagaagatgagacactgccca	46400
QY	4321	gttcccagacacatcagtaggaccttccacgaatgaggacatgacaaatgcagaaccttca	43800
Db	4641	gttcccagacacatcagtaggaccttccacgaatgaggacatgacaaatgcagaaccttca	47000
QY	4381	cctgcagtcgcaatgtagcagcagcgaacaaatcaagaagaatgtcgcctgtgtgtccccaag	44400
Db	4701	cctgcagtcgcaatgtagcagcagcgaacaaatcaagaagaatgtcgcctgtgtgtccccaag	47600
QY	4441	gcaaggggggtgtgctcctcctccacaagaacaaacacatgcagatatcccttcagaacctg	45000
Db	4761	gcaaggggggtgtgctcctcctccacaagaacaaacacacatgcagatatcccttcagaacctg	48200
QY	4501	acaaggaagaagaacattctggaattatcctgtgaagaagctatgtgcacatatgaacgcaaaagc	45600
Db	4821	acaaggaagaagaacattctggaattatcctgtgaagaagctatgtgcacatatgaacgcaaaagc	48800
QY	4561	ttaaagaaacaagatctcgtgtgaatgaatttaggtacagcggcgtcttccctgtgtgtcagt	46200
Db	4881	ttaaagaaacaagatctcgtgtgaatgaatttaggtacagcggcgtcttccctgtgtgtcagt	49400
QY	4621	aattactcaagacttctcctccgagtcagaagaatttaatgatgccaataacaaatgaagaaa	46800
Db	4941	aattactcaagacttctcctccgagtcagaagaatttaatgatgccaataacaaatgaagaaa	50000
QY	4681	caacccaagaagcgtgcgaaggaagaattctgcagatcagatttctcaacagcttggagaattt	47400
Db	5001	caacccaagaagcgtgcgaaggaagaattctgcagatcagatttctcaacagcttggagaattt	50600
QY	4741	atgacagaagctcgcgaacccaagaataatgtcaaatgtgtgttcaataacaaggctgtgcacat	48000
Db	5061	atgacagaagctcgcgaacccaagaataatgtcaaatgtgtgttcaataacaaggctgtgcacat	51200
QY	4801	ggaatcagactctttccctgaatgttcatacaacaatgtccattctccgggccaacctgtcaaaag	48600
Db	5121	ggaatcagactctttccctgaatgttcatacaacaatgtccattctccgggccaacctgtcaaaag	51800
QY	4861	ggagagaaccccttagccaattatgtgaattactgtttccaatcccttcacacttcacaaag	49200
Db	5181	ggagagaaccccttagccaattatgtgaattactgtttccaatcccttcacacttcacaaag	52400
QY	4921	cagcagactctcgaaggtgtgctctgtatgaccacacaatgtagatgtctgtgttccatctgt	49800
Db	5241	cagcagactctcgaaggtgtgctctgtatgaccacacaatgtagatgtctgtgttccatctgt	53000
QY	4981	gtacattcttgcaatgtcccttcgtcccaagcagaactttgtcgaattccctgattcccaaggagcgg	50400
Db	5301	gtacattcttgcaatgtcccttcgtcccaagcagaactttgtcgaattccctgattcccaaggagcgg	53600
QY	5041	gtcagcaagaacaaacacctgcagcttcaacagtgagtgagagcctgtcatctatcagctc	51000

PR 26-OCM-1999; 99EP-0402668.
 PR 01-MAR-2000; 2000US-0186260.
 XX
 PA (AVET) AVENTIS PHARMA SA.
 XX
 PI Deneffe P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;
 PI Lemoine C, Duvenger N, Jaye M, Searious GH, Kemaley A, Brewer HB;
 PI Dean M;
 XX
 DR WPI; 2001-316327/33.
 DR P-PSDB; AA002176.
 XX
 PT New human ABC1 nucleic acids and polypeptides for treating
 PT atherosclerosis, malaria and diabetes
 XX
 PS Claim 1; Page 204-208; 368pp; English.
 CC
 CC The sequence represents the coding sequence #1 of human ABC1. The
 CC nucleic acid sequence, primers and probes derived from the ABC1 sequence,
 CC and polypeptides and vectors are useful for the prevention of
 CC atherosclerosis, in a subject affected by a dysfunction in the reverse
 CC transport of cholesterol. The polypeptide encoded by the ABC1 gene is
 CC useful for screening for an active ingredient for the prevention or
 CC treatment of a disease resulting from dysfunction in the reverse
 CC transport of cholesterol. The nucleic acids and polypeptides are also
 CC useful for treating and preventing cardiovascular and neurological
 CC pathologies, and other diseases e.g. Tangier disease, lecithin-
 CC cholesterol (LCAT) deficiency, malaria and diabetes.
 CC
 SQ Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other:

Query Match 99.7%; Score 6784.8; DB 22; Length 9741;
 Best Local Similarity 99.8%; Pred No. 0;
 Matches 6792; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 atggtctgttgccctcagctgaggtgctgctgtgtggaagaacctcacttcagaagaaga 60
 DB 185 atgctgtgttgccctcagctgaggtgctgctgtgtggaagaacctcacttcagaagaaga 244
 QY 61 caaacatgcaagctgttactggaagtgctgctgctcttattctctctgtatc 120
 DB 245 caaacatgcaagctgtgctgctgctgctgctgctcttattctctctgtatc 304
 QY 121 tctgtctgctgagctaccacacctatgaacaacatgaatgcatcttcaataaagcc 180
 DB 305 tctgtctgctgagctaccacacctatgaacaacatgaatgcatcttcaataaagcc 364
 QY 181 atgacctctgcaggaacactctctgtgttcaaggagatcatctgtatgccaacacccc 240
 DB 365 atgacctctgcaggaacactctctgtgttcaaggagatcatctgtatgccaacacccc 424
 QY 241 tgttccgttacccgactctgtggaggtctcccgaggtgttggaaccttacaataacc 300
 DB 425 tgttccgttacccgactctgtggaggtctcccgaggtgttggaaccttacaataacc 484
 QY 301 atgttggtctgcctgttctcagaatgctcgaggtctcttita taagccagaagaacacc 360
 DB 485 atgttggtctgcctgttctcagaatgctcgaggtctcttita taagccagaagaacacc 544
 QY 361 agcatgaagagacatgcaaggttcttggaacatatacagcagatacaagaataccagctca 420
 DB 545 agcatgaagagacatgcaaggttcttggaacatatacagcagatacaagaataccagctca 604
 QY 421 aacttgaagcttcaagattctctgtgtgacaatgaacacctctcgtggttctctataacc 480
 DB 605 aacttgaagcttcaagattctctgtgtgacaatgaacacctctcgtggttctctataacc 664
 QY 481 aacctctctctcccaagctactgtgtgacaagaatgctgaggtctgtatctatctccac 540
 DB 665 aacctctctctcccaagctactgtgtgacaagaatgctgaggtctgtatctatctccac 724
 QY 541 aagtatatttgcaggtctacaggttatacttgacaagctcgtgcaatgcatcaataaaca 600

DB 725 aagtatatttgcaggtctacaggttatacttgacaagctcgtgcaatgcatcaataaaca 784
 QY 601 gaagagatgtatccaactgtgtgacccaagaagcttctgagcttctgtgctaccacaagag 660
 DB 785 gaagagatgtatccaactgtgtgacccaagaagcttctgagcttctgtgctaccacaagag 844
 QY 661 aaactgtctgcagcagagagatctctgttcccaacatggaacatcttcaagccaatctgt 720
 DB 845 aaactgtctgcagcagagagatctctgttcccaacatggaacatcttcaagccaatctgt 904
 QY 721 agaacaactaactatcatctccctcccgagcaagagagctgtgtgaagccacaanaaca 780
 DB 905 agaacaactaactatcatctccctcccgagcaagagagctgtgtgaagccacaanaaca 964
 QY 781 ttgtctcagatgtctggagctctgtgcccagagctgttccagatgagaagagctgtgagac 840
 DB 965 ttgtctcagatgtctggagctctgtgcccagagctgttccagatgagaagagctgtgagac 1024
 QY 841 atgcagcagaggtgagtgatgttcttgaccaaagtgaacagctccacccccaatc 900
 DB 1025 atgcagcagaggtgagtgatgttcttgaccaaagtgaacagctccacccccaatc 1084
 QY 901 taccaggtctgtgtcgtatgtctgtgctgctgagatcccgagagaggggctgtgaatacag 960
 DB 1085 taccaggtctgtgtcgtatgtctgtgctgctgagatcccgagagaggggctgtgaatacag 1144
 QY 961 tctctcaactgtatgagagacaacaactacaagaacctcttcttgaggcaatgagctgag 1020
 DB 1145 tctctcaactgtatgagagacaacaactacaagaacctcttcttgaggcaatgagctgag 1204
 QY 1021 gaagtgctggaacctcttatgacaactctacaactcttaatgcaatgattgataag 1080
 DB 1205 gaagtgctggaacctcttatgacaactctacaactcttaatgcaatgattgataag 1264
 QY 1081 aattgagatgaatgctctctctcccgacattctcggaagaagctcgagccgctgtcgt 1140
 DB 1265 aattgagatgaatgctctctctcccgacattctcggaagaagctcgagccgctgtcgt 1324
 QY 1141 gggaaatctctgtatatacactgtacactccagccacaagagctgcatgtgagtgagac 1300
 DB 1325 gggaaatctctgtatatacactgtacactccagccacaagagctgcatgtgagtgagac 1384
 QY 1201 aagacctccagagactggctgtgttccatgacttggaagagatgtgagggaactagc 1260
 DB 1385 aagacctccagagactggctgtgttccatgacttggaagagatgtgagggaactagc 1444
 QY 1261 cccaagatctgacacttcatggaagaacagccaagaataatggaaccttgcggatgtgtg 1320
 DB 1445 cccaagatctgacacttcatggaagaacagccaagaataatggaaccttgcggatgtgtg 1504
 QY 1321 gacagcagggagcaatgacactcttcttggaacagagcttggaatgctatgtgaagcc 1380
 DB 1505 gacagcagggagcaatgacactcttcttggaacagagcttggaatgctatgtgaagcc 1564
 QY 1381 caagacatctgtggtgttcttgccaagcaccacaagaatgtccagtcacatgtgttct 1440
 DB 1565 caagacatctgtggtgttcttgccaagcaccacaagaatgtccagtcacatgtgttct 1624
 QY 1441 ggtgacacctggaagaagacttccaacgagactaaccaggaacatccgagacatatacgc 1500
 DB 1625 ggtgacacctggaagaagacttccaacgagactaaccaggaacatccgagacatatacgc 1684
 QY 1501 ttcatgagatgttcaaacctggaacagctggaacccatgacacaagaatctggtccatc 1560
 DB 1685 ttcatgagatgttcaaacctggaacagctggaacccatgacacaagaatctggtccatc 1744
 QY 1561 aacaagtccaatgagctgtggaatgagagagagcttctggtctgtatctgttccatgtga 1620
 DB 1745 aacaagtccaatgagctgtggaatgagagagagcttctggtctgtatctgttccatgtga 1804
 QY 1621 attactccaagcagcatgtgactgtgcccacatcatgtcaagtacaagaatccgaatgtgacat 1680

Db 1805 attactcagcgacgtatgactgcccacatctgtaacagatccgaatgagactt 1864
Qy 1681 gacatctgagagagacaataataatacaagatggttactggagacctgctctgagct 1740
Db 1865 gacaaatgtagagagagacaataataatacaagatggttactggagacctgctctgagct 1924
Qy 1741 gacctcttgagagacatcggttaactctgggggggctctgacctacttgacagatggtg 1800
Db 1925 gacctcttgagagacatcggttaactctgggggggctctgacctacttgacagatggtg 1984
Qy 1801 gacagagacacatcaatcggttgctgacgggacacggagaaacacgggtctacataatgcaa 1860
Db 1985 gacagagagacacatcaatcggttgctgacgggacacggagaaacacgggtctacataatgcaa 2044
Qy 1861 cagatgacctatccctgctgacgttgagacacatctctgaggggtgagagccggtcaatg 1920
Db 2045 cagatgacctatccctgctgacgttgagacacatctctgaggggtgagagccggtcaatg 2104
Qy 1921 cccctcttcaatgacgttgacgttgacgttgacgttgacgttgacgttgacgttgacgttg 1980
Db 2105 cccctcttcaatgacgttgacgttgacgttgacgttgacgttgacgttgacgttgacgttg 2164
Qy 1981 tatgagaaagagagacacggctgaaagagacatgacgtgacatgagcctgagacacagcata 2040
Db 2165 tatgagaaagagagacacggctgaaagagacatgacgtgacatgagcctgagacacagcata 2224
Qy 2041 cctctggtttagctggttcaatlaagtaagctcaatctcctctctgtagagcgtgacctgcta 2100
Db 2225 cctctggtttagctggttcaatlaagtaagctcaatctcctctctgtagagcgtgacctgcta 2284
Qy 2101 gtggttcaatctgaaagttagaaacacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 2160
Db 2285 gtggttcaatctgaaagttagaaacacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 2344
Qy 2161 ttccctgctggtttagctggtttagaaacatctcgtgacgtgacgtgacgtgacgtgacgtgac 2220
Db 2345 ttccctgctggtttagctggtttagaaacatctcgtgacgtgacgtgacgtgacgtgacgtgac 2404
Qy 2221 tccagaaacacacgtgagagacgttggggggacatcatcaatctcaacgtgtagacctggcc 2280
Db 2405 tccagaaacacacgtgagagacgttggggggacatcatcaatctcaacgtgtagacctggcc 2464
Qy 2281 taagttccctggtttagctggtttagaaacatctcgtgacgtgacgtgacgtgacgtgacgtgac 2340
Db 2465 taagttccctggtttagctggtttagaaacatctcgtgacgtgacgtgacgtgacgtgacgtgac 2524
Qy 2341 ctgctgctcctcgtggtttagctggtttagaaacatctcgtgacgtgacgtgacgtgacgtgac 2400
Db 2525 ctgctgctcctcgtggtttagctggtttagaaacatctcgtgacgtgacgtgacgtgacgtgac 2584
Qy 2401 ggcattggaagttagctggtttagaaacatctcgtgacgtgacgtgacgtgacgtgacgtgac 2460
Db 2585 ggcattggaagttagctggtttagaaacatctcgtgacgtgacgtgacgtgacgtgacgtgac 2644
Qy 2461 ctcaacacatctgacatctcgtggtttagaaacatctcgtgacgtgacgtgacgtgacgtgac 2520
Db 2645 ctcaacacatctgacatctcgtggtttagaaacatctcgtgacgtgacgtgacgtgacgtgac 2704
Qy 2521 taacattgaggtgctcttccagggacatgagaaattccagggccctggtatcttccctg 2580
Db 2705 taacattgaggtgctcttccagggacatgagaaattccagggccctggtatcttccctg 2764
Qy 2581 accaagttcctactggtttagagagaaatgagatgagaaagacacacgtggttccaaacag 2640
Db 2765 accaagttcctactggtttagagagaaatgagatgagaaagacacacgtggttccaaacag 2824
Qy 2641 aagagaatctcagaatctgcatgagagagaaacacacacacacacacacacacacacacacac 2700
Db 2825 aagagaatctcagaatctgcatgagagagaaacacacacacacacacacacacacacacacac 2884
Qy 2701 attcagaacctggttaagaatctacacagatgagatgagaggtggtgctgagctgagcag 2760
Db 2885 attcagaacctggttaagaatctacacagatgagatgagaggtggtgctgagctgagcagcag 2944

Qy 2761 ctgaaattttatgaggggcccagatcaactccttctggtgcccacaaatgagcgggaaagacg 2820
Db 2945 ctgaaattttatgaggggcccagatcaactccttctggtgcccacaaatgagcgggaaagacg 3004
Qy 2821 accacacatctcaatctcagacgggttcttcccccagacctcggggacacggctacacatctg 2880
Db 3005 accacacatctcaatctcagacgggttcttcccccagacctcggggacacggctacacatctg 3064
Qy 2881 ggaagaaacatctcagacgggttcttcccccagacctcggggacacggctacacatctg 2940
Db 3065 ggaagaaacatctcagacgggttcttcccccagacctcggggacacggctacacatctg 3124
Qy 2941 cataagcgtcgttctgacatgctgacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 3000
Db 3125 cataagcgtcgttctgacatgctgacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 3184
Qy 3001 aaagggctcctctgagaaagacgtgaaagcggagatgagagacagatggccctgagatggt 3060
Db 3185 aaagggctcctctgagaaagacgtgaaagcggagatgagagacagatggccctgagatggt 3244
Qy 3061 ttgacatcaagacacgttgaagaaacaaacacacacacacacacacacacacacacacacac 3120
Db 3245 ttgacatcaagacacgttgaagaaacaaacacacacacacacacacacacacacacacacac 3304
Qy 3121 ctatctggtgacctgaccttctgctgggggacatcaagttgcatctctgagatgaaacacaca 3180
Db 3305 ctatctggtgacctgaccttctgctgggggacatcaagttgcatctctgagatgaaacacaca 3364
Qy 3181 gctggtgtgagaccttaactcccgagggagataatgagagcgtcgtctgaataacacagaa 3240
Db 3365 gctggtgtgagaccttaactcccgagggagataatgagagcgtcgtctgaataacacagaa 3424
Qy 3241 ggcggacacacatctcctctctacacacacacacacacacacacacacacacacacacac 3300
Db 3425 ggcggacacacatctcctctctacacacacacacacacacacacacacacacacacacac 3484
Qy 3301 atgacacatctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 3360
Db 3485 atgacacatctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 3544
Qy 3361 cagctggagaaacagctacatcctcctcctcctcctcctcctcctcctcctcctcctcctc 3420
Db 3545 cagctggagaaacagctacatcctcctcctcctcctcctcctcctcctcctcctcctcctc 3604
Qy 3421 tccctgagaaacagctacatcctcctcctcctcctcctcctcctcctcctcctcctcctc 3480
Db 3605 tccctgagaaacagctacatcctcctcctcctcctcctcctcctcctcctcctcctcctc 3664
Qy 3481 agcagttctgactgctgacctgagcagacacatgagagatgagacacgtctgacacatctgac 3540
Db 3665 agcagttctgactgctgacctgagcagacacatgagagatgagacacgtctgacacatctgac 3724
Qy 3541 tctgtatctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 3600
Db 3725 tctgtatctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 3784
Qy 3601 gggcattgagacatctgctgctgacatgagagcgtctgaagagagagccttctgtgaa 3660
Db 3785 gggcattgagacatctgctgctgacatgagagcgtctgaagagagagccttctgtgaa 3844
Qy 3661 cctcttcaatgagatgagatgagacggcctctcagacgttggacattctcagatgagacatca 3720
Db 3845 cctcttcaatgagatgagatgagacggcctctcagacgttggacattctcagatgagacatca 3904
Qy 3721 gagacgacctggagaaacatactcctcaagctgagcgaagagagatggtgagatggtgag 3780
Db 3905 gagacgacctggagaaacatactcctcaagctgagcgaagagagatggtgagatggtgag 3964
Qy 3781 acctcagaatgtaaccttgcagcagaagaacagacggccttgcggagacagacagac 3840
Db 3965 acctcagaatgtaaccttgcagcagaagaacagacggccttgcggagacagacagac 4024

QY	3841	tgcttcgcgcgcgttcaactggaagatgtagtgcgtgcgtatcccaatgattctgtacatagacc	3900
Db	4025	tgcttcgcgcgcgttcaactggaagatgtagtgcgtgcgtatcccaatgattctgtacatagacc	4084
QY	3901	gaatccagagaaacagactgtctcaagtggagatgtagtgcgaaggtccatcaaggttga	3966
Db	4085	gaatccagagaaacagactgtctcaagtggagatgtagtgcgaaggtccatcaaggttga	4144
QY	3961	ggtctgaaacttaacagcaacagttgtgaccttgtgtgaaagagactgtctaattgc	4020
Db	4145	ggtctgaaacttaacagcaacagttgtgaccttgtgtgaaagagactgtctaattgc	4204
QY	4021	agacggagatccggaagaagattttttgtccagattgtcttcgcagctgtgtttctgcatt	4088
Db	4205	agacggagatccggaagaagattttttgtccagattgtcttcgcagctgtgtttctgcatt	4264
QY	4081	ggccttggttttaacgcctgatctgtgccaccttgtggcaagtaccacgccttgtaacttaag	4140
Db	4265	ggccttggttttaacgcctgatctgtgccaccttgtggcaagtaccacgccttgtaacttaag	4324
QY	4141	cccttgatgtacaacagaaacagtaaacatttgtacgaatgtagtctcctggaagacggga	4200
Db	4325	cccttgatgtacaacagaaacagtaaacatttgtacgaatgtagtctcctggaagacggga	4384
QY	4201	acccttggaactcttaaaagcccttaacccaagaccctggtctcggagaccgcctgtatgga	4260
Db	4385	acccttggaactcttaaaagcccttaacccaagaccctggtctcggagaccgcctgtatgga	4444
QY	4261	ggaatacccaatcccaagacagcctctgcacagggaggaagatggaacaactgtgccca	4320
Db	4445	ggaatacccaatcccaagacagcctctgcacagggaggaagatggaacaactgtgccca	4504
QY	4321	gttccccaagaccatcatggaacctcttcacgaatggaactgtgacaatgcagaaccttca	4380
Db	4505	gttccccaagaccatcatggaacctcttcacgaatggaactgtgacaatgcagaaccttca	4564
QY	4381	cctgtgacgacagttgtagcagcgacaatatcaagaagatgtgcctgtgtgtccccaagg	4440
Db	4565	cctgtgacgacagttgtagcagcgacaatatcaagaagatgtgcctgtgtgtccccaagg	4624
QY	4441	ggaaggggggcgtgcctcctccacaagaataaacaacacgcgcagatatccttcagagctt	4500
Db	4625	ggaaggggggcgtgcctcctccacaagaataaacaacacgcgcagatatccttcagagctt	4684
QY	4501	acaaggaagaacaattctcggaattctgtgtgaaagcgtatgtgcagatcatagccaagc	4560
Db	4685	acaaggaagaacaattctcggaattctgtgtgaaagcgtatgtgcagatcatagccaagc	4744
QY	4561	ttaaagaacaagatctcgtggatgtgaattgaattgttgsgsggttttcctgtgtgaagt	4620
Db	4745	ttaaagaacaagatctcgtggatgtgaattgaattgttgsgsggttttcctgtgtgaagt	4804
QY	4621	aattctcaagcaacttcctccagtgcaagaagttaatgtatgcatacaaaatgaaga	4680
Db	4805	aattctcaagcaacttcctccagtgcaagaagttaatgtatgcatacaaaatgaaga	4864
QY	4681	caactaagcctgggcaagggacagttctggaatgtgattcttccaacagttggggaagtt	4740
Db	4865	caactaagcctgggcaagggacagttctggaatgtgattcttccaacagttggggaagtt	4924
QY	4741	atgacagagactgtgacaaccaagaataatgtcaaggtgtgtgttcaatacaagggctgcat	4800
Db	4925	atgacagagactgtgacaaccaagaataatgtcaaggtgtgtgttcaatacaagggctgcat	4984
QY	4801	gcaataagcctttcttcgtgaatgtcttaacaaatgcatcttcctcgggccaactgtgaaag	4860
Db	4985	gcaataagcctttcttcgtgaatgtcttaacaaatgcatcttcctcgggccaactgtgaaag	5044
QY	4861	ggagagaacacttaacatataatggaattactgtcttcaatctccctggaattccaag	4920
Db	5045	ggagagaacacttaacatataatggaattactgtcttcaatctccctggaattccaag	5104
QY	4921	cagagagcttcgaaggtgtgctctgtatgaccacacagatgagatgtccttgtgtccatctgt	4980

Db	5105	cagcagctctcagaggtgtgctccggtatgcacatcagtgatgtctgtgctatcgt	5166
Qy	4881	gtcatctttgcgaatgtctctgtgtccagcagcttgttgatctctgataccaagagcgg	5040
Db	5165	gtcatctttgcgaatgtctctgtgtccagcagcttgttgatctctgataccaagagcgg	5224
Qy	5041	gtcagcaagaacaaacacctgagctacacgtacagtagagtagagccttcatctacgtgctc	5100
Db	5225	gtcagcaagaacaaacacctgagctacacgtacagtagagtagagccttcatctacgtgctc	5288
Qy	5101	tctaatctgtctcgtggatgatagtgcaatlaagttgtccctgcacacctggatcatatcac	5160
Db	5285	tctaatctgtctcgtggatgatagtgcaatlaagttgtccctgcacacctggatcatatcac	5348
Qy	5161	ttcatctgttcacagagaagttccatgtgtgtccctccagcaatctgctgtgtacgctt	5220
Db	5345	ttcatctgttcacagagaagttccatgtgtgtccctccagcaatctgctgtgtacgctt	5404
Qy	5221	ctacatttgcgtalaggttggtlcatcatcaacacttctacgtaccagcctcttgtctc	5280
Db	5405	ctacatttgcgtalaggttggtlcatcatcaacacttctacgtaccagcctcttgtctc	5468
Qy	5281	aaatctccacagacagcctatagtggtgtctacacagcgttgacctctcatgtgcatat	5340
Db	5465	aaatctccacagacagcctatagtggtgtctacacagcgttgacctctcatgtgcatat	5524
Qy	5341	ggcagcgttgcacacctgtgtcgttgagcgtttcacccagataagcttgataatacat	5400
Db	5525	ggcagcgttgcacacctgtgtcgttgagcgtttcacccagataagcttgataatacat	5584
Qy	5401	gatatctcgaagtcgcgtgttcttgatcttccacatatttgcctgtagcagagctcatc	5460
Db	5585	gatatctcgaagtcgcgtgttcttgatcttccacatatttgcctgtagcagagctcatc	5644
Qy	5461	gacatcgttgcgaanaacagcgaatgtgcgtacgtgcgccttgaaagtttggggagatcgcctt	5520
Db	5645	gacatcgttgcgaanaacagcgaatgtgcgtacgtgcgccttgaaagtttggggagatcgcctt	5704
Qy	5521	gtgtcaccatatctcttgggacttgggtggagcgaacaccttcgcacatgvcggttgaaag	5580
Db	5705	gtgtcaccatatctcttgggacttgggtggagcgaacaccttcgcacatgvcggttgaaag	5764
Qy	5581	gtgtggttcttccctcatctacgttctcgtatccaataagaattcttcatacggccagacct	5640
Db	5765	gtgtggttcttccctcatctacgttctcgtatccaataagaattcttcatacggccagacct	5824
Qy	5641	gtcaaatgcgaagctatctcctctgaatgatagtaaagtgtgagcgggaaagacag	5700
Db	5825	gtcaaatgcgaagctatctcctctgaatgatagtaaagtgtgagcgggaaagacag	5884
Qy	5701	aaaattctcttgatgttgagcgcgaagaatgaaatcttggaaatacaaggaatttgacgaata	5760
Db	5885	aaaattctcttgatgttgagcgcgaagaatgaaatcttggaaatacaaggaatttgacgaata	5944
Qy	5761	tatagaaggaagcggagcctgtcgttgcacaggaatttgcgttggagcatctctcctgtgag	5820
Db	5945	tatagaaggaagcggagcctgtcgttgcacaggaatttgcgttggagcatctctcctgtgag	6004
Qy	5821	tgcttgggtccctggaggaagttaatgggtcttgtaaaaatacaactttaaagtgttaca	5880
Db	6005	tgcttgggtccctggaggaagttaatgggtcttgtaaaaatacaactttaaagtgttaca	6064
Qy	5881	ggagatatacactgttaccagagagatgtcttcccttaacaaaatagtatcttcaaac	5940
Db	6065	ggagatatacactgttaccagagagatgtcttcccttaacaaaatagtatcttcaaac	6124
Qy	5941	atcataaagtaactaagaacataggctactgtccctcagtttgatgcatacaagagctg	6000
Db	6125	atcataaagtaactaagaacataggctactgtccctcagtttgatgcatacaagagctg	6184
Qy	6001	ttgacttgggagagacacgtgtgagttcttctgtccctttgagagagttccagagaaag	6060

```

Db      6185  ttgactggagagaaacagtgagltcttgccttttgagagagttccagagaaagaa 6244
QY      6061  gttgcaaggttctgagtgagtcgaatctggaactggccctgagagatgagaaagaa 6120
        |||||||
Db      6245  gttgcaaggttctgagtgagtcgaatctggaactggccctgagagatgagaaagaa 6304
QY      6121  tatgctgtaactatagtgagagcaaaagcaagctctctacagagcattgattatc 6180
        |||||||
Db      6305  tatgctgtaactatagtgagagcaaaagcaagctctctacagagcattgattatc 6364
QY      6181  gggggggcccttggtgttcttgatgaaccaccacagagatgagatcccaagccgg 6240
        |||||||
Db      6365  gggggggcccttggtgttcttgatgaaccaccacagagatgagatcccaagccgg 6424
QY      6241  cggctcttgagaaatgtgacctaaagtgtgtcaagagagggagatcagtagtctta 6300
        |||||||
Db      6425  cggctcttgagaaatgtgacctaaagtgtgtcaagagagggagatcagtagtctta 6484
QY      6301  tctcataagatgagaaatgtgacctaaagtgtgtcaagagagggagatcagtagt 6360
        |||||||
Db      6485  tctcataagatgagaaatgtgacctaaagtgtgtcaagagagggagatcagtagt 6544
QY      6361  aggttcagtgctctgagagtgccagacatctaaagaaataggtttgagatggtata 6420
        |||||||
Db      6545  aggttcagtgctctgagagtgccagacatctaaagaaataggtttgagatggtata 6604
QY      6421  atagttgacgaatagcaaggttccaaacccgagctgagagctgtccagagattctt 6480
        |||||||
Db      6605  atagttgacgaatagcaaggttccaaacccgagctgagagctgtccagagattctt 6664
QY      6481  ctgtgctctcttgagagtggtctaaagagaaacacccgagacatgctacatatac 6540
        |||||||
Db      6665  ctgtgctctcttgagagtggtctaaagagaaacacccgagacatgctacatatac 6724
QY      6541  ccatctcattatcttctctgagagatattcagatcctctccagagcaaaagcga 6600
        |||||||
Db      6725  ccatctcattatcttctctgagagatattcagatcctctccagagcaaaagcga 6784
QY      6601  ctccacataagagactactctgtttctcagacaaacattgacaaatatttgaactt 6660
        |||||||
Db      6785  ctccacataagagactactctgtttctcagacaaacattgacaaatatttgaactt 6844
QY      6661  gccaaagagcaaaatgagtgagaccacttaaaagacctcattacacaaacagaca 6720
        |||||||
Db      6845  gccaaagagcaaaatgagtgagaccacttaaaagacctcattacacaaacagaca 6904
QY      6721  gtatgagagcttgagtgctcacaatcttctacagagatgagaagtgagaagctat 6780
        |||||||
Db      6905  gtatgagagcttgagtgctcacaatcttctacagagatgagaagtgagaagctat 6964
QY      6781  gtaagagaatcctgttcatacgg 6804
        |||||||
Db      6965  gtaagagaatcctgttcatacgg 6988

```

RESULT 12

AA506121 standard; cDNA; 9854 BP.

AA506121:

12-SEP-2001 (first entry)

Human ABC1 DNA sequence #2.

Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;

cardiovascular; neurological; Tangier disease; LCAT deficiency;

lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.

OS Homo sapiens.

XX Key

PH CDS

Location/Qualifiers
298..7078

```

FT      /*tag= a
        /product= "Human ABC1 protein"
PI      WO200130848-A2.
        03-MAY-2001.
        26-OCT-2000; 2000MO-EP10886.
        26-OCT-1999; 99EP-0402668.
        01-MAR-2000; 2000US-0186260.
        (AVER ) AVENTIS PHARMA SA.
PI      Denelle P, Rosier-Montus M, Arnaud-Reguigne I, Prades C, Naudin L;
        Lemoine C, Duvenger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
        Dean M;
        WPI: 2001-316327/33.
        P-PSDB; AAU02176.
        New human ABC1 nucleic acids and polypeptides for treating
        atherosclerosis, malaria and diabetes -
        Claim 1: Page 209-213; 368pp; English.
        The sequence represents the coding sequence #2 of human ABC1. The
        nucleic acid sequence, primers and probes derived from the ABC1 sequence,
        and polypeptides and vectors are useful for the prevention of
        atherosclerosis, in a subject affected by a dysfunction in the reverse
        transport of cholesterol. The polypeptide encoded by the ABC1 gene is
        useful for screening for an active ingredient for the prevention or
        treatment of a disease resulting from dysfunction in the reverse
        transport of cholesterol. The nucleic acids and polypeptides are also
        useful for treating and preventing cardiovascular and neurological
        pathologies, and other diseases e.g. Tangier disease, lecithin-
        cholesterol (LCAT) deficiency, malaria and diabetes.
        CC      Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other:
        SQ
        Query Match      99.7%; Score 6784.8; DB 22; Length 9854;
        Best Local Similarity 99.08%; Pred. No. 0;
        Matches 6792; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
        QY      1 atggctgttgagcctcagctgaggtgtgtgtgtggaagaacctcacttcagaagaaga 60
        |||||||
        Db      298 atggctgttgagcctcagctgaggtgtgtgtgtggaagaacctcacttcagaagaaga 357
        |||||||
        QY      61 caaacatgtcagctgttacttggaagtggtgctgtcctctatattcttctgtatctgac 120
        |||||||
        Db      358 caaacatgtcagctgtgctggaagtggtgctgtcctctatattcttctgtatctgac 417
        |||||||
        QY      121 tctgttgagctgagctacccaacctatgaacaacatgaaatgcaatttccaaataagcc 180
        |||||||
        Db      418 tctgttgagctgagctacccaacctatgaacaacatgaaatgcaatttccaaataagcc 477
        |||||||
        QY      181 atgccccttcaggaacaactccttggtgtcaggggtatctcgttaatgccaaacccc 240
        |||||||
        Db      478 atgccccttcaggaacaactccttggtgtcaggggtatctcgttaatgccaaacccc 537
        |||||||
        QY      241 tgttcgttacccgactccttgaggaggtcccgaggtgttggaaactttaacaatcc 300
        |||||||
        Db      538 tgttcgttacccgactccttgaggaggtcccgaggtgttggaaactttaacaatcc 597
        |||||||
        QY      301 atgtgagctccggttctcagatgctcggaggtcttttatacagccagaagacacc 360
        |||||||
        Db      596 atgtgagctccggttctcagatgctcggaggtcttttatacagccagaagacacc 657
        |||||||
        QY      361 agcatgaagagatgccaaggtcttgagaacattacagcagatcaagaatccagctca 420
        |||||||
        Db      658 agcatgaagagatgccaaggtcttgagaacattacagcagatcaagaatccagctca 717

```


Db 2878 accaagttactgtgttggcgaggaagtgatgaaagagccaacctgttccaacag 2937
Qy 2641 aagagaatgtcagaatctgcatagtgagaggaaccaccaacttgaagctgggcgttcc 2700
Db 2938 aagagataatcagaatctgcatagtgagaggaaccaccaacttgaagctgggcgttcc 2997
Qy 2701 attcagaacctgttaaagcttaccaggaatggatgaaagtggtgtgtcgaatggcttggca 2760
Db 2998 attcagaacctgttaaagcttaccaggaatggatgaaagtggtgtgtcgaatggcttggca 3057
Qy 2761 ctgaattttatgagggccaagataccaccttcccttccctggccaatgagcgaggaaagcg 2820
Db 3058 ctgaattttatgagggccaagataccaccttcccttccctggccaatgagcgaggaaagcg 3117
Qy 2821 accacatgtcaatccctgcagcggtgttcccccgaacctgggagccaacctataacctg 2880
Db 3118 accacatgtcaatccctgcagcggtgttcccccgaacctgggagccaacctataacctg 3177
Qy 2881 ggaagaagacattccgcttgaagatgagcaacatccgcaagaacctggggtctgtcccaag 2940
Db 3178 ggaagaagacattccgcttgaagatgagcaacatccgcaagaacctggggtctgtcccaag 3237
Qy 2941 cataaagtgctgttgcatactgcatactgcataagacaacatctgttctatgtcccgcttg 3000
Db 3238 cataaagtgctgttgcatactgcatactgcataagacaacatctgttctatgtcccgcttg 3297
Qy 3001 aagaagtgcttgcataagacaacgttgaagcgagagatgagcgagatgagccctgtgattgtgt 3060
Db 3298 aagaagtgcttgcataagacaacgttgaagcgagagatgagcgagatgagccctgtgattgtgt 3357
Qy 3061 ttgccttcaagcgagcttgaagaacaaacaaacagccttcagagtggaatgagaagaaag 3120
Db 3358 ttgccttcaagcgagcttgaagaacaaacaaacagccttcagagtggaatgagaagaaag 3417
Qy 3121 ctatctgtgacctgtgccttgcgcggggagatcaagttgtcatcttcgtgaataccaca 3180
Db 3418 ctatctgtgacctgtgccttgcgcggggagatcaagttgtcatcttcgtgaataccaca 3477
Qy 3181 gctgtgtgtgaaccttaccctccgcaggggaatatgtggaatctgtctgtgaataccagaca 3240
Db 3478 gctgtgtgtgaaccttaccctccgcaggggaatatgtggaatctgtctgtgaataccagaca 3537
Qy 3241 ggcgcgacccaatttctcttaccacacacacatgaaagcgagacgcttccctggggagag 3300
Db 3538 ggcgcgacccaatttctcttaccacacacacatgaaagcgagacgcttccctggggagag 3597
Qy 3301 atgtgcatacttcccatgtgggaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3360
Db 3598 atgtgcatacttcccatgtgggaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3657
Qy 3361 cagctgtggaacaggtctactaccctgacctgtgttaagaagaatgtggaatccctccctcagt 3420
Db 3658 cagctgtggaacaggtctactaccctgacctgtgttaagaagaatgtggaatccctccctcagt 3717
Qy 3421 tccctgcagaaacagtaagtaacactgtgtcaatccttgaanaaagagacagtggttttccag 3480
Db 3718 tccctgcagaaacagtaagtaacactgtgtcaatccttgaanaaagagacagtggttttccag 3777
Qy 3481 agcagttctgtatgtcgtgcctgtggcgagacatgagatgagacgctgtgacatcgatgttc 3540
Db 3778 agcagttctgtatgtcgtgcctgtggcgagacatgagatgagacgctgtgacatcgatgttc 3837
Qy 3541 tctgttatcttccaaacctcatcagaagaacatgtgtctgaanaacgggtgtgtggaagcata 3600
Db 3838 tctgttatcttccaaacctcatcagaagaacatgtgtctgaanaacgggtgtgtggaagcata 3897
Qy 3601 gggcagtgagctgacatactgt 3660
Db 3898 gggcagtgagctgacatactgt 3957
Qy 3661 ctctttcatgagatgtgagacggcttccagacctgtggcatcttctgttatagtgcatctca 3720
Db 3958 ctctttcatgagatgtgagacggcttccagacctgtggcatcttctgttatagtgcatctca 4017
Qy 3721 gtagcgaaccttggaaataatattccccaaggtggcggaagagtgagggtgtgtgtgtgtgtgtgt 3780
Db 4018 gtagcgaaccttggaaataatattccccaaggtggcggaagagtgagggtgtgtgtgtgtgtgtgt 4077
Qy 3781 acctcagatgtgaccttgcagcaagacgaacagcgagcgaccttccgggagacagcagc 3840
Db 4078 acctcagatgtgaccttgcagcaagacgaacagcgagcgaccttccgggagacagcagc 4137
Qy 3841 tgttcttgccttccatcagaaatgagt 3900
Db 4138 tgttcttgccttccatcagaaatgagt 4197
Qy 3901 gaattccagagacagactgtgtcagtggaatgagatgagtgagtgagtgagtgagtgagtgagtgag 3960
Db 4198 gaattccagagacagactgtgtcagtggaatgagatgagtgagtgagtgagtgagtgagtgagtgag 4257
Qy 3961 ggtctgaaacttacacagacagatgt 4020
Db 4258 ggtctgaaacttacacagacagatgt 4317
Qy 4021 agacggaagtcggaagaagatgt 4080
Db 4318 agacggaagtcggaagaagatgt 4377
Qy 4081 ggcctgtgttgcagcctgt 4140
Db 4378 ggcctgtgttgcagcctgt 4437
Qy 4141 ccctgtgattgaacagacagatgacacattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4200
Db 4438 ccctgtgattgaacagacagatgacacattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4497
Qy 4201 accctggaactttaaagccctccacaaagacccctggcttggagaccgctgtatgaa 4260
Db 4498 accctggaactttaaagccctccacaaagacccctggcttggagaccgctgtatgaa 4557
Qy 4261 ggaacccaatcccaagacagccttgcagggagagggagagtgagccaatgtgccca 4320
Db 4558 ggaacccaatcccaagacagccttgcagggagagggagagtgagccaatgtgccca 4617
Qy 4321 gttccccaagacatgtgaccttccccaagatggagacatgtgagacatgtgagacatgtgagacat 4380
Db 4618 gttccccaagacatgtgaccttccccaagatggagacatgtgagacatgtgagacatgtgagacat 4677
Qy 4381 cctgtatgacagtgatgacagcgaacaaatcaagaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4440
Db 4678 cctgtatgacagtgatgacagcgaacaaatcaagaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4737
Qy 4441 gcaagggt 4500
Db 4738 gcaagggt 4797
Qy 4501 acaggaagaacatcttgcagttatctgt 4560
Db 4798 acaggaagaacatcttgcagttatctgt 4857
Qy 4561 ttaagaagaacagatgt 4620
Db 4858 ttaagaagaacagatgt 4917
Qy 4621 aatatcaagcattctcctgcagtgaaagatgaaatgagtgacatacaaaatgaaagaa 4680
Db 4918 aatatcaagcattctcctgcagtgaaagatgaaatgagtgacatacaaaatgaaagaa 4977
Qy 4681 caactaaagctgtggcagaagagctgt 4740
Db 4978 caactaaagctgtggcagaagagctgt 5037
Qy 4741 atgacagagctgtgacacagaataatgt 4800
Db 5038 atgacagagctgtgacacagaataatgt 5097

```
OY 4801 gcaatcagctcttctcgtgaatgatacaaatgcatcttcgggccaactgcaaaag 4860
|||||
Db 5098 gcaatcagctcttctcgtgaatgatacaaatgcatcttcgggccaactgcaaaag 5157
OY 4861 ggaagaagacccttaagcattatggaattactgcttcaatcaatcccggaattcaacaag 4920
|||||
Db 5158 ggaagaagacccttaagcattatggaattactgcttcaatcaatcccggaattcaacaag 5217
OY 4921 cagaagctcttaagagtggtgctctgatacaacatcaatgagatgctctgtgtccatctgt 4980
|||||
Db 5218 cagaagctcttaagagtggtgctctgatacaacatcaatgagatgctctgtgtccatctgt 5277
OY 4981 gtcactcttggaatgctcttcgtccagcagctcttgctatctccggaacagagcg 5040
|||||
Db 5278 gtcactcttggaatgctcttcgtccagcagctcttgctatctccggaacagagcg 5337
OY 5041 gtcagcaagcaaaacacacgtgcaatgcaatgagagtgaaagcctgtcatctatgctc 5100
|||||
Db 5338 gtcagcaagcaaaacacacgtgcaatgcaatgagagtgaaagcctgtcatctatgctc 5397
OY 5101 tctaattctgtaagatgatagtgaatgagtggtgctccgcaacgtgcatatcatc 5160
|||||
Db 5398 tctaattctgtaagatgatagtgaatgagtggtgctccgcaacgtgcatatcatc 5457
OY 5161 tcaatctgcttccagcagaagctcctatgcttccccaacatctgctgtgtagccct 5220
|||||
Db 5458 tcaatctgcttccagcagaagctcctatgcttccccaacatctgctgtgtagccct 5517
OY 5221 ctactcttgctgatagggtgataatcaacacctctatgtaacccaacgtctgtgttc 5280
|||||
Db 5518 ctactcttgctgatagggtgataatcaacacctctatgtaacccaacgtctgtgttc 5577
OY 5281 aagatccccaagcagcactatgctgtgctcaacagcgtagaacctcttctgcatat 5340
|||||
Db 5578 aagatccccaagcagcactatgctgtgctcaacagcgtagaacctcttctgcatat 5637
OY 5341 ggcagcgtagccaccttctgtgctgagcgctgttcaacgaacataagctgataatcaat 5400
|||||
Db 5638 ggcagcgtagccaccttctgtgctgagcgctgttcaacgaacataagctgataatcaat 5697
OY 5401 gatactctgaagtcggtgttctgatacttcccaatcttctgctggaagagagccatc 5460
|||||
Db 5698 gatactctgaagtcggtgttctgatacttcccaatcttctgctggaagagagccatc 5757
OY 5461 gacatggtgaaaaaacagcgaatgctgatagcttggaaggttggggagagatcgctt 5520
|||||
Db 5758 gacatggtgaaaaaacagcgaatgctgatagcttggaaggttggggagagatcgctt 5817
OY 5521 ggtccacattatcttgggaactgtgtggaacgaacacacacacacacacacacacac 5580
|||||
Db 5818 ggtccacattatcttgggaactgtgtggaacgaacacacacacacacacacacacac 5877
OY 5581 gttgtgtcttccctcaatactgttctgatacagatacagattcttcaacagccagact 5640
|||||
Db 5878 gttgtgtcttccctcaatactgttctgatacagatacagattcttcaacagccagact 5937
OY 5641 gtaaatgcaaaactatcttccctgaatgataagatgaagatgtaagcggaagagacag 5700
|||||
Db 5938 gtaaatgcaaaactatcttccctgaatgataagatgtaagatgtaagcggaagagacag 5997
OY 5701 aagaattctgattgtggaagcgcaagatgacatcttagaataaagaagttagcagaata 5760
|||||
Db 5998 aagaattctgattgtggaagcgcaagatgacatcttagaataaagaagttagcagaata 6057
OY 5761 tatagaaggaagcgaagcgtgctgttagcaggaattgctggaatccctcctgtgag 5820
|||||
Db 6058 tatagaaggaagcgaagcgtgctgttagcaggaattgctggaatccctcctgtgag 6117
OY 5821 tgccttggtctcttggtggttaatggtgctggaataatcaacttcaagaatgtaaca 5880
|||||
Db 6118 tgccttggtctcttggtggttaatggtgctggaataatcaacttcaagaatgtaaca 6177
OY 5881 ggaagatacactgttaccagagagatgcttcccttaacaaaatagatattatcaaac 5940
|||||

Db 6178 ggaagatacactgttaccagagagatgcttcccttaacaaaatagatattatcaaac 6237
OY 5941 atccatgaagatcatcaagaagaatggtctacgtccctcaagtgtatgatacacaagctg 6000
|||||
Db 6238 atccatgaagatcatcaagaagaatggtctacgtccctcaagtgtatgatacacaagctg 6297
OY 6001 ttgacttggaaggaacacgttggaatcttcttgccttttgagaagagagtcocagaagaaga 6060
|||||
Db 6298 ttgacttggaaggaacacgttggaatcttcttgccttttgagaagagagtcocagaagaaga 6357
OY 6061 gtttgcaaggttgggtgagtggtgagcttcggaactggtgctctgtgaatgatagaanaa 6120
|||||
Db 6358 gtttgcaaggttgggtgagtggtgagcttcggaactggtgctctgtgaatgatagaanaa 6417
OY 6121 tatgctgtaactatagtggaaggaacaaacgaagcctctcaagcgaatgagcttgatc 6180
|||||
Db 6418 tatgctgtaactatagtggaaggaacaaacgaagcctctcaagcgaatgagcttgatc 6477
OY 6181 ggcgggctcctgtgtgttcttgatagaacccaacaggaatgatacacaagcccg 6240
|||||
Db 6478 ggcgggctcctgtgtgttcttgatagaacccaacaggaatgatacacaagcccg 6537
OY 6241 cgttcttggaatgtgcccataagtggttcaagagagggagatcaatgagcttcaaca 6300
|||||
Db 6538 cgttcttggaatgtgcccataagtggttcaagagagggagatcaatgagcttcaaca 6597
OY 6301 tctcaatgatagaagaatgtaagaactcttgcataagatgataatgataatgataatgata 6360
|||||
Db 6598 tctcaatgatagaagaatgtaagaactcttgcataagatgataatgataatgataatgata 6657
OY 6361 aggttcaggtgcttgggaagtggtccagatcttaaaaaataggttggagatggttataca 6420
|||||
Db 6658 aggttcaggtgcttgggaagtggtccagatcttaaaaaataggttggagatggttataca 6717
OY 6421 atagttgatagaatgagcaggttccaaacccgagcctggaagcctgccaagattcttggga 6480
|||||
Db 6718 atagttgatagaatgagcaggttccaaacccgagcctggaagcctgccaagattcttggga 6777
OY 6481 ctgtgattctctggaaggtgtcttaaaagaagaacacccggaacatgatacacaacagct 6540
|||||
Db 6778 ctgtgattctctggaaggtgtcttaaaagaagaacacccggaacatgatacacaacagct 6837
OY 6541 ccatctcatatcttctctgccaagatattagacatctctcccgagacaacaaagcga 6600
|||||
Db 6838 ccatctcatatcttctctgccaagatattagacatctctcccgagacaacaaagcga 6897
OY 6601 ctccacatagaagaactactgttcttccagaacacacttgacaagaattgtgaactt 6660
|||||
Db 6898 ctccacatagaagaactactgttcttccagaacacacttgacaagaattgtgaactt 6957
OY 6661 gccaaagcaaaagttagatgatacacttaaaagacacttccatctacacaaaacagaca 6720
|||||
Db 6958 gccaaagcaaaagttagatgatacacttaaaagacacttccatctacacaaaacagaca 7017
OY 6721 gtagtgagcttggaagcttcacacacttcttcaagaatgaagaatgtaagaagactat 6780
|||||
Db 7018 gtagtgagcttggaagcttcacacacttcttcaagaatgaagaatgtaagaagactat 7077
OY 6781 gtagtgagcttggaagcttcacacacttcttcaagaatgaagaatgtaagaagactat 7077
|||||
Db 7078 gtagtgagcttggaagcttcacacacttcttcaagaatgaagaatgtaagaagactat 7101

RESULT 13
ID AAK51683 standard; cDNA; 7281 BP.
XX AAK51683;
AC AAK51683;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 228.
DE
```


XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine: peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation; ss.

XX Homo sapiens.
 XX MO200157190-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US04098.

XX 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620323.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.

XX (HYSE-) HISEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX WPI; 2001-476283/51.
 DR P-PDB; AAM78550.

XX Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -

XX Claim 1; Page 1086-1096; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78523-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other:

Query Match 99.7%; Score 6783.2; DB 22; Length 7281;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 6791; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1 atgctctgttgccctcagctgagctgtgctgtgctgtggaagaacctcattcagaagaaga 60
 |||
 DB 342 atgctgtgttgccctcagctgagctgtgctgtgctgtggaagaacctcattcagaagaaga 401
 OY 61 caacatgtcagctgttactggaagtgtgctgtgctgttattattcttcctgattcgtgac 120
 |||
 DB 402 caacatgtcagctgttactggaagtgtgctgtgctgttattattcttcctgattcgtgac 461
 OY 121 tctgtgtgctgagctacccacccctatgaaacatgatgatcatttccaaataaagcc 180
 |||
 DB 462 tctgtgtgctgagctacccacccctatgaaacatgatgatcatttccaaataaagcc 521
 OY 181 atgcctctgcaggaacctctctgtgtgctcaggagattatctgtatgcacaacaccc 240
 |||

DB 522 atgcctctgcaggaacctctctgtgtgctcaggagattatctgtatgcacaacaccc 581
 OY 241 ttttcgttaccacgaacctctgtggtgagctcccggaatttttggaaacttaacaatcc 300
 |||
 DB 582 ttttcgttaccacgaacctctgtggtgagctcccggaatttttggaaacttaacaatcc 641
 OY 301 attgtgctgcgcctgttttcagatgctcgagctctcttatacaacccaagaacac 360
 |||
 DB 642 attgtgctgcgcctgttttcagatgctcgagctctcttatacaacccaagaacac 701
 OY 361 agcatgaagaagacatgcgaagaattcttgaaacattacagcagatcaagaatccagctca 420
 |||
 DB 702 agcatgaagaagacatgcgaagaattcttgaaacattacagcagatcaagaatccagctca 761
 OY 421 aacttgaagcttcaagatttctgtgtggaacatgaacactctctgtgttccatatacac 480
 |||
 DB 762 aacttgaagcttcaagatttctgtgtggaacatgaacactctctgtgttccatatacac 821
 OY 481 aactctctctcccaagctactgttgacaagaatgctgagagctgtatgtatctccac 540
 |||
 DB 822 aactctctctcccaagctactgttgacaagaatgctgagagctgtatgtatctccac 881
 OY 541 aaggtatttttgaaggtctaccagttacatttgacaagctgtgtgaatgtataatca 600
 |||
 DB 882 aaggtatttttgaaggtctaccagttacatttgacaagctgtgtgaatgtataatca 941
 OY 601 gaagagatgatacactgtgtgacccaagaagtcttgagctttgtgcttcccaagaag 660
 |||
 DB 942 gaagagatgatacactgtgtgacccaagaagtcttgagctttgtgcttcccaagaag 1001
 OY 661 aactgtgctgcagcagagagatctgttcccaacatgagacatctctgaaacaaatcc 720
 |||
 DB 1002 aactgtgctgcagcagagagatctgttcccaacatgagacatctctgaaacaaatcc 1061
 OY 721 agaacactaaactctacatctccctcccgagcaagagctgtgtgaaacaaaaca 780
 |||
 DB 1062 agaacactaaactctacatctccctcccgagcaagagctgtgtgaaacaaaaca 1121
 OY 781 ttcttcatagtcttggtgctctggtccagagctgttcaagatgaagaagctgtgac 840
 |||
 DB 1122 ttcttcatagtcttggtgctctggtccagagctgttcaagatgaagaagctgtgac 1181
 OY 841 atgcgaagaggtgtgatttcttgacaaatgtgaacagctcagctctcccaacaaatc 900
 |||
 DB 1182 atgcgaagaggtgtgatttcttgacaaatgtgaacagctcagctctcccaacaaatc 1241
 OY 901 taccagctgtgtctgtatttctgtcgggcatcccgaggagggggtctgaagaatcaag 960
 |||
 DB 1242 taccagctgtgtctgtatttctgtcgggcatcccgaggagggggtctgaagaatcaag 1301
 OY 961 tctctcaactgtatgagacaacaactacaagccctcttggaggcaatgagctgag 1020
 |||
 DB 1302 tctctcaactgtatgagacaacaactacaagccctcttggaggcaatgagctgag 1361
 OY 1021 gaagatgtcgaacactctctatgacaactctacaaccccttactgcaattattgtgag 1080
 |||
 DB 1362 gaagatgtcgaacactctctatgacaactctacaaccccttactgcaattattgtgag 1421
 OY 1081 aattgagatgattctcttcccgatattctgaaagctctgaaagcgtgtcgtt 1140
 |||
 DB 1422 aattgagatgattctcttcccgatattctgaaagctctgaaagcgtgtcgtt 1481
 OY 1141 gggaagatctcttatacactgtacatccagcacaaggaagtcatggtcgtatgaaac 1200
 |||
 DB 1482 gggaagatctcttatacactgtacatccagcacaaggaagtcatggtcgtatgaaac 1541
 OY 1201 aagacattccaggaagcgtctgttccatgatctgaaaggaatgtggaggaagaactcaac 1260
 |||
 DB 1542 aagacattccaggaagcgtctgttccatgatctgaaaggaatgtggaggaagaactcaac 1601
 OY 1261 cccaagatctgaccttcatatgaaagaacagccaagaatgtgacctgtccgagatgctgtt 1320
 |||
 DB 1602 cccaagatctgaccttcatatgaaagaacagccaagaatgtgacctgttcgagatgctgtt 1661

QY	1321	gacagcagggagacaatagcacctctttgggaacagcaatlbgatggtctatgatltgacacgc	1380
Db	1662	gacacgacagggacaacaatgacacacttttggaaacagacagttgatgtctatgttggacagcc	1721
QY	1381	caagcagatcggtggcgctttttggccaagcaccccgaaagatgctccagtlcaatggttct	1440
Db	1722	caagacacacggtggcgcttttttggccaagcaccccgaaagatgctccagtlcaatggttct	1781
QY	1441	gtgtacacccctggagagaaagccttccaagagacccaacaaagcaatccgagacatcttcgc	1500
Db	1782	gtgtacacccctggagagaaagccttccaagagacccaacaaagcaatccgagacatcttcgc	1841
QY	1501	ttccatgggggtgtgttgcacactgcgtgaacaagctgaacacccatagcaagaagctctgcatac	1560
Db	1842	ttccatgggggtgtgttgcacactgcgtgaacaagcctgaagaaccccatagcaagaagctctgcatac	1901
QY	1561	aacaaggtccacgtgagcgtcgtctgagatgagagagaatctctggcgcgtattgtgttcaatcgga	1620
Db	1902	aacaaggtccacgtgagcgtcgtctgagatgagagagaatctctggcgcgtattgtgttcaatcgga	1961
QY	1621	attactccaggcagcattgagctgccccatcatalgtcaagtacagaatccgaatggagacat	1680
Db	1962	attactccaggcagcattgagctgccccatcatalgtcaagtacagaatccgaatggagacat	2021
QY	1681	gacaaatgtggagagagacaataataacaaagatgtgtactttggagacccgtgcctcgagct	1740
Db	2022	gacaaatgtggagagagacaataataacaaagatgtgtactttggagacccgtgcctcgagct	2081
QY	1741	gacccctttgagagacatgctggtactcgtcgggggggttcctgcctactcttgacagatgtgtg	1800
Db	2082	gacccctttgagagacatgctggtactcgtcgggggggttcctgcctactcttgacagatgtgtg	2141
QY	1801	gagcagagcaatcacaacaggtgctgcgtgaagggcacccggaaagaaactggtgtctataltgcaa	1860
Db	2142	gagcagagcaatcacaacaggtgctgcgtgaagggcacccggaaagaaactggtgtctataltgcaa	2201
QY	1861	cagatgcccctatccctgttactglttgaatgacatcttctcggcggtgatgtagccgttcaatg	1920
Db	2202	cagatgcccctatccctgttactglttgaatgacatcttctcggcggtgatgtagccgttcaatg	2261
QY	1921	cccccttcaatgacgcgtgcgtcgtgatttactcaatgtgcgtctgtatcatcaagaaggtacatcgtg	1980
Db	2262	cccccttcaatgacgcgtgcgtcgtgatttactcaatgtgcgtctgtatcatcaagaaggtacatcgtg	2321
QY	1981	tatbagaaggagagacacgcgtcgaagaagacaacacgtgcgtacacatggggccctggacaacagacata	2040
Db	2322	tatbagaaggagagacacgcgtcgaagaagacaacacgtgcgtacacatggggccctggacaacagacata	2381
QY	2041	ctctcgtgttagctggtgtcatcaatagtlagctcatcctctctcttcttgtagcgtcttgccgtcta	2100
Db	2382	ctctcgtgttagctggtgtcatcaatagtlagctcatcctctctcttcttgtagcgtcttgccgtcta	2441
QY	2101	gtgtgtacccctgtaagttaagaagaacccgtgcgtccctacaaatgtatcccaagcgtggtgttgc	2160
Db	2442	gtgtgtacccctgtaagttaagaagaacccgtgcgtccctacaaatgtatcccaagcgtggtgttgc	2501
QY	2161	ttctcgtgtcgtgttctgtctgtgtgaacaacccbtgaatgctctctctgtatagacacactcttc	2220
Db	2502	ttctcgtgtcgtgttctgtctgtgtgaacaacccbtgaatgctctctctgtatagacacactcttc	2561
QY	2221	ttccagagccaacccctgtagcagacacccgtggggagatcatcaactcaacgtcgtatccctgcgcc	2280
Db	2562	ttccagagccaacccctgtagcagacacccgtggggagatcatcaactcaacgtcgtatccctgcgcc	2621
QY	2281	taagctcgtgtgtgtgcatatgacagactacatgtggtcttcaacatcaagaatccttcgtctagc	2340
Db	2622	taagctcgtgtgtgtgcatatgacagactacatgtggtcttcaacatcaagaatccttcgtctagc	2681
QY	2341	ctctccttctccctgtggccttttgggttggcgtgtgaatcaacttgcctctttttagagagag	2400
Db	2682	ctctccttctccctgtggccttttgggttggcgtgtgaatcaacttgcctctttttagagagag	2741

[illegible]

|||||
Db 3822 agcagttcgtatgctgacctggcagccatctgagatgacacgctgcacatctgactgctc 3881
QY 3541 tctgtcatctcaacctcatcaaggagatgctgtcgaagcccgctggtgtgaagacata 3600
Db 3882 tctgtcatctcaacctcatcaaggagatgctgtcgaagcccgctggtgtgaagacata 3941
QY 3601 gggcatgagctgacatagtctgacataatgaagctgctaaaggagggagccctgtgtaa 3660
Db 3942 gggcatgagctgacatagtctgacataatgaagctgctaaaggagggagccctgtgtaa 4001
QY 3661 cctcttcagagatctgagacccggtctccagacctgggcatcttctagtatgacatctca 3720
Db 4002 cctcttcagagatctgagacccggtctccagacctgggcatcttctagtatgacatctca 4061
QY 3721 gagaagacctggaagaaatctctcaagctgctcgaagagatggtgggtgagctgag 3780
Db 4062 gagaagacctggaagaaatctctcaagctgctcgaagagatggtgggtgagctgag 4121
QY 3781 acctcagatgctacccctgccaagacgaacagcgggccctcggggagacagcagagc 3840
Db 4122 acctcagatgctacccctgccaagacgaacagcgggccctcggggagacagcagagc 4181
QY 3841 tgtcttcgccccttcaactgaatgactgctgtgaatccaatgacttctgacatgaccca 3900
Db 4182 tgtcttcgccccttcaactgaatgactgctgtgaatccaatgacttctgacatgaccca 4241
QY 3901 gaatccagaagagacagactgtctcagtgagatgataggcaaaaggtctctaccaggtgaaa 3960
Db 4242 gaatccagaagagacagactgtctcagtgagatgataggcaaaaggtctctaccaggtgaaa 4301
QY 3961 ggtctggaacctatacagaacagatgtggtgaccttgtgtgaagaagctctaaatgcc 4020
Db 4302 ggtctggaacctatacagaacagatgtggtgaccttgtgtgaagaagctctaaatgcc 4361
QY 4021 agacgagatcgcgaagatcttctgtcagatgtctctgccaagctgtgttctgtcgtcat 4080
Db 4362 agacgagatcgcgaagatcttctgtcagatgtctctgccaagctgtgttctgtcgtcat 4421
QY 4081 gacctgtgtctcagacctgactgctgacaccttggcaagctaccagacctgtaacttaag 4140
Db 4422 gacctgtgtctcagacctgactgctgacaccttggcaagctaccagacctgtaacttaag 4481
QY 4141 cccctgagatgatacagaacagatcacattgttcaagaatgactgctcctgaagacacgga 4200
Db 4482 cccctgagatgatacagaacagatcacattgttcaagaatgactgctcctgaagacacgga 4541
QY 4201 accctggaactcttaaacgacctcaacaaagacctggtctcggaagcccgctgataggaa 4260
Db 4542 accctggaactcttaaacgacctcaacaaagacctggtctcggaagcccgctgataggaa 4601
QY 4261 ggaaaacccaatcccaagaacagccctgccaagcggaaggaagagatgagacacatcccca 4320
Db 4602 ggaaaacccaatcccaagaacagccctgccaagcggaaggaagagatgagacacatcccca 4661
QY 4321 gtctcccaagacatcatgagacccctctccagatgaggaactggaacaaatgtaagaaccttca 4380
Db 4662 gtctcccaagacatcatgagacccctctccagatgaggaactggaacaaatgtaagaaccttca 4721
QY 4381 cctgtcatgccaagtgtagcagcgacaaatcaagaagaatgctgctgtgtgtcccccaggg 4440
Db 4722 cctgtcatgccaagtgtagcagcgacaaatcaagaagaatgctgctgtgtgtcccccaggg 4781
QY 4441 gcaaggggggctgctcctccacaagaagaacaaacacatctcagatactcctccagacccg 4500
Db 4782 gcaaggggggctgctcctccacaagaagaacaaacacatctcagatactcctccagacccg 4841
QY 4501 acaagaagaacacatttcgattatctgtgtgaagaagatglatgtgcagatcatagccaaaagc 4560
Db 4842 acaagaagaacacatttcgattatctgtgtgaagaagatglatgtgcagatcatagccaaaagc 4901
QY 4561 ttaagaagaacatctggtgtgaatgaaattagatgtggtgcttccctcggtgtcagt 4620
|||||

Db 4902 ttaagaagaacatctggtgtgaatgagtttagatgtggcgcttccctcggtgtcagt 4961
QY 4621 aataactaaagacatctcctccagatcaagaagttaattatgccaatcaaaatgaagaa 4680
Db 4962 aataactaaagacatctcctccagatcaagaagttaattatgccaatcaaaatgaagaa 5021
QY 4681 cccctaaagcttgccaagaagacagctctgcagatcgatcttcccaacagcttggaagatt 4740
Db 5022 cccctaaagcttgccaagaagacagctctgcagatcgatcttcccaacagcttggaagatt 5081
QY 4741 atgacagagctgagacacagaataatgtlcaaggtgtgttcaataaacaaggctgtgcat 4800
Db 5082 atgacagagctgagacacagaataatgtlcaaggtgtgttcaataaacaaggctgtgcat 5141
QY 4801 gcaatcagctcttccctgaatgtcatcaacaatgccaattcccgggccaactgcaaaag 4860
Db 5142 gcaatcagctcttccctgaatgtcatcaacaatgccaattcccgggccaactgcaaaag 5201
QY 4861 ggaagaaaccttccagcatatgaaatctgcttcaatctcaatccctgaaatctcaacaag 4920
Db 5202 ggaagaaaccttccagcatatgaaatctgcttcaatctcaatccctgaaatctcaacaag 5261
QY 4921 cagcagctctcagaaggtggtctgtatgacacacatcagatgagatgtcctgtgtccactgt 4980
Db 5262 cagcagctctcagaaggtggtctgtatgacacacatcagatgagatgtcctgtgtccactgt 5321
QY 4981 gtatcttggcaatgtcctctgtcccaagcacttgtcgtatctccatccatcagaagcgg 5040
Db 5322 gtatcttggcaatgtcctctgtcccaagcacttgtcgtatctccatccatcagaagcgg 5381
QY 5041 gtccagcaagcaaaaacacctgagatctcatlcaagtggaatgaaagcctgtcaatctactgctc 5100
Db 5382 gtccagcaagcaaaaacacctgagatctcatlcaagtggaatgaaagcctgtcaatctactgctc 5441
QY 5101 tccaatttggctcgggaatgtgtgcaaatagcgtgtccctggccaacatgctgtatatac 5160
Db 5442 tccaatttggctcgggaatgtgtgcaaatagcgtgtccctggccaacatgctgtatatac 5501
QY 5161 ttcatctgctccagcagaagctcatgtgtctcccaacacatgctgtgtcagacct 5220
Db 5502 ttcatctgctccagcagaagctcatgtgtctcccaacacatgctgtgtcagacct 5561
QY 5221 ctactcttgcgtatgtgtgtgtatcaacacatctctcatgtacccaagctccttgtgtctc 5280
Db 5562 ctactcttgcgtatgtgtgtgtatcaacacatctctcatgtacccaagctccttgtgtctc 5621
QY 5281 aagatccccaagcagaacacatgtgtgtgtccacaacagcgttaaccttcaatgtgacataat 5340
Db 5622 aagatccccaagcagaacacatgtgtgtgtccacaacagcgttaaccttcaatgtgacataat 5681
QY 5341 ggcagcgtgcccacaccttgtgtcgtgagctgttaccgcgaataaagctgaataatacat 5400
Db 5682 ggcagcgtgcccacaccttgtgtcgtgagctgttaccgcgaataaagctgaataatacat 5741
QY 5401 gatactctgaagctccgtgttcttgatcttcccaatcttctgtgtggaaggggtctatc 5460
Db 5742 gatactctgaagctccgtgttcttgatcttcccaatcttctgtgtggaaggggtctatc 5801
QY 5461 gacatgtgtgaaaaaacccggaatgagctgtatgaccttggaaggttttggggagatctgctt 5520
Db 5802 gacatgtgtgaaaaaacccggaatgagctgtatgaccttggaaggttttggggagatctgctt 5861
QY 5521 gtgtacacatatactgtggaactgtgtggaagcaaacctcttcgacatggtcgatgaaagg 5580
Db 5862 gtgtacacatatactgtggaactgtgtggaagcaaacctcttcgacatggtcgatgaaagg 5921
QY 5581 gtgtgttcttccatctactgttcttgatccagttacagattcttcaatcgccagacct 5640
Db 5922 gtgtgttcttccatctactgttcttgatccagttacagattcttcaatcgccagacct 5981
QY 5641 gtaaatgcaaaagctatctcctgtgaatgataatgaaatgtgtgaagcgggaagacag 5700
Db 5982 gtaaatgcaaaagctatctcctgtgaatgataatgaaatgtgtgaagcgggaagacag 6041
|||||

QY	5701	agaattcttgaagtgaggagcccaagaatgacattttagaatcaaggagtttgcagaata	5760
Db	6042	agaattcttgaagtgaggagcccaagaatgacattttagaatcaaggagtttgcagaata	6101
QY	5761	tataagaagaagccggaagccctgcgtttgacagagatttgcgttggcattccctctgtag	5820
Db	6102	tataagaagaagccggaagccctgcgtttgacagagatttgcgttggcattccctctgtag	6161
QY	5821	tgctttgggtcccttgggaggttaatggggcttqgaaatcatcaacttcaagtttaaca	5880
Db	6162	tgctttgggtcccttgggaggttaatggggcttqgaaatcatcaacttcaagtttaaca	6221
QY	5881	ggagaataccactgttaccagaagagagatgcttcttccaacaaatagatcttccaac	5940
Db	6222	ggagaataccactgttaccagaagagagatgcttcttccaacaaatagatcttccaac	6281
QY	5941	atccaatgaatgacatcagaacatlggctactgacctcaagtttgaatgcatacagaatg	6000
Db	6282	atccaatgaatgacatcagaacatlggctactgacctcaagtttgaatgcatacagaatg	6341
QY	6001	ttgacttgggaagaagaacccgtggaggttccttggccctttgaaggagggtcccaagaaga	6060
Db	6342	ttgacttgggaagaagaacccgtggaggttccttggccctttgaaggagggtcccaagaaga	6401
QY	6061	gttggcaaggttctgtgaagtgagcgatctcgaaacttggccctgttaagtaagagaaaaa	6120
Db	6402	gttggcaaggttctgtgtgaagtgagcgatctcgaaacttggccctgttaagtaagagaanaa	6461
QY	6121	tatgtgtgttaactataatgtgaagcaacaaacgcaagctctcaagccatgagctttgac	6180
Db	6462	tatgtgtgttaactataatgtgaagcaacaaacgcaagctctctcaagccatgagctttgac	6521
QY	6181	ggcgggacctctctgtgtgttctctgtgaatgaaaccacacagagatgattcccaagcccg	6240
Db	6522	ggcgggacctctctgtgtgttctctgtgtgaatgaaaccacacagagatgattcccaagcccg	6581
QY	6241	cggttcttgtgaatttgcacctgaagtgtttgtccaaggaggagatcaagtagtgattaca	6300
Db	6582	cggttcttgtgaatttgcacctgaagtgtttgtccaaggaggagatcaagtagtgattaca	6641
QY	6301	tctcatagtaagaaatgtgaagctcttgcactagaatgagcaatcatgtgtcaatga	6360
Db	6642	tctcatagtaagaaatgtgaagctcttgcactagaatgagcaatcatgtgtcaatga	6701
QY	6361	aggttcacggtgacctgtgcagatgtccgaactctaaaaatagtttggagatggttataca	6420
Db	6702	aggttcacggtgacctgtgcagatgtccgaactctaaaaatagtttggagatggttataca	6761
QY	6421	atagtttacgaatagacaaggtcccaaccgggacctggaagcctgtgccaggtttcttga	6480
Db	6762	atagtttacgaatagacaaggtcccaaccgggacctggaagcctgtgccaggtttcttga	6821
QY	6481	cttgcattctccctgggaagtgttctaaaaagaacaacggaatcatgctacaaatlaacagct	6540
Db	6822	cttgcattctccctgggaagtgttctaaaaagaacaacggaatcatgctacaaatlaacagct	6881
QY	6541	ccaattctatattcttcttggccggagatattcagcattcctctcccgagaacaaagcga	6600
Db	6882	ccaattctatattcttcttggccggagatattcagcattcctctcccgagaacaaagcga	6941
QY	6601	ctccacaatagaactactctgtttctcagaacaacttgcacgaagtatttggacttt	6660
Db	6942	ctccacaatagaactactctgtttctcagaacaacttgcacgaagtatttggacttt	7001
QY	6661	ggcaaggacccaagtgatgataaccactttaaagaactctcatatacaaaaaacagaca	6720
Db	7002	ggcaaggacccaagtgatgataaccactttaaagaactctcatatacaaaaaacagaca	7061
QY	6721	gtatgtgagcttgcattctcacaacttttctcaagatgagaagaatgaaaagctat	6780
Db	7062	gtatgtgagcttgcattctcacaacttttctcaagatgagaagaatgaaaagctat	7121

Qy	6781	gtatgaagaatcctgltcatacyg	6804
Db	7122	gtatgaagaatcctgltcatacyg	7145

RESULT 14
ABA09200

ABA09200

ID	ABA09200 standard; cDNA; 7086 BP.
----	-----------------------------------

AC ABA09200;
xy

DT 11-JAN-2002 (first entry)

Human ABCA1 homologue-encoding cDNA, SEQ ID NO:976.

KM Human; cytokine; cell proliferation; cell differentiation; growth factor;
KM haematopoiesis regulation; tissue growth; immunomodulator; activin;
KM inhibin; chemokinesis; chemokinesis; chromolysis; oncogenesis;
KM proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KM myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KM chronic inflammatory condition; proliferative retinopathy;
KM atherosclerosis; coronary heart disease; arterial ischaemia;
KM bone disorder; osteoporosis; vascular growth disorder;
KM tissue regeneration; wound healing; infection; immune disorder;
KM cell culture; drug screening; gene therapy; antiinflammatory;
KM antisthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KM cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KM antifungal; vulnery; antitumor; ss.

OS Homo sapiens

PN WO200157188-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US03800.

PR 03-FEB-2000; 2000US-0496914.

XX
DA (HYGE-) HYGE0 TWO

XX	
PT	Mand VM T in C

XX
DP WBT: 2003-457740/40

DR P-PSDB; ABB11956.
XY

PT	Human proteins and DNA encoding
DT	+ treating or modifying

PT e.g. arthritis and cancer -
XY

PS Claim 1; Page 833-835; 1963pp; English.
XX

CC	Sequences	ABBI0981-ABBI12330	represent
CC	Sequences	ABA0825-ABA08574	represent

invention also relates to vectors and recombinant host cells comprising nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haematopoietic regulatory activity; tissue growth factor activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis, depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include

CC cancers, hematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), CC proliferative retinopathy, atherosclerosis, coronary heart disease, CC arterial ischemia, bone disorders (e.g., osteoporosis), and abnormal CC vascular growth. Polypeptides involved with tissue regeneration and CC repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with CC immunomodulatory activities may be used in the treatment of viral, CC bacterial and fungal infections in addition to immune disorders. CC Polypeptides with growth factor activity may be used in cell cultures to CC promote cell growth. For example, such polypeptides may be used to CC manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness. CC autoimmune disease or accidental damage. The polypeptides and nucleotides CC may also be used in the diagnosis of the above conditions, and in drug CC screening techniques. The present sequence represents a cDNA encoding a CC novel human polypeptide of the invention.

XX Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;

Query Match

Best Local Similarity 99.4%; Score 6762.2; DB 22; Length 7086;
Matches 6770; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 atggtctgttggtcctcagctcagctggtctgctgtgtggaagaacctcattcagaagaaga 60
DB 304 atggtctgttggtcctcagctcagctggtctgctgtgtggaagaacctcattcagaagaaga 363
QY 61 caaactatcagctgtactgtgaagtgctgctgctcctatcttactctcagctcagctg 120
DB 364 caaactatcagctgtactgtggaagtgctgctgctcctatcttactctcagctcagctg 423
QY 121 tctgttctgctgctgctcagctcagctcagctcagctcagctcagctcagctcagctc 180
DB 424 tctgttctgctgctgctcagctcagctcagctcagctcagctcagctcagctcagctc 483
QY 181 atgcccctcaggaagaacctcctgtgctcagggagatctcgtatgccaacacccc 240
DB 484 atgcccctcaggaagaacctcctgtgctcagggagatctcgtatgccaacacccc 543
QY 241 tgttccgtacccagctcctcctggtggaagctcccgagctgtgttggaacttaacaaatcc 300
DB 544 tgttccgtacccagctcctcctggtggaagctcccgagctgtgttggaacttaacaaatcc 603
QY 301 atgtgtgctgctgctgtctcagatgctcggagctccttcttatacagccgaagaagacc 360
DB 604 atgtgtgctgctgctgtctcagatgctcggagctccttcttatacagccgaagaagacc 663
QY 361 agctatgagagacatgctcgaagctcgtgagacattacagagatcgaagaatccagctca 420
DB 664 agctatgagagacatgctcgaagctcgtgagacattacagagatcgaagaatccagctca 723
QY 421 aacttgagagctcgaagcttctcctgtgtgagacatgaaacctctctggttctcctatcac 480
DB 724 aacttgagagctcgaagcttctcctgtgtgagacatgaaacctctctggttctcctatcac 783
QY 481 aactctctctcccaagctcactgtgagacagatgctgagggctgtgctatcttccac 540
DB 784 aactctctctcccaagctcactgtgagacagatgctgagggctgtgctatcttccac 843
QY 541 aaggtatcttttgcaagctcagcttaccatttgcaagctctgtgcaatgtgataaataca 600
DB 844 aaggtatcttttgcaagctcagcttaccatttgcaagctctgtgcaatgtgataaataca 903
QY 601 gaagaagatgatacaactgtgtgacaaagatttctgagcttgtgtgcttaccacaagagag 660
DB 904 gaagaagatgatacaactgtgtgacaaagatttctgagcttgtgtgcttaccacaagagag 963
QY 661 aaactgtgtcagcagagcagagctatctcgttcccaactgagacatcccgaaagccaatctgt 720
DB 964 aaactgtgtcagcagagcagagctatctcgttcccaactgagacatcccgaaagccaatctgt 1023

QY 721 agaactaaactctacatctcctccctccagcagaagagctgtgctgagccacaacaaca 780
DB 1024 agaactaaactctacatctcctccctccagcagaagagctgtgctgagccacaacaaca 1083
QY 781 ttgtctgatactctgtgagctctgtgccaagagctgttctgacatgaaagctgtgtgac 840
DB 1084 ttgtctgatactctgtgagctctgtgccaagagctgttctgacatgaaagctgtgtgac 1143
QY 841 atgcagcagaggtgtgagttcttctgacccaatgtgaaacgctcagctctccacccaatc 900
DB 1144 atgcagcagaggtgtgagttcttctgacccaatgtgaaacgctcagctctccacccaatc 1203
QY 901 taccaggtgtgtctcgtatgtctgtgctgctgagccagcagaggggggtgtgaagatcaag 960
DB 1204 taccaggtgtgtctcgtatgtctgtgctgctgagccagcagaggggggtgtgaagatcaag 1263
QY 961 tctctcaactgtatgaggaacaacaactacaaagccctcttggaggaatgacatgtgag 1020
DB 1264 tctctcaactgtatgaggaacaacaactacaaagccctcttggaggaatgacatgtgag 1323
QY 1021 gaagatgtctgaacctcttctatgacaaactctacactcctctcgaatgtatgataag 1080
DB 1324 gaagatgtctgaacctcttctatgacaaactctacactcctctcgaatgtatgataag 1383
QY 1081 aattgtgagctagctcctctctcccgcatlactctgaaagctcgaagccgctgtcgtt 1140
DB 1384 aattgtgagctagctcctctctcccgcatlactctgaaagctcgaagccgctgtcgtt 1443
QY 1141 gggaaagatcctgtatatacaccctgacacatccagccaaagcaggtgtcatgtcgaagtgaac 1200
DB 1444 gggaaagatcctgtatatacaccctgacacatccagccaaagcaggtgtcatgtcgaagtgaac 1503
QY 1201 aagaccttccaggaactgctgtgttccatgatactctggaagcattgtggaagaaactcagc 1260
DB 1504 aagaccttccaggaactgctgtgttccatgatactctggaagcattgtggaagaaactcagc 1563
QY 1261 cccaagatctgagctctcatgagagaacagccaagaatgagactgtccgagatgtgtt 1320
DB 1564 cccaagatctgagctctctcatgagagaacagccaagaatgagactgtccgagatgtgtt 1623
QY 1321 gacagcagggagaaatgagacacttctgggaacagcaggtgtgaggtttagttgagcagcc 1380
DB 1624 gacagcagggagaaatgagacacttctgggaacagcaggtgtgaggtttagttgagcagcc 1683
QY 1381 caagacatctgtgctgttcttggccaagcaccagagagatgtccaatgcaatagttct 1440
DB 1684 caagacatctgtgctgttcttggccaagcaccagagagatgtccaatgcaatagttct 1743
QY 1441 gtgtacacctgagagaagcttctcaacagagactaaacagagcaatcccgacataltcgc 1500
DB 1744 gtgtacacctgagagaagcttctcaacagagactaaacagagcaatcccgacataltcgc 1803
QY 1501 ttcatgtgagttgttcaaccttgaaacagctcagaacccatagcaacgaagctcgtctac 1560
DB 1804 ttcatgtgagttgttcaaccttgaaacagctcagaacccatagcaacgaagctcgtctac 1863
QY 1561 aacaagtccatgtgagctgtgtgagtgagagaagcttctgtgctgagttgtgttcaactgga 1620
DB 1864 aacaagtccatgtgagctgtgtgagtgagagaagcttctgtgctgagttgtgttcaactgga 1923
QY 1621 atctaccagcagcagcatgtgagctgtcccatcatgtlccaagtatacaagatccgaatgacat 1680
DB 1924 atctaccagcagcagcatgtgagctgtcccatcatgtlccaagtatacaagatccgaatgacat 1983
QY 1681 gacaatgtgtgagaggaataataatcaagatgtgtgtatgtggaacctgtgtccctcgaagct 1740
DB 1984 gacaatgtgtgagaggaataataatcaagatgtgtgtatgtgtggaacctgtgtccctcgaagct 2043
QY 1741 gacctcttgagagacatgtgctgagctgtggtggtggtctgctactctgaggaatgtgtgt 1800
DB 2044 gacctcttgagagacatgtgctgagctgtggtggtggtctgctactctgaggaatgtgtgt 2103
QY 1801 gagcaggaatcatcatgaggtgtgtgacgggcaaccgagaagaataatgtgtctatattgcaa 1860

Db 2104 gagcaggaacatcaccagagggctgacgagcagcaggaagaaactgggtctatgacaa 2163
QY 1861 cagaatgacctaccctgttcaagttgatacatcttctcgggggtgagaaacgcatg 1920
Db 2164 cagatgacctaccctgttcaagttgatacatcttctcgggggtgagaaacgcatg 2223
QY 1921 ccccttctcatgagcgtcgccctgattactcaagtcgtgctgatacatcaaggcatcgtg 1980
Db 2224 ccccttctcatgagcgtcgccctgattactcaagtcgtgctgatacatcaaggcatcgtg 2283
QY 1981 tatgagaagagagcagcgcgtgaagagacatcgcgatacctgagccctggaacaacata 2400
Db 2284 tatgagaagagagcagcgcgtgaagagacatcgcgatacctgagccctggaacaacata 2343
QY 2041 ctctggttttagctggttcatatgatacctcatctctctctctgtagagcgtgagcgtgta 2100
Db 2344 ctctggttttagctggttcatatgatacctcatctctctctctgtagagcgtgagcgtgta 2403
QY 2101 gtggtcatcctgagatgagaacacgctgctccctacagtgatcccgagcgtggtgtgttc 2160
Db 2404 gtggtcatcctgagatgagaacacgctgctccctacagtgatcccgagcgtggtgtgttc 2463
QY 2161 ttcctgtccgt 2220
Db 2464 ttcctgtccgt 2523
QY 2221 tccagagcccaacccctgagcagcgtgtggtggtgacatctactctcagctgtactcctcc 2280
Db 2524 tccagagcccaacccctgagcagcgtgtggtggtgacatctactctcagctgtactcctcc 2583
QY 2281 taagtcctgt 2340
Db 2584 taagtcctgt 2643
QY 2341 ctgctgtctctctgt 2400
Db 2644 ctgctgtctctctgt 2703
QY 2401 ggcattgagagtgagtgagggagcaaacctgtttgagagtcctgtgagagaaatgagcttcaat 2460
Db 2704 ggcattgagagtgagtgagggagcaaacctgtttgagagtcctgtgagagaaatgagcttcaat 2763
QY 2461 ctcaacactctgacatccatgatagtgtgtgtgaacacttctctatgaggtgatagacgtg 2520
Db 2764 ctcaacactctgacatccatgatagtgtgtgtgaacacttctctatgaggtgatagacgtg 2823
QY 2521 taacattgagagctgtcttctcagggccagtaacgaattccagggccctggtatttctctgtc 2580
Db 2824 taacattgagagctgtcttctcagggccagtaacgaattccagggccctggtatttctctgtc 2883
QY 2581 accaagtcctactgt 2640
Db 2884 accaagtcctactgt 2943
QY 2641 aagagaagatgtaagaatctgcatagagagaggaacccacacacttgaagctgtggtgtgtcc 2700
Db 2944 aagagaagatgtaagaatctgcatagagagaggaacccacacacttgaagctgtggtgtgtcc 3003
QY 2701 attcagaacactgtgtaaaatctacagagatgagatgaaagtgtgctgtcatatgagctgtgca 2760
Db 3004 attcagaacactgtgtaaaatctacagagatgagatgaaagtgtgctgtcatatgagctgtgca 3063
QY 2761 ctggaattttatgagagggcagagatcaactctctctgtgagccacatgagagcgggagagag 2820
Db 3064 ctggaattttatgagagggcagagatcaactctctctgtgagccacatgagagcgggagagag 3123
QY 2821 accacacatgtaactctgaacgggtgtgtcccccagacactcggagacacgacctactcctgt 2880
Db 3124 accacacatgtaactctgaacgggtgtgtcccccagacactcggagacacgacctactcctgt 3183
QY 2881 ggaagaaacattcgtctgtgagatgagcaacatccgcagaaacctgtgggtgtgtgtccag 2940
Db 3184 ggaagaaacattcgtctgtgagatgagcaacatccgcagaaacctgtgggtgtgtgtccag 3243
QY 2941 cataagctgt 3000
Db 3244 cataagctgt 3303
QY 3001 aagaggctctctgagaagacgltgaagcggagatgagatgagatgagccctgtgagttgtgt 3060
Db 3304 aagaggctctctgagaagacgltgaagcggagatgagatgagatgagccctgtgagttgtgt 3363
QY 3061 tgcgcatacgaagaatctgaaaaagcaaaacgaagccagctgtgaagtgtggaatgacagaag 3120
Db 3364 tgcgcatacgaagaatctgaaaaagcaaaacgaagccagctgtgaagtgtggaatgacagaag 3423
QY 3121 ctatctgt 3180
Db 3424 ctatctgt 3483
QY 3181 gctgt 3240
Db 3484 gctgt 3543
QY 3241 ggcgcacacattatctctctacacacacatgagatgagagagagcgtcctgtggtgagag 3300
Db 3544 ggcgcacacattatctctctacacacacatgagatgagagagagcgtcctgtggtgagag 3603
QY 3301 attgcacatcctcccatgaggagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3360
Db 3604 attgcacatcctcccatgaggagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3663
QY 3361 cagctggggaagagcttactactgtacactgtgtgtaagaagaatgagatccctcctcagt 3420
Db 3664 cagctggggaagagcttactactgtacactgtgtgtaagaagaatgagatccctcctcagt 3723
QY 3421 tctctgcaagaaacagtagtagacactgtgtacatccctgaaagagagagcagtggttctcag 3480
Db 3724 tctctgcaagaaacagtagtagacactgtgtacatccctgaaagagagagcagtggttctcag 3783
QY 3481 agcaggtctctgt 3540
Db 3784 agcaggtctctgt 3843
QY 3541 tctgtatctctcaacccatccatcaggaagacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3600
Db 3844 tctgtatctctcaacccatccatcaggaagacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3903
QY 3601 gggcatgagctgacactatgt 3660
Db 3904 gggcatgagctgacactatgt 3963
QY 3661 ctcttcatgagatgtatgacgggtctcagagccctgagacattcttaattatgtgacatcca 3720
Db 3964 ctcttcatgagatgtatgacgggtctcagagccctgagacattcttaattatgtgacatcca 4023
QY 3721 gagaagacactggaagaataatctccaaagvtggtcgaagaagatggtgtgtgtgtgtgtgt 3780
Db 4024 gagaagacactggaagaataatctccaaagvtggtcgaagaagatggtgtgtgtgtgtgtgt 4083
QY 3781 accctcagatgttactctgtgcaagcagaagcaaaacggggtccttgggggcaagcagagc 3840
Db 4084 accctcagatgttactctgtgcaagcagaagcaaaacggggtccttgggggcaagcagagc 4143
QY 3841 tgtcttgcgcgttctactctgagatgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3900
Db 4144 tgtcttgcgcgttctactctgagatgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4203
QY 3901 gaatccagagaagacagactgt 3960
Db 4204 gaatccagagaagacagactgt 4263
QY 3961 ggtcggaaacttacaagcaagcaggt 4020
Db 4264 ggtcggaaacttacaagcaagcaggt 4323

QY 4021 agacgagatcggaagatcttctgcagatgtcttcgacgctgtcttcgcat 4080
|||||
Db 4324 agacgagatcggaagatcttctgcagatgtcttcgacgctgtcttcgcat 4383
QY 4081 gacctgtgtcagcctgtcgtccaccccttggcaagtaaccagcctgtgaactca 4140
|||||
Db 4384 gacctgtgtcagcctgtcgtccaccccttggcaagtaaccagcctgtgaactca 4443
QY 4141 cccctgtgttaacagaaagtaacacattgtcagcaatgatgtccctgagagacggga 4200
|||||
Db 4444 cccctgtgttaacagaaagtaacacattgtcagcaatgatgtccctgagagacggga 4503
QY 4201 acccttgaaactttaaacgctcccaacaaagccctgtgctggagaccgctgttgaa 4260
|||||
Db 4504 acccttgaaactttaaacgctcccaacaaagccctgtgctggagaccgctgttgaa 4563
QY 4261 ggaatacccaatcccaagacacgctgtccagcagggaggaagatggaaccactgccca 4320
|||||
Db 4564 ggaatacccaatcccaagacacgctgtccagcagggaggaagatggaaccactgccca 4623
QY 4321 gtcccccagacatactgaactcttccagaatgggaactggacaatacgccttca 4380
|||||
Db 4624 gtcccccagacatactgaactcttccagaatgggaactggacaatacgccttca 4683
QY 4381 cctgtcacgtcagtgtagcagcgacaataatcaagaaatgtctgtgtgtcccccagg 4440
|||||
Db 4684 cctgtcacgtcagtgtagcagcgacaataatcaagaaatgtctgtgtgtcccccagg 4743
QY 4441 gcaagggggctgcctcctccacaagaacaaacacacgagataccttcagagacctg 4500
|||||
Db 4744 gcaagggggctgcctcctccacaagaacaaacacacgagataccttcagagacctg 4803
QY 4501 acaggaagaacacattcggatatactgtgtgaagacgtatgtgcagatacgaacaaagc 4560
|||||
Db 4804 acaggaagaacacattcggatatactgtgtgaagacgtatgtgcagatacgaacaaagc 4863
QY 4561 ttaaaagaacaaagatcgtgtgtgaatgttaagtatgagtgagggcttccctgggtgtcagt 4620
|||||
Db 4864 ttaaaagaacaaagatcgtgtgtgaatgttaagtatgagtgagggcttccctgggtgtcagt 4923
QY 4621 aatacccaagcacttctcctccagatcaagaagttaatgatgcatacacaacaaatgaagaa 4680
|||||
Db 4924 aatacccaagcacttctcctccagatcaagaagttaatgatgcatacacaacaaatgaagaa 4983
QY 4681 caactaaagctggcacaagacagttctgcagatcgaattctcaaacagcttgggaagatt 4740
|||||
Db 4984 caactaaagctggcacaagacagttctgcagatcgaattctcaaacagcttgggaagatt 5043
QY 4741 atgacagagctggacacacgaagaaatgtcaaggtgtgttcaatacaagggctggcat 4800
|||||
Db 5044 atgacagagctggacacacgaagaaatgtcaaggtgtgttcaatacaagggctggcat 5103
QY 4801 gcaatagccttctcctgaatgtcatcaacaatgcatctcccgggccaactgcgaag 4860
|||||
Db 5104 gcaatagccttctcctgaatgtcatcaacaatgcatctcccgggccaactgcgaag 5163
QY 4861 ggaagaaacccatgacatataatgaatgaatgttcaatcatccctgtgaactcaacaa 4920
|||||
Db 5164 ggaagaaacccatgacatataatgaatgaatgttcaatcatccctgtgaactcaacaa 5223
QY 4921 cagcaagctcctcagaggtgtcctgtgagcaacacaaatgagtgctgtgtccatctt 4980
|||||
Db 5224 cagcaagctcctcagaggtgtcctgtgagcaacacaaatgagtgctgtgtccatctt 5283
QY 4981 gtatctcttgcaatgtcctcgtccagcagcgttgcgtatctccctgtccagggcg 5040
|||||
Db 5284 gtatctcttgcaatgtcctcgtccagcagcgttgcgtatctccctgtccagggcg 5343
QY 5041 gtcaagcaagcaaaacacctgcagttcatcatgtgagtggaagcctgtcatctacgtgctc 5100
|||||
Db 5344 gtcaagcaagcaaaacacctgcagttcatcatgtgagtggaagcctgtcatctacgtgctc 5403

QY 5101 tctaatttgcctggatataatgaatgaatgttccctgcacacatgcatatcatc 5160
|||||
Db 5404 tctaatttgcctggatataatgaatgaatgttccctgcacacatgcatatcatc 5463
QY 5161 ttaatctgtctccagcagaatctctaagtgtccccaacaaatcgtcgtgtgacgacct 5220
|||||
Db 5464 ttaatctgtctccagcagaatctctaagtgtccccaacaaatcgtcgtgtgacgacct 5523
QY 5221 ctacttctgtgtatgtgtgttcaatcaaaccttcaatgtatcaaccagcctctgtgttc 5280
|||||
Db 5524 ctacttctgtgtatgtgtgttcaatcaaaccttcaatgtatcaaccagcctctgtgttc 5583
QY 5281 aagatccccaagcacaagcctatgtgtgtcacaacgctgtgaaccttcatatgtgaat 5340
|||||
Db 5584 aagatccccaagcacaagcctatgtgtgtcacaacgctgtgaaccttcatatgtgaat 5643
QY 5341 ggcagcgttgcacacctgtgtgtgagcgtgtcaacgacaataagctgaataataat 5400
|||||
Db 5644 ggcagcgttgcacacctgtgtgtgagcgtgtcaacgacaataagctgaataataat 5703
QY 5401 gatactcgaagctcgt 5460
|||||
Db 5704 gatactcgaagctcgt 5763
QY 5461 gacatgtgtgaataaaccaagcagaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5520
|||||
Db 5764 gacatgtgtgaataaaccaagcagaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5823
QY 5521 gtgtcacatatacttggagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5580
|||||
Db 5824 gtgtcacatatacttggagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5883
QY 5581 gt 5640
|||||
Db 5884 gt 5943
QY 5641 gtaaatgtcaaaagctatccctcctgaatgaatgaatgaatgtgtgaagcgggaagacag 5700
|||||
Db 5944 gtaaatgtcaaaagctatccctcctgaatgaatgaatgaatgtgtgaagcgggaagacag 6003
QY 5701 agaatcttgaatgt 5760
|||||
Db 6004 agaatcttgaatgt 6063
QY 5761 tataagaagaagcgggaagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5820
|||||
Db 6064 tataagaagaagcgggaagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6123
QY 5821 tgccttgggtcctcctggaggttaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5880
|||||
Db 6124 tgccttgggtcctcctggaggttaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6183
QY 5881 ggaagataccactgttaccagaagagatgtcttcccttaacaaatagatatacaaac 5940
|||||
Db 6184 ggaagataccactgttaccagaagagatgtcttcccttaacaaatagatatacaaac 6243
QY 5941 atccatgaagatatacaagaacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6000
|||||
Db 6244 atccatgaagatatacaagaacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6303
QY 6001 ttgacttggagagaaacacgtgtgaagttcttgccttctgtgaagagagtcacgaagaa 6060
|||||
Db 6304 ttgacttggagagaaacacgtgtgaagttcttgccttctgtgaagagagtcacgaagaa 6363
QY 6061 gtgtgcaaggt 6120
|||||
Db 6364 gtgtgcaaggt 6423
QY 6121 tatgtgtgttaactatagtgaggggacaaacgcaagccttcaacgcaatgtgtgtgt 6180
|||||
Db 6424 tatgtgtgttaactatagtgaggggacaaacgcaagccttcaacgcaatgtgtgtgt 6483
QY 6181 ggcgggctcctcgt 6240


```
Db 6484 ggcgggacctcctctgtgtgttcttgatgaaccaccacagcagatgatacccaagccgg 6543
Qy 6241 cggctctgtggaattgtgcccctaagtgttgaaggaaggagatcaatagtgctaca 6300
Db 6544 cggctctgtggaattgtgcccctaagtgttgaaggaaggagatcaatagtgctaca 6603
Qy 6301 tctcatagatggaagaatgtaagctcttgcacatagatggaatgcaatgtaagatga 6360
Db 6504 tctcatagatggaagaatgtaagctcttgcacatagatggaatgcaatgtaagatga 6663
Qy 6361 aggttcaggtctggtcagatggtccagatcctaaataatggttggagatggttaca 6420
Db 6664 aggttcaggtctggtcagatggtccagatcctaaataatggttggagatggttaca 6723
Qy 6421 atagttgacgaatagcaagggtccaaacccgagcttgaaagctgtccagatcttcttga 6480
Db 6724 atagttgacgaatagcaagggtccaaacccgagcttgaaagctgtccagatcttcttga 6783
Qy 6481 ctggcatttctctggaagtgttctaaagaagaacaccggaacatgtctacaatccagctt 6540
Db 6784 ctggcatttctctggaagtgttctaaagaagaacaccggaacatgtctacaatccagctt 6843
Qy 6541 ccattctcattatctctcgcgcagatatacagatcctccccaagagcaaaagcga 6600
Db 6844 ccattctcattatctctcgcgcagatatacagatcctccccaagagcaaaagcga 6903
Qy 6601 ctccacataagaactactctgttctcagaacaacttgacaaatatttgaactt 6660
Db 6904 ctccacataagaactactctgttctcagaacaacttgacaaatatttgaactt 6963
Qy 6661 gccaaagaccaaagtgaatgtaagccacttaaaagacctcctcatcacaaaaacagaca 6720
Db 6964 gccaaagaccaaagtgaatgtaagccacttaaaagacctcctcatcacaaaaacagaca 7023
Qy 6721 gtagtggagctgtcagttctacatcttctcagaagatgagaagaatgaaagctat 6780
Db 7024 gtagtggagctgtcagttctacatcttctcagaagatgagaagaatgaaagctat 7083
Qy 6781 gta 6783
Db 7084 gta 7086

RESULT 15
AAK52667
ID AAK52667 standard; cDNA; 7086 BP.
XX
AC AAK52667;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 2196.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
```

```
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
DR P-PSDB: AAM79534.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PR useful in diagnosis and gene therapy -
```

Claim 1; Page 4558-4560; 6221pp; English.

The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.

CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.

Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;

Query Match 99.4%; Score 6762.2; DB 22; Length 7086;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6770; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

```
Qy 1 atggttttggtcctcagctgaggttctgtgtggaagaaccctcatcagaagaga 60
Db 304 atggtctgtgtcccaagctgaggtctgtgtggaagaaccctcatcagaagaga 363
Qy 61 caaatatgcatgtgttactggaagtgtgcctggtcctattatctctcatcgtatc 120
Db 364 caaatatgcatgtgttactggaagtgtgcctggtcctattatctctcatcgtatc 423
Qy 121 tctgttgctgagctacccaacctatgaacaacatgaatgcatcttccaataaagcc 180
Db 424 tctgttgctgagctacccaacctatgaacaacatgaatgcatcttccaataaagcc 483
Qy 181 atgcccctgcaagaacactcctctgggttcaggagatcatctgtaagcaaacacccc 240
Db 484 atgcccctgcaagaacactcctctgggttcaggagatcatctgtaagcaaacacccc 543
Qy 241 tgttcctgtacccgactcctggtggaagctcccgaggtgtgtggaacttaacaatcc 300
Db 544 tgttcctgtacccgactcctggtggaagctcccgaggtgtgtggaacttaacaatcc 603
Qy 301 attgtggtcgcgtgttctcagatgctcgcggagctcttttatcacccagaagaaccc 360
Db 604 attgtggtcgcgtgttctcagatgctcgcggagctcttttatcacccagaagaaccc 663
Qy 361 agcatgaagacatgcgcaaaagttctgagaacatctacagacagatcaagaatccagctca 420
Db 664 agcatgaagacatgcgcaaaagttctgagaacatctacagacagatcaagaatccagctca 723
Qy 421 aacttgaagctcaagatctcctgtgtgacaatgaacactctctgtgttccatatacc 480
Db 724 aacttgaagctcaagatctcctgtgtgacaatgaacactctctgtgttccatatacc 783
Qy 481 aacctctctccaagatctactgtgacaagatgcttgagggtgtgtcatcttcac 540
```


Db 784 aacctctctcccaagaagtctactgtgacagaatgctgagggctgtagtcatctccac 843
QY 541 aaggtattttgcaagggtaccagttacatttgacaagtctgttcaatgatacaaatca 600
Db 844 aaggtattttgcaagggtaccagttacatttgacaagtctgttcaatgatacaaatca 903
QY 601 gaagagatgattcaactgtgtgacccaagaattcttgagcttctgtgcttcccaaggag 660
Db 904 gaagagatgattcaactgtgtgacccaagaattcttgagcttctgtgcttcccaaggag 963
QY 661 aaactgtgtcagcagcagagagtagtctgttccacaatgacatccctgaacatccctg 720
Db 964 aaactgtgtcagcagcagagtagtctgttccacaatgacatccctgaacatccctg 1023
QY 721 agaaactaaactaaactaaactaaactaaactaaactaaactaaactaaactaaactaa 780
Db 1024 agaaactaaactaaactaaactaaactaaactaaactaaactaaactaaactaaactaa 1083
QY 781 ttgtgtcagtagtctgtgagctctgtgcccagagagctgttccagatgagagctgtgag 840
Db 1084 ttgtgtcagtagtctgtgagctctgtgcccagagagctgttccagatgagagctgtgag 1143
QY 841 atgcaagcagagagtagtctgttccgaacatgtagaagctccagctccctccaccacaa 900
Db 1144 atgcaagcagagagtagtctgttccgaacatgtagaagctccagctccctccaccacaa 1203
QY 901 taccaggtctgtgtctcgtatgtctgtcgtgagctcccgagagagggggtctgaagatac 960
Db 1204 taccaggtctgtgtctcgtatgtctgtcgtgagctcccgagagagggggtctgaagatac 1263
QY 961 tctctcaactgtgtatgtagagacaacaactaaagccctcttggagggcaatgagcactag 1020
Db 1264 tctctcaactgtgtatgtagagacaacaactaaagccctcttggagggcaatgagcactag 1323
QY 1021 gaagatgtcgaacactctatagacaactctacaactccttactgtacatgatttgaag 1080
Db 1324 gaagatgtcgaacactctatagacaactctacaactccttactgtacatgatttgaag 1383
QY 1081 aattggaggtcagtcctcttcccgcatctatctggaagctctgaagccgctgtctgt 1140
Db 1384 aattggaggtcagtcctcttcccgcatctatctggaagctctgaagccgctgtctgt 1443
QY 1141 gggaagatccgttatacaactctgacatcccaagcagatgatactgagagtgagac 1200
Db 1444 gggaagatccgttatacaactctgacatcccaagcagatgatactgagagtgagac 1503
QY 1201 aagacctccaggaactggtgtgttccatgatactggaagagatgtggaaggaactcagc 1260
Db 1504 aagacctccaggaactggtgtgttccatgatactggaagagatgtggaaggaactcagc 1563
QY 1261 cccaagatctgagcttctatggaagaacagccaagaatgagacctgttccgagatgtgtg 1320
Db 1564 cccaagatctgagcttctatggaagaacagccaagaatgagacctgttccgagatgtgtg 1623
QY 1321 gacagcagggacaatgacacacttctggaacacagcagctgtagtgccttagatggaacac 1380
Db 1624 gacagcagggacaatgacacacttctggaacacagcagctgtagtgccttagatggaacac 1683
QY 1381 caagacatctgtgtgttcttggccaagcaccagaagatgtccagtaatgtgtct 1440
Db 1684 caagacatctgtgtgttcttggccaagcaccagaagatgtccagtaatgtgtct 1743
QY 1441 ggtgtacacctggaagagacttcaacagagataccagcagcatccggaacatctctgc 1500
Db 1744 ggtgtacacctggaagagacttcaacagagataccagcagcatccggaacatctctgc 1803
QY 1501 ttcatgtgagtggttcaacctgacaagcttagaacatcagacaagaagctgtgctatc 1560
Db 1804 ttcatgtgagtggttcaacctgacaagcttagaacatcagacaagaagctgtgctatc 1863
QY 1561 aacaagatccatgagagctgtctggaatgagaggaagttctgtgctgtatctgttcaactg 1620
Db 1864 aacaagatccatgagagctgtctggaatgagaggaagttctgtgctgtatctgttcaactg 1923

QY 1621 attactcagcagcagatctgagctgtcccatcatgctcaagtlacaagaatccgaatgagacat 1680
Db 1924 attactcagcagcagatctgagctgtcccatcatgctcaagtlacaagaatccgaatgagacat 1983
QY 1681 gacaaatgtgagagagacaataaataaagatgagatgagatgagatgagatgagatgagat 1740
Db 1984 gacaaatgtgagagagacaataaataaagatgagatgagatgagatgagatgagatgagat 2043
QY 1741 gaacctttagagacatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1800
Db 2044 gaacctttagagacatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2103
QY 1801 gagaagcacaatcatcaagagctgtgagacagcagcagaagaagaactgtgtctatagca 1860
Db 2104 gagaagcacaatcatcaagagctgtgagacagcagcagaagaagaactgtgtctatagca 2163
QY 1861 cagatgccctatccctgttctatgtagatcatcttctgtgagtgatgagccggtcatg 1920
Db 2164 cagatgccctatccctgttctatgtagatcatcttctgtgagtgatgagccggtcatg 2223
QY 1921 cccctcttcatgagcgtgtgctgtgatttactcagtggtgtgatatcatcaaggatctgt 1980
Db 2224 cccctcttcatgagcgtgtgctgtgatttactcagtggtgtgatatcatcaaggatctgt 2283
QY 1981 tatgagaagagagagcagcgtggaagaagacatgcggaatcatgagcgtggaacaacagata 2040
Db 2284 tatgagaagagagagcagcgtggaagaagacatgcggaatcatgagcgtggaacaacagata 2243
QY 2041 ctctgtgttagctgtgtatcatgtagtcatctctctcttctgtgagcgtgtgctgtat 2100
Db 2344 ctctgtgttagctgtgtatcatgtagtcatctctctcttctgtgagcgtgtgctgtat 2403
QY 2101 gtgtgtatctctgaaatgagaaactgtgtcctctacagtgatcccaagcgtgtgtgtgtc 2160
Db 2404 gtgtgtatctctgaaatgagaaactgtgtcctctacagtgatcccaagcgtgtgtgtgtc 2463
QY 2161 ttctgtgtcgt 2220
Db 2464 ttctgtgtcgt 2523
QY 2221 tccagagcccaactgtgagcagcagctgtgtgagagatcatctacttccagcgtgtatccct 2280
Db 2524 tccagagcccaactgtgagcagcagctgtgtgagagatcatctacttccagcgtgtatccct 2583
QY 2281 taagtcctgt 2340
Db 2584 taagtcctgt 2643
QY 2341 ctgtgtgtcctgt 2400
Db 2644 ctgtgtgtcctgt 2703
QY 2401 ggcactgtgagtgagtgagacaactgttctgaagatctctgtgtgagagagatgagcttcaat 2460
Db 2704 ggcactgtgagtgagtgagacaactgttctgaagatctctgtgtgagagagatgagcttcaat 2763
QY 2461 ctcaacactctgacttccatgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2520
Db 2764 ctcaacactctgacttccatgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2623
QY 2521 tacattgagctgtcttccagcagctagcgaatctccagcgcctgtgtatcttctcctg 2580
Db 2824 tacattgagctgtcttccagcagctagcgaatctccagcgcctgtgtatcttctcctg 2683
QY 2581 accaagttctactgt 2640
Db 2884 accaagttctactgt 2943
QY 2641 aagaagatgtcaagaatctgtcatgtgagaggaagaacccaacttgaagcgtgtgtgtgtgtgt 2700
Db 2944 aagaagatgtcaagaatctgtcatgtgagaggaagaacccaacttgaagcgtgtgtgtgtgtgt 3003

QY	2701	atccaagaacctggtcaaaaagctctacacgagatggagatgaaagctgctgtctgcatgagcttgcca	2760
Db	3004	atccaagaacctggtcaaaaagctctacacgagatggagatgaaagctgctgtctgcatgagcttgcca	3063
QY	2761	ctgaatttttatgtagggccagagatccactccctctctctgtgcccacaatggaagccggaggaagcg	2830
Db	3064	ctgaatttttatgtagggccagagatccactccctctctctgtgcccacaatggaagccggaggaagcg	3123
QY	2821	accaacatgttaataccctgacccgggtgtgttccccccgactccgtgggacccgctcaatccctg	2880
Db	3124	accaacatgttaataccctgacccgggtgtgttccccccgactccgtgggacccgctcaatccctg	3183
QY	2881	ggaanaagacatctgctctctgagatcgagacacatcccgacaaacccctgggggtctgtctccag	2940
Db	3184	ggaanaagacatctgctctctgagatcgagacacatcccgacaaacccctgggggtctgtctccag	3243
QY	2941	cataacgtgtgtgtttgacatgctgacgtgtctcgaaacacatctgttctatgtgcccgttg	3000
Db	3244	cataacgtgtgtgtttgacatgctgacgtgtctcgaaacacatctgttctatgtgcccgttg	3303
QY	3001	aaagggctctctctgaaagcacgtgaaaggcggaagatgaaacaaatgacctgagatgtgt	3060
Db	3304	aaagggctctctctgaaagcacgtgaaaggcggaagatgaaacaaatgacctgagatgtgt	3363
QY	3061	ttgcacatcaagcaagctcgaaagcaaaacaaagccagctgtccaggtcgagatgcaagaaag	3120
Db	3364	ttgcacatcaagcaagctcgaaagcaaaacaaagccagctgtccaggtcgagatgcaagaaag	3423
QY	3121	ctatctgtgtgctctgctgaccttgctcgcyggagatctaaggtgttcatctctgatagaaaccca	3180
Db	3424	ctatctgtgtgctctgctgaccttgctcgcyggagatctaaggtgttcatctctgatagaaaccca	3483
QY	3181	gctggtgtgagacctctacccctcccgacagggagatactggagctgctgctgaataacccgaaca	3240
Db	3484	gctggtgtgagacctctacccctcccgacagggagatactggagctgctgctgaataacccgaaca	3543
QY	3241	ggccgcacacattatctctctacacacacatgatagaaagcgagacgtccctggggagaaag	3300
Db	3544	ggccgcacacattatctctctacacacacatgatagaaagcgagacgtccctggggagaaag	3603
QY	3301	attgcacatcatctcccatctggaaagctgtgctgtgtgtgtctccctgtttcttgaaagac	3360
Db	3604	attgcacatcatctcccatctggaaagctgtgctgtgtgtgtgtctccctgtttcttgaaagac	3663
QY	3361	cagctggggaacaggtctactacacgtgacctgtgtaagaagaagatgtgaaatccctccagt	3420
Db	3664	cagctggggaacaggtctactacacgtgacctgtgtaagaagaagatgtgaaatccctccagt	3723
QY	3421	tcctgcggaagaacagtaagtaacatctgtgtataccctggaanaagaaagacaagtgtttctcag	3480
Db	3724	tcctgcggaagaacagtaagtaacatctgtgtataccctggaanaagaaagacaagtgtttctcag	3783
QY	3481	agcagcttctgatagtctgacctggcgagcgacgcacatgaaagtgaaacgctcaacatcgatctc	3540
Db	3784	agcagcttctgatagtctgacctggcgagcgacgcacatgaaagtgaaacgctcaacatcgatctc	3843
QY	3541	tctgctatctccacccctcatcagagaaagcatgtgtctgaaagcccgctgtgtggaagacata	3600
Db	3844	tctgctatctccacccctcatcagagaaagcatgtgtctgaaagcccgctgtgtggaagacata	3903
QY	3601	gggacatagctgacactgctgtgctgcacatactgaagctgcctcaagaggaggagcccttgtagaa	3660
Db	3904	gggacatagctgacactgctgtgctgcacatactgaagctgcctcaagaggaggagcccttgtagaa	3963
QY	3661	ctcttccaatgagatgtgatacgcggtctccaagacctgagaccttctagattatgacatcca	3720
Db	3964	ctcttccaatgagatgtgatacgcggtctccaagacctgagaccttctagattatgacatcca	4023
QY	3721	gagacgagcccttgaaagaagaataattccctcaaggtgtgcacgaagagatgtgggtgtgagtctgag	3780
Db	4024	gagacgagcccttgaaagaagaataattccctcaaggtgtgcacgaagagatgtgggtgtgagtctgag	4083
QY	3781	accctcaatgtgataccttgccagagaagaacgaacacagctgggacctctctgggggaacaaagcgc	3840

Db	4084	accctcaagatcgttacccttcgccaagacagaaacagccggcccttcgggagcaagcagagc	4143
Qy	3841	tgctctgcgcccttccacttgaaagatgatgcgcctgcgataccaaatgatattctgacatagacc	3900
Db	4144	tgtcttcgcgccttccacttgaaagatgatgcgcctgcgataccaaatgatattctgacatagacc	4203
Qy	3901	gaatccaaagagacacagacttgcctcagtgaggatgagatgagcaaaagggtccacacagtgtaa	3966
Db	4204	gaatccaaagagacacagacttgcctcagtgaggatgagatgagcaaaagggtccacacagtgtaa	4263
Qy	3961	ggcttgaaactatcacagcaacagatttgtagcccttcttgtagaagagactgtctaattgc	4020
Db	4264	ggcttgaaactatcacagcaacagatttgtagcccttcttgtagaagagactgtctaattgc	4322
Qy	4021	agaacgagtcgaaagaatttttgcacagattgtcttcagctgtgttctgcacat	4088
Db	4324	agaacgagtcgaaagaatttttgcacagattgtcttcagctgtgttctgcacat	4383
Qy	4081	ggcccttggttcacagcctgatactgcaccccttggcaagtaaccacagccctgtgaacttcag	4140
Db	4384	ggcccttggttcacagcctgatactgcaccccttggcaagtaaccacagccctgtgaacttcag	4443
Qy	4141	cccttgatgtatacaacagacagatatacatttgtagcaaatgatgtcttcagtaggacaggg	4200
Db	4444	cccttgatgtatacaacagacagatatacatttgtagcaaatgatgtcttcagtaggacaggg	4503
Qy	4201	acccttggaactcttaaacgcctctacacaaagaccctggtcttcgggagcccgctgtatgaa	4266
Db	4504	acccttggaactctcttaaacgcctctacacaaagaccctggtcttcgggagcccgctgtatgaa	4563
Qy	4261	ggaaaccccaatcccaagacagccctgcgcaagcagggaggaagatgtagacacatgcacca	4320
Db	4564	ggaaaccccaatcccaagacagccctgcgcaagcagggaggaagatgtagacacatgcacca	4622
Qy	4321	gttccccaagaccatcattggaactcttccgaatctgggaactctgacaactctgagaacccttca	4380
Db	4624	gttccccaagaccatcattggaactcttccgaatctgggaactctgacaactctgagaacccttca	4683
Qy	4381	cctgcatgcacgctgtagcagcgacaaatcacaagaatctgcctctgtgtccccaagg	4440
Db	4684	cctgcatgcacgctgtagcagcgacaaatcacaagaatctgcctctgtgtgtccccaagg	4743
Qy	4441	gcaagggggctgtcctcctccacaagaacaaacacatgcagatataccttccaggaactg	4500
Db	4744	gcaagggggctgtcctcctccacaagaacaaacacatgcagatataccttccaggaactg	4803
Qy	4501	acaggaagaacacatttggatattctgtgtaagaactatgtgcagatctaaagtcagcaaaagc	4566
Db	4804	acaggaagaacacacatttggatattctgtgtaagaactatgtgcagatctaaagtcagcaaaagc	4863
Qy	4561	ttaagaacacagatctcgtgtgaatgagtttagtgtagcgggcttttccctgggtgcagt	4620
Db	4864	ttaagaacacagatctcgtgtgaatgagtttagtgtagcgggcttttccctgggtgcagt	4923
Qy	4621	aatactcaagcaacttctcctcggagtccaagaagttaatgatgccaatacaacaaatgaagaa	4680
Db	4924	aatactcaagcaacttctcctcggagtccaagaagttaatgatgccaatacaacaaatgaagaa	4983
Qy	4681	caacctaaagctgcgccaagggacgtctcgcagatctcgatttccaaacagcttggagaattt	4740
Db	4984	caacctaaagctgcgccaagggacgtctcgcagatctcgatttccaaacagcttggagaattt	5043
Qy	4741	atgacaagcactggaaccacagaataatgltcaagtgtagtccaatacaaaaggctgacat	4800
Db	5044	atgacaagcactggaaccacagaataatgltcaagtgtagtccaatacaaaaggctgacat	5103
Qy	4801	gcaatcagccttcttcctgaatgtatcatcaaaatgcaatcttccgggccaactgtgaag	4860
Db	5104	gcaatcagccttcttcctgaatgtatcatcaaaatgcaatcttccgggccaactgtgaag	5163
Qy	4861	ggagagaacccctagacattatgtgaatctgcttccaatcacccttgatctcaacag	4920

Db 5164 ggagagaaacctagaccatlatgaaatctactgcttccatccatccctgatacccaag 5223
QY 4921 cagcagctctcaagagtgctctgataggacacatcagtgagatgcttctgttccatcgt 4980
Db 5224 cagcagctctcaagagtgctctgataggacacatcagtgagatgcttctgttccatcgt 5283
QY 4981 gtcacctctgcaatgcttctcgttccacagcagcttctgctatctccatccagagcgg 5040
Db 5284 gtcacctctgcaatgcttctcgttccacagcagcttctgctatctccatccagagcgg 5343
QY 5041 gtcacagaaagcaaaacacctgcatcagtgagtgagagcctgtcatctactgctc 5100
Db 5344 gtcacagaaagcaaaacacctgcatcagtgagtgagagcctgtcatctactgctc 5403
QY 5101 tctaatctgtctggagatctgcaatcagttgctcctccagcaactgtgataatc 5160
Db 5404 tctaatctgtctggagatctgcaatcagttgctcctccagcaactgtgataatc 5463
QY 5161 ttcactgcttccacagaaagtcctatgtctcctccacaaactgtgctgtagccctt 5220
Db 5464 ttcactgcttccacagaaagtcctatgtctcctccacaaactgtgctgtagccctt 5523
QY 5221 ctaacttgcgtatgagtggttgcatacacaactctcatgtaaccagcctctgtgttc 5280
Db 5524 ctaacttgcgtatgagtggttgcatacacaactctcatgtaaccagcctctgtgttc 5583
QY 5281 aagatccccaagcaacagcctatgtgtctcaacagcgtgcaacctctcatatggcataat 5340
Db 5584 aagatccccaagcaacagcctatgtgtctcaacagcgtgcaacctctcatatggcataat 5643
QY 5341 ggcagcgtgcccacaccttgtgtctggaagctgttcaacagcaaaatagctgataataat 5400
Db 5644 ggcagcgtgcccacaccttgtgtctggaagctgttcaacagcaaaatagctgataataat 5703
QY 5401 gataccctgaagctgcgtgttcttgatcttccacacatttctcctgggagcagggctatc 5460
Db 5704 gataccctgaagctgcgtgttcttgatcttccacacatttctcctgggagcagggctatc 5763
QY 5461 gacatggtgtaaaaaacagagcaaatgtgctgatagcctctgaaaaagtttgggaaaaacgcgttt 5520
Db 5764 gacatggtgtaaaaaacagagcaaatgtgctgatagcctctgaaaaagtttgggaaaaacgcgttt 5823
QY 5521 ggtgtaaccattatcttctggaactgtgtggaacgaaaactctcgcataggccgttgaaagg 5580
Db 5824 ggtgtaaccattatcttctggaactgtgtggaacgaaaactctcgcataggccgttgaaagg 5883
QY 5581 gttggttctctccatcactgtctctgataccagtaacagattctctcatcagggccagacct 5640
Db 5884 gttggttctctccatcactgtctctgataccagtaacagattctctcatcagggccagacct 5943
QY 5641 gtaaatgcaaaagctactcctctcgtgaatgaaatgaaatgtaagatgtgaaaggcggaagacag 5700
Db 5944 gtaaatgcaaaagctactcctctcgtgaatgaaatgaaatgtaagatgtgaaaggcggaagacag 6003
QY 5701 agaattctgtgtgtggaagcgcaaatgacatctttagaataatcaagaggttgacgaagata 5760
Db 6004 agaattctgtgtgtggaagcgcaaatgacatctttagaataatcaagaggttgacgaagata 6063
QY 5761 tatagaaagaaagcggaagcgcgtctgacaggaatttgcgtgggacattctccctcgtgag 5820
Db 6064 tatagaaagaaagcggaagcgcgtctgacaggaatttgcgtgggacattctccctcgtgag 6123
QY 5821 tgccttgggctcctggaggttaatlgaggcttgaanaatcatcaacttcaagaatgttaca 5880
Db 6124 tgccttgggctcctggaggttaatlgaggcttgaanaatcatcaacttcaagaatgttaca 6183
QY 5881 ggaagataccactgttaccagaggaatgtcttcccttaacaaatagtatctatcaaac 5940
Db 6184 ggaagataccactgttaccagaggaatgtcttcccttaacaaatagtatctatcaaac 6243
QY 5941 atccatgaagtaactcagaacatgtactgcccctcagttttagtgcatacagaagctg 6000
Db 6244 atccatgaagtaactcagaacatgtactgcccctcagttttagtgcatacagaagctg 6303

QY 6001 ttgactggagagaacacgtaggaattcttctgccccttctgagagagtgatcccaagaagaa 6060
Db 6304 ttgactggagagaacacgtaggaattcttctgccccttctgagagagtgatcccaagaagaa 6363
QY 6061 gttggcaaggttggtagtgaggcagatccgaaactgggctctgaaatgtgaagaaaaa 6120
Db 6364 gttggcaaggttggtagtgaggcagatccgaaactgggctctgaaatgtgaagaaaaa 6423
QY 6121 tatgttgtaactaagtggaagcaacaacagcaagctctctiaacaacatgagtttgatc 6180
Db 6424 tatgttgtaactaagtggaagcaacaacagcaagctctctiaacaacatgagtttgatc 6483
QY 6181 ggcgggctcctctgtgtgttctctgtagaagcaacccaacagagatgatacccaagccgg 6240
Db 6484 ggcgggctcctctgtgtgttctctgtagaagcaacccaacagagatgatacccaagccgg 6543
QY 6241 cgttctctggaattgtgcccctaagtggtgtcaaggaagggaatcagatagtgcttaca 6300
Db 6544 cgttctctggaattgtgcccctaagtggtgtcaaggaagggaatcagatagtgcttaca 6603
QY 6301 tctcaatagatbggaagaatgtgaagctcttgcactaggaatggcaatcaltgctcaatgga 6360
Db 6604 tctcaatagatbggaagaatgtgaagctcttgcactaggaatggcaatcaltgctcaatgga 6663
QY 6361 aggttcaaggtgcttggcagatgctccagcatcttaaaaaataggttctgagatgttataca 6420
Db 6664 aggttcaaggtgcttggcagatgctccagcatcttaaaaaataggttctgagatgttataca 6723
QY 6421 alagtgtaacgaatagcagaggtccaaacccggaacctgaagcctgtccaggaattctcttga 6480
Db 6724 alagtgtaacgaatagcagaggtccaaacccggaacctgaagcctgtccaggaattctcttga 6783
QY 6481 ctggcaattctctggaagtggttcttaaaagaaacacccggaacatgtctacaataccagctt 6540
Db 6784 ctggcaattctctggaagtggttcttaaaagaaacacccggaacatgtctacaataccagctt 6843
QY 6541 ccaatctcatatctctctcgtgcagagatatcagatctctccagagcgaaagcgga 6600
Db 6844 ccaatctcatatctctctcgtgcagagatatcagatctctccagagcgaaagcgga 6903
QY 6601 ctccacatagaagactactcgttcttctcagacaacacacttgaaccaatgttgaactt 6660
Db 6904 ctccacatagaagactactcgttcttctcagacaacacacttgaaccaatgttgaactt 6963
QY 6661 gccaaagaaacaaatgtagtgaatgacacttaaaaagacctctcatatacaaaaacagaca 6720
Db 6964 gccaaagaaacaaatgtagtgaatgacacttaaaaagacctctcatatacaaaaacagaca 7023
QY 6721 gtagtgagcgttgcaattctcaacatcttcttaagagatgagaagtgaaagaaagctat 6780
Db 7024 gtagtgagcgttgcaattctcaacatcttcttaagagatgagaagtgaaagaaagctat 7083
QY 6781 gta 6783
Db 7084 gta 7086

Search completed: September 14, 2002, 08:00:35
Job time: 73347 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2002, 07:22:46 ; Search time 20132.5 Seconds
(without alignments)
7072.350 Million cell updates/sec

Title: US-09-595-526b-1_COPY_291_7094
Perfect score: 6804
Sequence: 1 atggctgtgtgagctcagc.....gaagaatcctgttcatacgg 6804

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_da.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vl.*
30: em_hg_hum.*
31: em_hg_inv.*
32: em_hg_other.*
33: em_hg_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
------------	-------------	--------	-------	-------------

1	6804	100.0	10442	6	AX060713	AX060713 Sequence
2	6804	100.0	10442	6	AX060892	AX060892 Sequence
3	6804	100.0	10442	9	AF285167	AF285167 Homo sapi
4	6802.4	100.0	10474	6	AX060719	AX060719 Sequence
5	6802.4	100.0	10474	6	AX060721	AX060721 Sequence
6	6802.4	100.0	10474	6	AX060898	AX060898 Sequence
7	6802.4	100.0	10474	6	AX060900	AX060900 Sequence
8	6796	99.8	7860	6	AX092594	AX092594 Sequence
9	6788	99.8	7260	6	AX233452	AX233452 Sequence
10	6784.8	99.7	9741	6	AX127830	AX127830 Sequence
11	6784.8	99.7	9741	6	AX139817	AX139817 Sequence
12	6784.8	99.7	9741	6	AX351038	AX351038 Sequence
13	6784.8	99.7	9854	6	AX127831	AX127831 Sequence
14	6784.8	99.7	9854	6	AX139818	AX139818 Sequence
15	6771.6	99.5	6786	6	AB055982	AB055982 Homo sapi
16	6770.8	99.5	7862	6	AX135712	AX135712 Sequence
17	6728	98.9	6880	6	AX233450	AX233450 Sequence
18	6728	98.9	6880	6	HSAD012376	HSAD012376 Homo sapi
19	6728	98.9	9497	6	AX059973	AX059973 Sequence
20	6728	98.9	9497	6	AF165281	AF165281 Homo sapi
21	6714	98.7	9495	6	AX059978	AX059978 Sequence
22	6609.2	82.2	7878	10	MMAR01	MMAR01 Mus muscu
23	5596.2	63.9	7074	5	AF362377	AF362377 Gallus ga
24	4347.6	28.4	7298	9	AF001945	AF001945 Homo sapi
25	1931.6	28.4	7709	4	BTU90126	BTU90126 Bos tauru
26	1931.6	28.3	7268	10	MMAR000149	MMAR000149 Mus muscu
27	1928.8	28.3	7323	9	BD005026	BD005026 Genes rel
28	1928.8	28.3	5097	6	AK027864	AK027864 Homo sapi
29	1922.8	28.3	5097	6	AK027864	AK027864 Homo sapi
30	1922.8	28.3	5097	6	AK027864	AK027864 Homo sapi
31	1918.8	28.2	7276	9	HS088667	HS088667 Homo sapi
32	1742.2	25.6	6704	9	AF328787	AF328787 Homo sapi
33	1735.8	25.5	6027	9	AB055390	AB055390 Homo sapi
34	1735.8	25.5	6432	6	AX320364	AX320364 Sequence
35	1735.8	25.5	6522	6	AX202218	AX202218 Sequence
36	1735.8	25.5	6588	6	AF250238	AF250238 Homo sapi
37	1735.8	25.5	6588	6	AX320362	AX320362 Sequence
38	1696	24.9	6607	6	AX080493	AX080493 Sequence
39	1696	24.9	6607	10	AF287141	AF287141 Mus muscu
40	1531.6	22.5	5762	6	AX080462	AX080462 Sequence
41	1465	21.5	5669	6	AX202220	AX202220 Sequence
42	985	14.5	7305	6	AX235953	AX235953 Sequence
43	985	14.5	7482	9	AF327657	AF327657 Homo sapi
44	985	14.5	8056	9	AF178941	AF178941 Homo sapi
45	985	14.5	8195	6	AX235951	AX235951 Sequence

ALIGNMENTS

RESULT 1	AX060713	10442 bp	DNA	linear	PAT 22-JAN-2001
LOCUS	AX060713	Sequence 1 from Patent WO0078972.			
DEFINITION	AX060713				
ACCESSION	AX060713.1	GI:12406103			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
	human.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 10442)				
AUTHORS	Lawn,R.M., Wade,D. and Garvin,M.				
TITLE	Regulation with binding cassette transporter protein abcl				
JOURNAL	Patent: WO 0078972-A 1 28-DEC-2000;				
	CV THERAPEUTICS, INC. (US)				
FEATURES					
source	1..10442				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
BASE COUNT	2898 a 2297 c 2408 g 2835 t				
ORIGIN					
					4 others

Db	6771	CTTSCATTTTCCTGGAAAGTCTCTAAAGAAACCGGAACCGAAATGCTACAAATCCAGCTT	6830
Qy	6541	ccalcctcattalcctctcttgcagagatltcagcatcctctccagagcaaaagcga	6600
Db	6831	CCATCTTCATTAATCTTCTCTGGCCAGGATATTCCAGCATCTCTCCGAGACAAAAGCGCA	6890
Qy	6601	ctccacatagaagaactactctgtttcttaagaacaactitgaaccaagtatttgyaactt	6660
Db	6891	CTCCACACTAGAAACACTACTCTGTCTCTAGAACAACTTGACCAAGATATTGGAACTTT	6950
Qy	6661	gcccaaggaaccaagtgatgatgacactttaaagaactctcatatcacaaaaacagaca	6720
Db	6951	GCCAGGACCCAAAGTGATGATGACCACTTAAAGACCTTCATTACACAAAACCGAGACA	7010
Qy	6721	gtatgtgaagcttgcagttctcacactctttctcacagatgtgaagaagctat	6780
Db	7011	GTAATGGACCTTCCACTTCTCACATCTTTCTACAGATGAGAAAGTGAAGAAACCTAT	7070
Qy	6781	gtatgaagaactcctgttcatacg	6804
Db	7071	GTATGAAGAAATCCTGTTCATACGG	7094

RESULT	2				
AX060892					
LOCUS		10442 bp	DNA	linear	PAT 22-JAN-2001
DEFINITION	Sequence 1 from Patent WO078971.				
ACCESSION	AX060892				
VERSION	AX060892.1	GI:12406270			

ORGANISM Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
1 (bases 1 to 10442)
Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
AIP binding cassette transporter protein abcl polypeptides
Patent: WO 0078971-A 1 28-DEC-2000;

FEATURES	SOURCE	LOCATION/QUALIFIERS
BASE COUNT	2898 a	1. 10442 /organism="Homo sapiens" /db_xref="taxon:9606"
ORIGIN	2297 c	2408 g 2835 t 4 others

Query Match	100.0%	Score 6804;	DB 6;	Length 10442;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 6804;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	atgctgttgagctcagctcagctgagttgtcgtcgtgtgagaacactcactttaagaagaga	60	
Db	291	ATGGCTGTGTGGCTCCACGCTGAGGTGGCTGTGTGGAAACCTCCTACTTTGAGGAAGA	350	
Qy	61	caaacatgctcagcgtctactcgtagaagctgagcctcgtcctatattcctatcgtatc	120	
Db	351	CAAACTGTCAGCTGTATTACTGGAAGTGGCGCTGGCTCTATTATCTTCCTGATCTGATC	410	
Qy	121	tctgttgctgagactccaccctcttgacaacatgaaatgactctttccaaataaagcc	180	
Db	411	TCTGTGTGGCTGACCTACCCACCTTATGAAACAATGAAATGCAATTTTCCAAATTAAGCC	470	
Qy	181	atgcgcctctgagaagaaactctcttggttcaggagatattatcgtlaatgacaacaccc	240	
Db	471	ATGCCCTCTGCAGGAACACTTCTCTGGGTTCAAGGAGATTATCTGTAATGCCAACAACCC	530	
Qy	241	tctttccgtttaccagactccctcggaggaagctcccgagattgtttggaacatttaacaatcc	300	
Db	531	TGTTTCCTGTACCCGACTCCTGGGGAAGCTCCCGGAGTTGTTGGAAACTTTAAACAAATCC	590	
Qy	301	attgtagctcgcctgttctcagatgctcgaaggctcttcttataagccagaagaacac	360	

Db	591	ATTGTGGCTGGCTGTTTCACAGATGCTGGAGCGTTCTTTATATACGACAAAGACACC	650
Qy	361	agcatgaaggacatbvcgcaaaagtlctgaacattacagcagatccaagaatccagctca	420
Db	651	AGCATGAAGGACATGCGCCAAAGTTCTGACAGACATTACAGACAGATCAACAAATTCACGTCA	710
Qy	421	aacttgaagcttcaaaagtttccgctgvggacaatgaacctctccctcgtgtccatcatcac	480
Db	711	AAC TTGAAGCTTCAAGATTTCCTGCTGGACAAATGAACCTTCTCGSCTTCTATATCAC	770
Qy	481	aacctctctcccaaaagttctactctggaacaagatctgaaggtctgaatgcatctccac	540
Db	771	AACCTCTCTCCCAAGTCTACTCTGGACAAAGTCTGAGGCTGATGTTATCTCTCAC	830
Qy	541	aagttatttttgcgaagctaccagttacatttgaacaagctbgtgaaatgataaaca	600
Db	831	AAGTATTTTTCGAAGGCTACCGAGTTACATTGACAAAGCTGTGCAATGATCAAAATCA	890
Qy	601	gaagatgattcaactctgtgtgaaccaaaagtlctcgaactctgctgtccaccaaaagag	660
Db	891	GAAAGATGATTCAACTTGGTGAACCAAGAAAGTTTGATGACTTGTGGCCTACCAAAAGAG	950
Qy	661	aaactgctcagcagcagcagagtaactcgtttccacacatgaaatccatgaacccatcgt	720
Db	951	AAACTGCTCGACGACGACGACGACGATCTTGTTCCAACTGACATCTTAAGCCATCTGT	1010
Qy	721	agaacactaaactctacatctccctcccgagaagagctgctcgaagcacaacaaaca	780
Db	1011	AGAACCTAAACTCTACATCTCCTTCCTCCGAGCAGAGACTGGCTGAAGCCACAAAAACA	1070
Qy	781	ttgcgtcactagctcttgggaactctgcccgaagagctgtlcaagcatgagaagctggaatgac	840
Db	1071	TTCGTGCTACTCTTGGGACTCTGCGCCAGAGACTGTACGATGAGAAGCTGGAGTGAC	1130
Qy	841	atgcgacagcagcagtgatgatttcttgaaccaatgtaaaagctcagctctccaccaaccaatc	900
Db	1131	ATGCGACAGCGAGGTGATGTTCTTGACCAATGTAAACGCTCCAGCTCTCCACCCCAATTC	1190
Qy	901	taccagagctgtgctcgtatgtlctgvggcaltcccgaaaggaggggggcttgaatacaag	960
Db	1191	TACAGAGCGCTGTGTCGATGTGTCGGGCGATCCGAGGAGGGGGGCTGTGAAGTCAAG	1250
Qy	961	tctctcaactgcttggagaaacaactataaagccctcttggaggcaatgagcactag	1020
Db	1251	TCTCTCACTGGTATGAGGACAAACAATACAAAGCCCTCTTGGAGCAATGCACTGAG	1310
Qy	1021	gaagaatgctgaacctctctacgaacatctacaaactcttactgcaatgatttgaatgaag	1080
Db	1311	GAAAGATGCGTGAACCTCTATGACAACTCTACAACTCTTACGCAATGATTGTGATGAAG	1370
Qy	1081	aatttggagctagctccctcttcccgcatatcttgaagaagctctgaagccgtgctgctt	1140
Db	1371	AATTGGAGCTAGTCCTTCTTCCGATTTATCTTGAAACCTCTGAAAGCCGCTGCTGTT	1430
Qy	1141	aggaagatcctctatacaccctggaactccagccaagcagatctcatgtgtagtgaag	1200
Db	1431	GGGAAGATCTGTATACACCTGACACTCCAGCCAAAGCAGGCTCATGSGCTGAGSTGAAC	1490
Qy	1201	aagaccttccaggaactgagctgtgttccatgattctggaagcctatgtggaagaaactcagc	1260
Db	1491	AAGACCTTCCAGGAAGCTGGCTGTCTTCCATGATCTGGAAGGCAATGGGAGGAACTCAAC	1550
Qy	1261	cccaaatcttgaaactctatggaagaacgccaagaanaatgaaactctgtccggaatgctgtg	1320
Db	1551	CCCAAGATCTGGAACCTTCTATGGAACAACAGCCAAACAATGCACTGTCTCCGGATGCGTTG	1610
Qy	1321	gacagcagggacaaatgacacacttltggaaacagcagtttggatgactatgtgacagcc	1380
Db	1611	GACAGCAGGGAAACAATGACCACTTTTGGGAACAGCAGTTGATGGCTTAATATTGGACAGCC	1670
Qy	1381	caagacatgtggcgttttlttggcaagaaccacagagatgtccacgcaagtaatgttct	1440

Db	1671	CAAGACATCGTGGCTTTTGGCCAAAGCCACCAGAGATGTCACATGCCAATAGGTTCT	1730
Qy	1441	gtglaacccctggagaaagcttcaagagactaaaccaaggcaatccgagaccatatccgc	1500
Db	1731	GGTACACCTGGAGGAAGCTTTCAAGAGACATACAGGCAATTCGGACATATCTGGC	1790
Qy	1501	ttcaatggatgtgtaacccctaaacctaagaaccatagcaacagaatctggtcatc	1560
Db	1791	TTTCATGCAATGTGTCAACTCAACCTCAACACCTCGAACCCTATACCAACAACTCGGCTCATC	1850
Qy	1561	aacaagttccatggagctgtctggaatgaaggaaagttctgagctgtatattgttcaatga	1620
Db	1851	AACAAGTCCATGAGACTGCTGGATGAGAGGAAGTTCTGGGCTGTGTGTGTTCATCGGA	1910
Qy	1621	attactccaagcagcatttgagctgtcctcccatcatgtcaagtacaaagatccgaaityacat	1680
Db	1911	ATTACTCCAGGACGACATTTGACCTCCCATCATCATGTCAAGTACAAAGATCCGAATGGAATTT	1970
Qy	1681	gacaatgtggaagagacaacaataaataagaatggtgtactggaagaccctgtctgaact	1740
Db	1971	GACAAATGTGGAGAGACAAATAAATAAAGATGTGCTACTGGACCTGTGTCTCGACT	2030
Qy	1741	gaaccccttgaagacatgacgtacgtcttgagggggcttcgactacttgcaatgtagt	1800
Db	2031	GACCCCTTTGAGACATGCGGTACGTGTGGGGGGCTTGCCCTACTTGACAGATGTGGTG	2090
Qy	1801	gagcagagcaatcatcaagaggtgtctacagagcagcaaaaacacggtgtcatatgcaa	1860
Db	2091	GAGCAGGCAATCATCAGGGTGTCTACCGGACCGGAAAGCAAAATGTGTCTATATGTGAA	2150
Qy	1861	cagatgtccctalcctccgttaacgttatgaatcatcttctgcgggtgatagacggcaatg	1920
Db	2151	CAGATGCCCTTACCTCTTACGTGTGATGACATCTTCTCGGGGTGATGACCGGTCAMTG	2210
Qy	1921	cccccttcaagaagcgtgcgtctgaattactaagtggtcgtgatatcaaaagggcatgtg	1980
Db	2211	CCCCCTTTCATGAGCTGTGGCTGTGATTTACTCATGTGGCTGTATCATCAAGGCAATCGTG	2270
Qy	1981	tatgaaagagagagacagcgtctgaagaagaccatbcagatcatgtgacctgaacaagcata	2040
Db	2271	TATGAGAAGGAGGACGACGCTGAAGAAAGAACATCGGATCATGGGCTGTGAACAACGATA	2330
Qy	2041	ctctggttttagcttggttcatatagtagccatctctctctctgtgagcgtgtgrectgta	2100
Db	2331	CTCTGGTTTACTGTGTTCATTAGTAAAGCTCATTTCCCTTGTGTGAGCGCTGGCTGTGTA	2390
Qy	2101	gtgtgtcatccctgaagattaggaaaacgtgcgtccctacagtgatccacagcgtgtgttctg	2160
Db	2391	GTGGTCAATCGTAAGATTAGGAACCTGTGGCTCAAGTGAATCCAGCGTGGTGTGTGTCTC	2450
Qy	2161	ttctctgtccgttgttctgtgtgtgtgacaatccctgcagtgctcttcgattagcacactctc	2220
Db	2451	TTCCGTGCCGTTTGTCTGTGGTGAACAACTCGACAGTGTCTTCTCATTTAGCACACTCTTC	2510
Qy	2221	lccagagcaacaacctgagcagcagccctgtgggggacatcatctacttaagcttacctgcc	2280
Db	2511	TCCAGAGCAAACTGTGAGAGAGCTGTGGGGGCAATCATTTACTTACCTGTACTCTGCC	2570
Qy	2281	taagtcctgtgtgtgtgcatgagcagactacgttggtgttacaactaagaatcttcgtacg	2340
Db	2571	TACGTCTGTGTGTGGCATGTGGCAGAGACTGTGCGGGCTTCACACTCAAAATCTTGCTGAGC	2630
Qy	2341	ctgtgtctccctgttgcttlttggtttgtgcttbtgagtacttggcccttttggaggagag	2400
Db	2631	CTGTGTCTCCTGTGGCTTTTGGGTTTGGCTGTAGTACTTTTGCCCTTTTGTGAAGAGCAG	2690
Qy	2401	ggcatgtgagtgcaatgaggaaacactgttttgaagtcctctgtgaggaagaatgagctloaat	2460
Db	2691	GGCAATTGAGATGAGTGGGACAAACCTGTTTGAGAGTCTCTGTGGAGAAAGATGGCTCAAT	2750
Qy	2461	ctcaacaccttcagatcccaatgtagtgcgtttttagacacttccctataggggtgtagactg	2520
Db	2751	CTCACCACTTCATCTCCATGATGAGTGTGATGACACTTCTCTATATGGGGTGAATGACTCGG	2810

QY	2521	taaatgtgagcgtgtcttctccagggcgaatagcgaattcccaagccctggtatattctcttgc	2580
Db	2811	ttacattgaaaggctgtcttctccaggccagatgacggaaatttcccaaggccctggtatatttcttgc	2870
QY	2581	accaagctccactatgttttggcaggaagtgaatgaagaagccacctgtgttccaacag	2640
Db	2871	accaggtcctactgttttggcaggaagtgaatgaagaagccacctgtgttccaacag	2930
QY	2641	aagagaatgtcgaatctgtcattggaaggaaccaaccaacttgaagcttggcggtgc	2700
Db	2931	aagagaatgtcgaatctgtcattggaaggaaccaaccaacttgaagcttggcggtgc	2990
QY	2701	atctgaagccttggttaaaagttaccggagatggatbaaagggtgtgtgatgtgcctgtga	2760
Db	2991	atttcgaaccttggttaaaagttaccggagatggatbaaagggtgtgtgatgtgcctgtga	3050
QY	2761	ctgaattcttcatgagggccagatcacctctctctgtggccaatgtgaagcg	2820
Db	3051	ctgaatttttttattgagggccagatcacctctctgtggccaatgtgaagcg	3110
QY	2821	accaccatgtcaatctctgaccgggtgtgttccccgaacctgtggcaacgctcaatccgt	2880
Db	3111	accaccatgtcaatctctgaccgggtgtgttccccgaacctgtggcaacgctcaatccgt	3170
QY	2881	ggaaaaagacattgcctctgtgaatgagacatctccgcagaacctgtgggtctgtcccaag	2940
Db	3171	ggaaaaagacattgcctctgtgaatgagacatctccgcagaacctgtgggtctgtcccaag	3220
QY	2941	cataaagtgtcgttttgaatgactgtcgtcgaagaacacatctgtgtctatgtccgcgttg	3000
Db	3231	cataaacgtcgttttgaatgactgtcgtcgaagaacacatctgtgtctatgtccgcgttg	3290
QY	3001	aaaggagctcttgaagaagcagctgaagaaggggaatggaacaaatgacctgtatgttgt	3060
Db	3291	aaaggagctcttgaagaagcagctgaagaaggggaatggaacaaatgacctgtatgttgt	3350
QY	3061	ttgcacatcaagcaagctgtaaaagcaaaacaagccagctgtccaggtgtgaattgcaagaag	3120
Db	3351	ttgcacatcaagcaagctgtaaaagcaaaacaagccagctgtccaggtgtgaattgcaagaag	3410
QY	3121	ctatctgtgagccttgagccttgttcggggagatcctaaggtgtcatctcgtgatgaaccaca	3180
Db	3411	ctatctgtgagccttgagccttgttcggggagatcctaaggtgtcatctcgtgatgaaccaca	3470
QY	3181	gctgtgtgtgaagcccttaccctccgcaggggaatatgtgaagctgtcttgaatatccgcaa	3240
Db	3471	gctgtgtgtgaagcccttaccctccgcaggggaatatgtgaagctgtcttgaatatccgcaa	3530
QY	3241	ggccgacacattatctctctacacaacacatgatatgaagcagcttctgtgggagcag	3300
Db	3531	ggccgacacattatctctctacacaacacatgatatgaagcagcttctgtgggagcag	3590
QY	3301	attgcacatcatctcccatgtggaagctgtgtctgttgggtcctctccgtgtttctgaagaac	3360
Db	3591	attgcacatcatctcccatgtggaagctgtgtctgttgggtcctctccgtgtttctgaagaac	3650
QY	3361	cagctgtggaacaggtactactactgtgacctgtgtcaagaagaatgttgaatcctctccctagt	3420
Db	3651	cagctgtggaacaggtactactactgtgacctgtgtcaagaagaatgttgaatcctctccctagt	3710
QY	3421	ctccgtgagaagaagtgatgagcactgtgtataacctggaaaaggaggaacgttgttctccag	3480
Db	3711	ctccgtgagaagaagtgatgagcactgtgtataacctggaaaaggaggaacgttgttctccag	3770
QY	3481	agcagctctgtatgtcgtccgtggaagcagcgacaaatggaatgtgaacgtgacacatcatgtatc	3540
Db	3771	agcagctctgtatgtcgtccgtggaagcagcgacaaatggaatgtgaacgtgacacatcatgtatc	3830
QY	3541	cttgtatcttccaactcaatcagaagaagtgtgtcttgaagcccggtgtgtgtgaagacata	3600
Db	3831	cttgtatcttccaactcaatcagaagaagtgtgtcttgaagcccggtgtgtgtgaagacata	3890

```
QY 3601 gggcatgagctgacctatgctgcacatagaagctgcttaaggagggagccttctgtgaa 3660
|||||
Db 3891 gggcatgagctgacctatgctgcacatagaagctgcttaaggagggagccttctgtgaa 3950
QY 3661 cttcttcagaattgagacggcgtctcagaacctgggcatcttcagttaatgagatccca 3720
|||||
Db 3951 cttcttcagaattgagacggcgtctcagaacctgggcatcttcagttaatgagatccca 4010
QY 3721 gagaagacctggaagaatattcctcaaggctggcgaagaagctggggctgagctgag 3780
|||||
Db 4011 gaaagacctggaagaatattcctcaaggctggcgaagaagctggggctgagctgag 4070
QY 3781 acctgaatgagcttgcacagaagaagaagcgcgcttcggggagagaagaagc 3840
|||||
Db 4071 acctgaatgagcttgcacagaagaagaagcgcgcttcggggagagaagaagc 4130
QY 3841 tgcctgcgcgttcacataagatgctgctgataccaatgattcgaatagaccga 3900
|||||
Db 4131 tgcctgcgcgttcacataagatgctgctgataccaatgattcgaatagaccga 4190
QY 3901 gaatccagaagaagacagcttgcctcaagtggatgagatggcaagaagctcctaccagtgaaa 3960
|||||
Db 4191 gaatccagaagaagacagcttgcctcaagtggatgagatggcaagaagctcctaccagtgaaa 4250
QY 3961 ggcctgaaactacagacaagaagcttggcgcccttctgtgaagaagacatcctaattgcc 4020
|||||
Db 4251 ggcctgaaactacagacaagaagcttggcgcccttctgtgaagaagacatcctaattgcc 4310
QY 4021 agacggagctggaagaagatttctgctcagatgtctctgacagctgtgttctgacatt 4080
|||||
Db 4311 agacggagctggaagaagatttctgctcagatgtctctgacagctgtgttctgacatt 4370
QY 4081 ggcctgtgtcagcctgagctgctgacaccccttggcaagtaaccagcctggaacttaag 4140
|||||
Db 4371 ggcctgtgtcagcctgagctgctgacaccccttggcaagtaaccagcctggaacttaag 4430
QY 4141 cccctgagtgtaacaagaacagatcacattgttcaagaatgagctgcctgaagaacaggaa 4200
|||||
Db 4431 cccctgagtgtaacaagaacagatcacattgttcaagaatgagctgcctgaagaacaggaa 4490
QY 4201 accctggaactcttaaacgcccctaccacaagaagcctgtgctcgggaacccgctgtatgaa 4260
|||||
Db 4491 accctggaactcttaaacgcccctaccacaagaagcctgtgctcgggaacccgctgtatgaa 4550
QY 4261 ggaagaccacatcccaagaagcgccttcgaagcgaaggaagaagctggaacatcccca 4320
|||||
Db 4551 ggaagaccacatcccaagaagcgccttcgaagcgaaggaagaagctggaacatcccca 4610
QY 4321 gtcccccagacatcatgagcctcttcacagaatgggaactggaacaaatgacgaaccttca 4380
|||||
Db 4611 gtcccccagacatcatgagcctcttcacagaatgggaactggaacaaatgacgaaccttca 4670
QY 4381 cctgcatgcaagtgtagcagcgaacaaatcaagaagaatgctgcctgtgtgtcccccaggg 4440
|||||
Db 4671 cctgcatgcaagtgtagcagcgaacaaatcaagaagaatgctgcctgtgtgtcccccaggg 4730
QY 4441 gcaaggggggcgtcctcctccacaagaagaagaacacactgcaatatccttcagaagcccg 4500
|||||
Db 4731 gcaaggggggcgtcctcctccacaagaagaagaacacactgcaatatccttcagaagcccg 4790
QY 4501 acagaagaacacatcttcagatctatctgtgtgaagacgtatgtgacatactagccaaaagc 4560
|||||
Db 4791 acagaagaacacatcttcagatctatctgtgtgaagacgtatgtgacatactagccaaaagc 4850
QY 4561 ttaagaagaagaatctgggtggaatgagcttaagatagcggccttccctgggtgtcagt 4620
|||||
Db 4851 ttaagaagaagaatctgggtggaatgagcttaagatagcggccttccctgggtgtcagt 4910
QY 4621 aatctcagaagcctcctccagagtcgaagaagtaatgatacctcaaaaagaagaaga 4680
|||||
Db 4911 aatctcagaagcctcctccagagtcgaagaagtaatgatacctcaaaaagaagaaga 4970
QY 4681 caactaaagctggcgaagaagacagctgtcagatcgatcttcacaacagcttgggaagatt 4740
|||||
Db 4971 caactaaagctggcgaagaagacagctgtcagatcgatcttcacaacagcttgggaagatt 5030
QY 4741 atgacagaagctggaacacagaataatgtcaagtggtgtltaataacaaggctgtgcat 4800
|||||
Db 5031 atgacagaagctggaacacagaataatgtcaagtggtgtltaataacaaggctgtgcat 5090
QY 4801 gcaatcagctcttcttcgaatgtcaataaagatgcattctccggggccaacctgcaag 4860
|||||
Db 5091 gcaatcagctcttcttcgaatgtcaataaagatgcattctccggggccaacctgcaag 5150
QY 4861 ggaagaacccctgacatattgaaatlaactgttcaatcaatccctgaaatcacaag 4920
|||||
Db 5151 ggaagaacccctgacatattgaaatlaactgttcaatcaatccctgaaatcacaag 5210
QY 4921 cagaagctcagaagtggtccttgatgacacaataagtaggtgtgctgtgtcatalgt 4980
|||||
Db 5211 cagaagctcagaagtggtccttgatgacacaataagtaggtgtgctgtgtcatalgt 5270
QY 4981 gtaactcttgcaatgtcctctgcccagaagccttctgctgatactcagtagagcg 5040
|||||
Db 5271 gtaactcttgcaatgtcctctgcccagaagccttctgctgatactcagtagagcg 5300
QY 5041 gtcagaagaacaaacacctgcaatcatcagtggaatggaagcctgtcatctagctc 5100
|||||
Db 5301 gtcagaagaacaaacacctgcaatcatcagtggaatggaagcctgtcatctagctc 5390
QY 5101 tctcaatttctggagatgtgtgcaaatcagctgtgtccctgcgaacatgtaatac 5160
|||||
Db 5391 tctcaatttctggagatgtgtgcaaatcagctgtgtccctgcgaacatgtaatac 5450
QY 5161 ttcatctgtctccagcagaagctcatalgtctcctccacaacatctgcctgttagccct 5220
|||||
Db 5451 ttcatctgtctccagcagaagctcatalgtctcctccacaacatctgcctgttagccct 5510
QY 5221 ctacttctgtctgagtggtgtgtaatacactctcaatgtacccaagcctctgtgtgtc 5280
|||||
Db 5511 ctacttctgtctgagtggtgtgtaatacactctcaatgtacccaagcctctgtgtgtc 5570
QY 5281 aagaatcccccagcagaagcctatgtgtgtcctcacaagcgtgaaccccttcaatggaat 5340
|||||
Db 5571 aagaatcccccagcagaagcctatgtgtgtcctcacaagcgtgaaccccttcaatggaat 5630
QY 5341 ggcagcgtggccaccccttgtgtgtgagctgttcaaccgacaataagctgaataatac 5400
|||||
Db 5631 ggcagcgtggccaccccttgtgtgtgagctgttcaaccgacaataagctgaataatac 5690
QY 5401 gatactctgaagcccggtgtcttgatcttccacatcttctgctgggaagaggtctatc 5460
|||||
Db 5691 gatactctgaagcccggtgtcttgatcttccacatcttctgctgggaagaggtctatc 5750
QY 5461 gacatgggtgaagaaacccgcaatgagctgagatgcccctggaaaggtlltggggaagatc 5520
|||||
Db 5751 gacatgggtgaagaaacccgcaatgagctgagatgcccctggaaaggtlltggggaagatc 5810
QY 5521 gtgtcacatattcttgggaactgtgtgtggaagcaaacctctgcgaatgagcgtgtgaag 5580
|||||
Db 5811 gtgtcacatattcttgggaactgtgtgtggaagcaaacctctgcgaatgagcgtgtgaag 5870
QY 5581 gtgtgtcttctccatattctgtgtgtgatacgaatgaagttcttaagggccagact 5640
|||||
Db 5871 gtgtgtcttctccatattctgtgtgtgatacgaatgaagttcttaagggccagact 5930
QY 5641 gtaaatgcaagatctcctcgaatgagatgaaatgaaatgtgagcggggaagacag 5700
|||||
Db 5931 gtaaatgcaagatctcctcgaatgagatgaaatgaaatgtgagcggggaagacag 5990
QY 5701 agaatctctgagtggtggaagccagaatgacatctagaatcaagaagtgtagcgaagata 5760
|||||
Db 5991 agaatctctgagtggtggaagccagaatgacatctagaatcaagaagtgtagcgaagata 6050
QY 5761 tatagaagaagcggaagcctgctgtgtgaagagattgtgtggggaattctcctcgtgtgag 5820
|||||
```

Dh 6051 TATAGAAAGGAGCGAGGCTGCTGTTGACAGATTTGCGGGGATTCCTCCGTGAG 6110
Qy 5821 tgcttggtccctggagatlaa-tygggctyggaaatcatcacttcaagaigttaaa 5880
Dh 6111 TGGTTTGGGCTCGGAGGTTAATGGGGCGGAAATCATCACTTCAAGATGTTTAA 6170
Qy 5881 ggaatccacactgtaccagagagatgcttctcttaacaaaataglatctataaac 5940
Dh 6171 GGAATATCCACTGTTACCCAGAGAGATGCTTCTTACAAAATATATCTTATCAAC 6230
Qy 5941 atccatgaatgatacagaaacatgggactgacctcagtttgatgcatcacagagcty 6000
Dh 6231 ATCCATGAAGTACATCAGAACATGGGCTACTGGCCCTCAGTTGATGCAACAGAGAG 6290
Qy 6001 ttgactgggagagaaacacgtyggagttcttgcctcttgagagagagtcaccaagaaga 6060
Dh 6291 TTGACTGGGAGAGAACCGTGAGATCTTTCCTTGTGAGAGAGATCCAGAGAAAGAA 6350
Qy 6061 gttgcaaggttggtgagtgagcgatcggaaactgggctctgtgaagatagagaagaaa 6120
Dh 6351 GTTGCAAGGTTGGTGAGTGGCGGATTCGGAACCTGGGCTCGTGAAGTATGAGAGAAAA 6410
Qy 6121 taatgctgtaactaagtgaggaagcaacaaacgcaagctctctcaagccatgcttgatc 6180
Dh 6411 TATGCTGTAAGTATAGTGAGAGCAACAAACGCAAGCTCTTACGCCATGGCTTTGATC 6470
Qy 6181 ggcgggacctctgtgtgttcttgatgagaccacacacagagcatgataccaaagccgg 6240
Dh 6471 GGGGGGCTCTCTGTTGGTGTGAGTGGAGAACCCACACAGCATGATCCCAAGCCCGG 6530
Qy 6241 cggctctgtggaatgtgcccctaaagtgtgtcaagaagggagatcagtagtcttaca 6300
Dh 6531 CGGTTCTGTGGAATGTTGGCCCTAAGTGTGTCAAGAGGGGAGATCAGTAGTCTTACA 6590
Qy 6301 tctcaatagatggaagaatgtgaagctcttgactagatgagcaatcaatgcaatgga 6360
Dh 6591 TCCATAGTATGGAAGAATGTAAGCTTTGCACTAGATGCAATGATGCAATGGA 6650
Qy 6361 aggttcagtgagctctggcagtgctcagcagcatctaaanaaatagtttgagagatgata 6420
Dh 6651 AGGTTTCAAGGCTTGGCAGTGTCCAGCATCTTAAATAATGATGTTGGATGTTTAA 6710
Qy 6421 atagttgacgaatagcaggggtccacacccggaactgaagcctgtccagatcttctga 6480
Dh 6711 ATAGTTGTAGCAATACAGAGGTCCACCGGACCTTAACCTGTCAGATTTCTTTGA 6770
Qy 6481 ctggaatctccggagagtggtctaaagaagaacacccggaacatgctacatacagctt 6540
Dh 6771 CTGGAATTTCTGGAAGTGTCTTAAAGAGAAACACCGGACATGCTACATACAGCTT 6830
Qy 6541 ccaatctcaatctctctgccaagatatcatcactctctccagagcaaaaagcga 6600
Dh 6831 CCATCTTCAATTAATCTTCTGGCCAGGATTAATCAGATCTCTCCAGAGCAAAAAGCA 6890
Qy 6601 ctccacatagaagactactctgttctcagacaacacttgaccaagatttgtaactt 6660
Dh 6891 CTCCACATAGGAAGACTACTCTGTTCTCAGACAACACTTGACCAAGTATTTGTAACCTT 6950
Qy 6661 gccaaagaccagaagatgatacacttaaaagacctctcttcaaaaaaacagaga 6720
Dh 6951 GCCAAGGACCAAGATGATGATACCACTTAAAGACCTCTTCAACAAAAAACAGACA 7010
Qy 6721 gtagtgaagcttgacagtttccatcttcttcaagagatgagaagaagtgaagaagcat 6780
Dh 7011 GTAGTGAAGCTTGACAGTCTTCTTCAACAGGATGAGAAGTGAAGAAAGCTAT 7070
Qy 6781 gtagaagaatccgttcaatcag 6804
Dh 7071 GTATGAAGAATCTCTTATACGG 7094

LOCUS AF285167 10442 bp mRNA linear PRI 09-AUG-2000
DEFINITION Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA,
complete cds.
ACCESSION AF285167
VERSION AF285167.1 GI:9755158
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Schwartz,K., Lawn,R.M. and Wade,D.P
ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
regulated by LXR
JOURNAL
REFERENCE
AUTHORS Lawn,R.M., Wade,D.P., Garvin,M.R., Wang,X., Schwartz,K.,
Porter,J.G., Sellhammer,J.J., Vaughan,A.M. and Oram,J.F.
Direct Submission
Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
3172 Porter Drive, Palo Alto, CA 94304, USA
FEATURES
source
location/Qualifiers
1..10442
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/map="q31"
/cell_type="fibroblast"
/tissue_type="skin"
1..10442
/gene="ABCA1"
291..7076
/gene="ABCA1"
/codon_start=1
/product="ATP-binding cassette transporter 1"
/protein_id="AAP8175.1"
/db_xref="GI:9755159"

RESULT 3
AF285167

/translation="MVCPEQLRLKLNLFRRRCQQLLEAVMLFTLLISVRL
SYPRYEDHECHFPNKAMPASAGTLPMVOGIIICANNPCFRYPGGAAGVGNFMSIV
ARLEFSDARLLLSOKDTSKMDKRYLRLQQLIKSSSKLLODFLVNDETFSGFLYH
NLSPKSTVDKMLRADVILHKVFLQYGLHLETLGKSGSEEMLODGEVRLGIP
KERLLAAERYLRNMDILKPLTLTLNSTSPKELAEATKTLISGLTADLBSMR
SMSDMQEVAFLLNNVSSSSSTIYQAVRIVCGHEGGGLKLSLMTEDNNYALF
GGNGEDAEFTYDNSTTPYCNDLMLNLESPSLRLIMALKPLGLILYDPDPAT
ROYVAELNKTFFDELAVFHDEGMWELSPKWTFMENSOEMDLVRLMLDSRNDHWE
QQLDGLDMTADIVAFLEKHEDEVSSNSVYTWRAFNEDNOLITIRFMECVNL
KLPIATEVWLINKSMELDEREFMAGIVETGTPGSLPIPHVKYKIMQIDNVENT
NKIKDGMWGPRADEPDMRYWGGFAVLQDVBOAIIIVLTPGPKTKGYVMQOPY
PCYVDIILFVMSRMLDKMTAMITSAVITIKGITYEAKRKETMRIMGDSILM
FSWFISLILPLVBSAGLVILALGNLPLSDSVFVLVFAVVTIIQCLISTLF
SRANLAAACGGIILFTLYLPLVLCVAMQDYVETLKFASLSPAVFGGCHYFALFE
BOGIGVQMDNLFPSPVEEDGFNLTTISIMSLDPTGLYVMTYIEAVFGQYGIPLPW
YFPCTKSYFGEESDEKSHSGNOKRMSICEEBETHLGLVSIONLVKYVRDMKY
AVDGLALNFEQOITSLFNGNGAGKTTTMSILTLGLPPPSGTATILGQIRSEMTIR
ONLGVCPHONHVLFDMLTVEHITMEVYARKLGSSEKHAKBOMALDYGRLSKSLKT
SOLSGMOKRLSALAFVGSKYVITIDEPYADVPISRGITVELIKTRQGTITLST
HHNDEADVADRLAIIISGLKCCVSSLELKNOLGTYLTLVKNKDVBSLSDSNSS
STVSYLKEDSVSSSSDAGLSGHESDLTIDVSAISMLIRKHSSEARLVDDICHEL
TYVLPYAKKEGAFVELFHEIDRLSDLGISYGLSETLEBIFLKVAEESGVADTS
DGLTPARRNRRAFGKOSCLRPTEEDADPMDSDIDPSRETDLSGMDGVSQYK
GMLKQOQFVALIMKRLLIARSRRKFFQIYVLPVAVCIATVLSIVPRCKYVSLE
LQPMWNEQYTVYSNDAPEDTGTIELNALTIDPGRGTRCMGNFIPTIDCOAGEEEN
TTAPVQVITMDLFPQNMWQNPSPACQCSQKIKMLPVCPPGAGGLPDPQKONTA
DILODKTGRNLSIDYLVKTYVOITAKSLKKIWNFRKRGGLFVSNQALPPODEVN
DAIKQMKRLKLAKSDASDRFLNSLGRKGIWNERKGGFLGVSNTQALPPODEVN
NALIRANLOKGENPSHYGITAFNHPNLTKOOLSEVALMTTSDVLSVCFYFASVS
PASEFVEILOERYSKAKHLOFTSGVKPVYVIMSNVYMCNVPVATVLIITFEFOO
KSYVSTNIPVIALILLILYKNSITPLMTYASVYKIPSTAYVILSVLEIGINSVA
TYVLELFTDNKLNNINDILKSVFLIPHECLFGLGLIDWKYKNQADALERGENKFS
PLSWDLVGRNLLPAAVEGVFPLIYVLIOYRPIPRPVNALSPLNDEDEVERERO
RLIDGGQNDIIEIKELTKIYRRKRKPAVDRCVGIPECEGGLGVNGASFTFKM
LNGDTVTGDAFLNNKNSILSNHHEHOMGVCPOFDAITELLTGREHVEFPALLRGY
PKREVKGVEWMAIRKLGLYKYEKTAAGNNSGKNKKLSTAMALIGPPVYVILDEPTTG

Dh 2271 TATGAGAGAGGACGCTGTAAGAGACCATGCGATCATGGGCTCGACAACAGATA 2330
Qy 2041 ctctggtttgctgtgttcaatagtagcctcaatctctctctgtgagcgtgagcgtgta 2100
Dh 2231 CTCTGGTTTGTAGCTGGTTTATAGGCTCATCTCTCTCTGTGAGCCCTGAGCTGCTGA 2390
Qy 2101 gtgtgtatccagaagttaggaaacctgtgacctacagttatccagcgtggtgtttgtc 2160
Dh 2391 GTGTGTATCTCTGAAAGTTAGAAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2450
Qy 2161 ttcctgtcgt 2220
Dh 2451 TTCTGTCTGT 2510
Qy 2221 ttcagagac 2280
Dh 2511 TCCAGAGCCAACTCGGAGAGACCTGTGGGGGATCATCTCTCTCTCTCTCTCTCTCTCT 2570
Qy 2281 taagctctgt 2340
Dh 2571 TAGGTCTGT 2630
Qy 2341 ctgtctgtctgt 2400
Dh 2631 CTGTCTGTCTGT 2690
Qy 2401 ggcatttgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2460
Dh 2691 GGCATTGTGAGTGCAGTGGAGCAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2750
Qy 2461 ctacacacttgcatactcatalgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2520
Dh 2751 CTCACACTTGCATCTCCATGTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2810
Qy 2521 taatttgagtggt 2580
Dh 2811 TACATTGAGGCTGT 2870
Qy 2581 accaagcttcaactgt 2640
Dh 2871 ACCAATCTCTACTGCTTTTGGCGAGCAAAATGTGTGTGTGTGTGTGTGTGTGTGTGT 2930
Qy 2641 aagagaatgtcagaatactgtcatalgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2700
Dh 2931 AAGAGAAATGTCAAAATGTCAATGTGAGAGAGAACCCACCTTGAAGTGGGCTGTGTC 2990
Qy 2701 attcagaacacgt 2760
Dh 2991 ATTCAAAACCTGT 3050
Qy 2761 ctgaaatttlaag 2820
Dh 3051 CTGAATTTTATAGAGGCGCAAGATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3110
Qy 2821 accacacatgtcaactcctgtacacacacacacacacacacacacacacacacacacac 2880
Dh 3111 ACCACCAATGTCAATCTGTGACCGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3170
Qy 2881 ggaagaagacattcgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2940
Dh 3171 GGAAGAAAGCAATTCGCTGTGAGATGTGACACCATCCCGGCAAACTTGGGGTCTGTGCC 3230
Qy 2941 cataacgt 3000
Dh 3231 CATTAACGT 3290
Qy 3001 aaagggtctctgtgaagacacgtgtgaagcggagatgtgagcagatgtgagcctgtgtgt 3060
Dh 3291 AAAGGGCTCTGTGAAGACAGCTGAAGCGGAGATGTGAGCGAGATGGCCCTGTGATGTGCT 3350
Qy 3061 ttgcatacaagaacacgtgtgaagacacacacacacacacacacacacacacacacacac 3120
Dh 3351 TTGCCATCAACGACGCTGAAGAAAGCAAAACCAAGCCAGCTGTGAGGTGAGATGTGAGAAAG 3410
Qy 3121 ctatctgt 3180
Dh 3411 CTATCTGT 3470
Qy 3181 gctgt 3240
Dh 3471 GCTGT 3530
Qy 3241 ggcgcacacattatctctctacacacacacacacacacacacacacacacacacacac 3300
Dh 3531 GGCCTCACCATTTATCTCTCTCAACACCAATGGATGAGAGGAGCTCTGTGGGAGACG 3350
Qy 3301 attgcacatcattccacatgt 3360
Dh 3591 ATTGCCATCATCTCCATGTGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3650
Qy 3361 cagctgt 3420
Dh 3651 CAGCTGT 3710
Qy 3421 tctgtcagaacacagtagtagcacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3480
Dh 3711 TCTGTCAAAACAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 3770
Qy 3481 agcagttctgt 3540
Dh 3771 AGCAGTTCTGT 3830
Qy 3541 tctgtctatctcaacactcatalgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3600
Dh 3831 TCTGTCTATCTCAACCTCATATAGAGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3890
Qy 3601 ggcagtgagctgaactatgt 3660
Dh 3891 GGCAGTGTGCTGT 3950
Qy 3661 ctcttcaatgt 3720
Dh 3951 CTCTTTTCAATGT 4010
Qy 3721 gagaagac 3780
Dh 4011 GAGAGACCTGTGAGAAATTTCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4070
Qy 3781 acctcagaatgt 3840
Dh 4071 ACCTCAGATGT 4130
Qy 3841 tgtctgt 3900
Dh 4131 TGTCTGT 4190
Qy 3901 gaatccag 3960
Dh 4191 GAATCCAG 4250
Qy 3961 ggtgtgaacttaacacagacacagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4020
Dh 4251 GGTGTGAACCTTACACAGCAACAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4310
Qy 4021 agacagagtgagaaagatttctgtcagatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4080
Dh 4311 AGACGAGTGTGGAAGAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4370
Qy 4081 ggcctgt 4140
Dh 4371 GGCCTTGT 4430
Qy 4141 cctgt 4200
Dh 4431 CCTGT 4490

Db 6651 AGGTTGAGGTCCTTGGCAGTGTCCAGCATCTAAATAATAGTTTGGAGATGGTTATACA 67110
Qy 6421 atagtgtaagaatagaaggggtccaaacggagctgaagctgtccagagatltcttga 6480
Db 6711 ATAGTTGACGAATAGCAGAGGTCCAAACCGAGCTGAAGCCTGTCCAGGATTTCTTGA 6770
Qy 6481 cttagcttctggaagtgtcttaagaagaacaacccggaactgtctacaalacagctt 6540
Db 6771 CTTCATTTCTCTGGAAGTGTCTTAAAGAGAAACACCGAAGCATGTACATATTCACACTT 6830
Qy 6541 ccacttcatatcttctctggtccagagatatctcagcatcctctccagagcaaaacgca 6600
Db 6831 CCATCTCATATCTCTCTGTGGCCAGATATTCAGCATCTCTCTCCAGACAAAACGCA 6890
Qy 6601 ctccacatagaagactactctgttctccagaacaacactgtgacaaagtattgtgaactt 6660
Db 6891 CTCCACATAGAGACTACTCTGTCTTCAAGAACAACTTGAACAAATTTGTGAATTT 6950
Qy 6661 gccaaagacaaagtgaatgaatgaacttaagaacactcattacacaaacacagaca 6720
Db 6951 GCCAAGACCAAGATGATGATGACACTTAAAGACCTCTCATTTACCAAAAACGACACA 7010
Qy 6721 gtagtggaagctgtcagcttccacatcttctcagaagaagaagtgaaagtgaaagaagctat 6780
Db 7011 GTAGTGAGCTGTGACGTTCTCACATCTTTCTACAGAGTGAAGAAGTGAAGAAGCTAT 7070
Qy 6781 gtaggaagaatcctgtctacacg 6804
Db 7071 GTATGAAGATCTCTGTTCATACG 7094

RESULT 4
AX060719 AX060719 10474 bp DNA linear PAT 22-JAN-2001
LOCUS Sequence 7 from Patent WO0078972.
DEFINITION AX060719
ACCESSION AX060719
VERSION AX060719.1 GI:12406108
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn, R.M., Wade, D., and Garvin, M.
TITLE Regulation with binding cassette transporter protein abcl
JOURNAL Patent: WO 0078972-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source Location/Qualifiers
1..10474
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others
ORIGIN

Query Match 100.0%; Score 6802.4; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 atgagctgttggtcagctcagctgaagtgctgctgtggaagaactccttccagaaga 60
Db 323 ATGGCTTTGTTGGCTCAGCTGAGGTGCTGTGGAAGAACCTCCTTCAGAAAGAA 382
Qy 61 caaacaatcagctgttactgaagtgtgctgctctctatcttctcctgactatc 120
Db 383 CAACAATGTCAGCTGTACTGGAAGTGGCTGCTCTATTATCTTCTGATTCGATC 442
Qy 121 tctgttgctgaagctacccacccatgaacaacatgaaatgcaatttccaaataagcc 180
Db 443 TCTGTTCGGCTGAGTACCCACCTATGAACAACATGAATGCCATTTCCTCAATTAAGCC 502
Qy 181 atgacctcgaagaaacttctctggtgtcaggggattatctgaatgaacaaaccc 240

Db 503 ATGCCCTTGACAGAACACTCTCTGGGTTTCAGGGGATTATCTGTAAATGCCAACAAACCC 562
Qy 241 ttttcggttaccagactcctctgggaggtcccggaagtgttggaacttaaaacaccc 300
Db 563 TGTTCCTGTACCCGACTCTCTGGGAGGCTCCCGAGTTGTTGGAACCTTTACAAATTC 622
Qy 301 atgttgctcgtgttctcagaatgtcgtgaggttcttatacagccagaagaacac 360
Db 623 ATGTGCTCGCCTGTCTCAAGATGCTCGAGGCTTCTTTATACAGCCAGAAAGACACC 682
Qy 361 agcatgaagaatcgtgaaagtcttgaaacattacagcagatcaaaatccaagcca 420
Db 683 AGCATGAAGACATGGGCAAACTTCTGAGAACATTTACGCAATCAAAATTCACGCTCA 742
Qy 421 aacttgaaagcttcaagattccttggttggaacaatgaacacttctctggttctcatalac 480
Db 743 AACTGAAAGCTTCAGATTTCTCGGTGACATGAACCTTCTGGTCTCTATATAC 802
Qy 481 aaactctctcccaagtctactgttgacaagaatgtcgaaggtcgtatcattctcac 540
Db 803 AACCTCTCTCCCAAGTCTACTGTGACAAAGATGCTGAGGGCTGATGTCATCTCCAC 862
Qy 541 aaggtattttgcaaggtctacagattacattgaacaagctgtgcaatgatacaaatca 600
Db 863 AAGGTATTTTTCAGAGGCTACAGATTACATTGACAACTGTGCAATGATCAAAATCA 922
Qy 601 gaagagatgattcaactgtgtggaacaagaagttctgagcttgtgcttcaacaaagag 660
Db 923 GAAGAGATGATTTCAACTGTGTGACCAAGATTTCTGAGCTTGTGGCTTCCCAAGAG 982
Qy 661 aaactgctcgaagcagagcaggtactgttcttccaaatggaacatccatgaacacactg 720
Db 983 AAACCTGCTGACGACGACGAGCTACTTCTGTCACAACTGACAACTCGAAGCAATCTG 1042
Qy 721 agaacactaaactctacatctcccttcccgacaagagctgtgctgaagccacaacaa 780
Db 1043 AGAACATAAATCTTACATCTCTCTCCGACGAAGAGTGGCTGAAGCCCAAAAACA 1102
Qy 781 ttgctgcatagcttgggaactctgtgccaagagctgttccagatgaagaagctgtgag 840
Db 1103 TTGCTGCAATGCTTGGAGCTGTGGCCGACGAGGCTGTGACCACTGAGAAAGTGAAGTGC 1162
Qy 841 atgcagcagagagtgatgttcttgaacaaatgtgaacagctcagctcctccacccaatc 900
Db 1163 ATGCGACAGAGAGTATTTCTGTACCAATGGAACAGCTCCACTCTCCACCAATTC 1222
Qy 901 taacagctgtgtctcgatgtgtctgtgctgctgagccacccgaagaggggctgaagaatca 960
Db 1223 TACCAAGCTGTGTCTCGTATGTGTGCGGCGCATCCGAGGAGGGGCTGAAGATCAAG 1282
Qy 961 tctctcaactgtatgaagacaacaactacaaagccctcttgaaggcaatgagctgag 1020
Db 1283 TCTCTCACTGTGTATGAGGACAACTACAAACCTCTTTGAGGCAATGGACTGAG 1342
Qy 1021 gaagatgtgaacactctatgaacaactctaaactcttactgaatgaatgtatgaag 1080
Db 1343 GAAGATGCTGAACCTCTATGACAACTTACAACTCTTACTGCAATGATTTGATGAAG 1402
Qy 1081 aatttgaggtcagctcttcttcccgatattctggaagaagctgaagccgctgtcgtt 1140
Db 1403 AATTTGAGTGTAGTCCCTTCCGATTAATGGAAGCTGGAAGCCGCTGCTGCTT 1462
Qy 1141 ggaagaatcctgtatacaccctgaacacccacgaagcagagctcatgtgtgagtgaaac 1200
Db 1463 GGGAAAGATCTGTATACACCTGACACTCCAGCCCAAGGCAAGCTGATGCTGAGGTGAAC 1522
Qy 1201 aagaacttccagaaactgtgtgttccatgaltctggaagagcaltgtggaagaaactcagc 1260
Db 1523 AAGACTTCCAGAACTGGCTGTCTTCATGATGTGGAAGGCAATGNGGAGAACTCAGC 1582
Qy 1261 cccaagatctggaactcctcaggaagaacagccaaagaatggaactgtcagatgtcgttg 1320
Db 1583 CCCAAGATCTGAGCTTTCATGAGAAACAGCCAAAGAAATGAGACCTTGTCCGATGCTGTG 1642

QY 1321 gacagcaggaacatgacacatttgggaacagcagttgagcttagattgacagcc 1380
|||||
DB 1643 GACAGCAGGAGCAATGACCATTTTGGGAACAGCATGGATGGCTTAGATTGACAGCC 1702
|||||
QY 1361 caagacatcgttggcglttggccaagcaaccagagatgtccagtcagtaagtctt 1440
|||||
DB 1703 CAAGCATCTGTTGGGCTTTTGGCCAGACCCAGAGATGTCCAGTCCAGTAATGGTTCT 1762
|||||
QY 1441 gttgacacctggagagaagcttcaacagagactaacagagcaatcccgacatactcgc 1500
|||||
DB 1763 GTGTACACTCTGGAGAGAAAGCTTTTCAACAGACATTAACCGCAATCCGGACATATCTCCG 1822
|||||
QY 1501 ttcatgagatgtgtcaacactgaaacagctagaaccataagcaagaagcttgcatac 1560
|||||
DB 1823 TTCAATGGATGTGTCAACCTTAACAAAGCTAGAACCCATAGCAACAGAACTGTGCTCATC 1882
|||||
QY 1561 aacaagttcaatggagatcgttggatgagaggaagtttgggtgtattgttcaactgga 1620
|||||
DB 1883 AACCAAGTCCATGAGAGCTGCTGATGAGAGAAAGTTCTGGCTGTGATTTGTCTCACTGGA 1942
|||||
QY 1621 attactcagcagcaatgagctgtgcccacatgtcaagtaacaagatccgaatgacatt 1680
|||||
DB 1943 ATTACTCCAGGAGCATGTGAGCTGTGCCCATCATGTCAAGTACAAAGATCCGAATGAGACATT 2002
|||||
QY 1681 gacaaatgtgagagaggaacaataaatacaagatgggttactgtggacctgtgtccagact 1740
|||||
DB 2003 GACAAATGTGAGAGAGCAAAATAAATCAAGATGGGTACTGGGACCTGTGCTCTGACACT 2062
|||||
QY 1741 gacctttagagagatgctgctgagctgtgggggggcttcgactacttbaagatgtgtg 1800
|||||
DB 2063 GACCCCTTGAAGAGATGCGTACCTGTGGGGGGCTTCGCCCTACTTCCGGGATGTGGTG 2122
|||||
QY 1801 gacgagcaatcatcaagggtgtctgacgagcaggaagaacactgtgtctataatgcaa 1860
|||||
DB 2123 GAGCAGGCAATCATCAGGAGGTGCTGACGGGCAACGAGAAAGAAAGTGTCTATATGCAA 2182
|||||
QY 1861 cagatgacctaccctgtttagcttgaagacatcttctgcgaggtgaatgaagcagctga 1920
|||||
DB 2183 CAGATGCTCCCTATCCCTGTTACCTGTATGATACATCTTCTGGGGTATGAGCGCGGCAATG 2242
|||||
QY 1921 ccccttcatagcgtgacctggaatttactcagctgagctgtatcatcaagagcaatcgt 1980
|||||
DB 2243 CCCCTTCTATGACGCTGGCCTGGATTTACTGAGGCTGTATCATCAAGGCAATCGG 2302
|||||
QY 1981 tatgagaaagagcagcgtctgaagaagacatgagatcaatggccttggaacaagcata 2040
|||||
DB 2303 TATGAGAAAGAGGACGCGCTGAAGAGACATGCGGATCATGGGCTGGACAAACAGCATA 2362
|||||
QY 2041 cctcgttttagctgttcaatagtttagcctcatctctctctgttgaagcgttgcgtcta 2100
|||||
DB 2363 CTCTGTTTAACTGCTGTTCAATGATAGCCATCTCTCTTCTGTGTAAGCGCTGGCTGCTTA 2422
|||||
QY 2101 gttgatactcctaagtttaagaaacactgtcctcactaagatgataccagcgtgtgttctc 2160
|||||
DB 2423 GTGGTATCTCTGAAGTTAGAAACCTGCTGCCCTACAGATGCCAGCGCTGTGTTGTC 2482
|||||
QY 2161 ttccgttccgttgttgcgtgtgtgaataacccgcagtgcttccctgattagcaactcttc 2220
|||||
DB 2483 TTCTCTGCTGCTGTTGCTGTGTAACATCTGCAATGCTTCTCTGATTAAGCAACACTCTTC 2542
|||||
QY 2221 tccagagccaacctggaagcaagcctgtgggagatcatcatctactcaagctgtactcgc 2280
|||||
DB 2543 TCCAGAGCCAACCTGACAGACGCTGTGGGCGATCATCTACTTCAAGCTGTACCTGCC 2602
|||||
QY 2281 taactcctgtgtgtgacatgagcaagactaagtgagcttcaacataaagatcttcgttagc 2340
|||||
DB 2603 TACGTCTCTGTGTGAGAGGAGGAGCTAGCTGTGGGCTTCAACACTCAAGATCTTCCGTAC 2662
|||||
QY 2341 ctgctgttccctgtgtgcttgggttggctgtgagtaacttggcccttttgaagagcag 2400
|||||
DB 2663 CTGCTGTCTCTGCTGCTGCTTTGGCTTTGGCTGTGATTAATCTTCCCTTTTGAAGGAGAG 2722

QY 2401 ggcattggagatgacgtgaggaacaaactgtttgagagctcctgttggaggaatgagcttcaat 2460
|||||
DB 2723 GGCATTGGAGTGGAGTGGGCAACCTGTTTGAAGTCTGTGGAGGAGAAATGCTTCAAT 2782
|||||
QY 2461 ctcaacacttgcatactcaatgacatgctgttgaacacttctctatgtgggtgaatgactgtg 2520
|||||
DB 2783 CTACACCACTTCATCTCCATGATGATGCTGTTGACACCTCTCTGATGGGGTGAATGACTGG 2842
|||||
QY 2521 taactgagctgtcttccaaagccagtaagaaatcccaagccctgtgtatttctctgc 2580
|||||
DB 2843 TACATTGAGCTCTCTTCCAGGCGCAGTACGGAAATCCAGAGCCCTGTGATTTCTTTC 2902
|||||
QY 2581 accaagcttcaactgtgttggcgagaaagtgaatgaagaagccaacctgtgttccaaacag 2640
|||||
DB 2903 ACCAAGTCTTACTGTGTTGGCGAGAAAGTGAATGAGAGAGCCACCTGTGTTCAACCAAG 2962
|||||
QY 2641 aagagatgtcagaatctcatgagaggaagaaacccaacttgaagcttggcgtgtctc 2700
|||||
DB 2963 AAGGAAATGTCAAAATCTCATGAGAGAACCCACCTTGAAGCTGGGCTGTCTC 3022
|||||
QY 2701 attcaagaacctgttaaaagtctcaacagagaatggaatgaagtgagctgtcgtgcgtgga 2760
|||||
DB 3023 ATTCAAGACCTGTGTAAGATCTACCGAGATGGATGAAGGTGGCTGTCAATGCTTGGA 3082
|||||
QY 2761 ctgagtttattgagggccagatcaacttcttctgtggccaatgagcggggaagagc 2820
|||||
DB 3083 CTGAAATTTTATGAGGCGCAGATCACCTCTTCTGTGGCCACAAATGAGCGGGGAAGAGC 3142
|||||
QY 2821 accacaaatgtcaatcttgaacgaggtgttcccccagacactcgggcaacgactaactcgt 2880
|||||
DB 3143 ACCACAAATGCAATCTGACCGGGGTGTCTCCCGCCAGCTCGGGCAACCGCTTCAATCTG 3202
|||||
QY 2881 ggaaaagaacatctgcttctgagatgaagacacatccaggaagaaacttggaggtctgtccag 2940
|||||
DB 3203 GGAAGAAACATCTGCTGTGATGAGACCATCCGGAGAACTGGGGCTGTCTCCAG 3262
|||||
QY 2941 cataagctgtcgttgaacatgctgactgtctgaagaacacatctgttctatgcccgcttg 3000
|||||
DB 3263 CATACGCTGCTGTTGACATGCTGATCTGGAAGAACATCTGCTTATGCGCCGCTTG 3322
|||||
QY 3001 aaaggtctcttgaagacagctgaagcggagatggaagcaagatgagccctgagatgttgt 3060
|||||
DB 3323 AAAAGGCTCTCTGGAAGACGTAAGCGGAGATGAGAGAGATGCGCTGGAATGTTGGT 3382
|||||
QY 3061 ttgcataaagcaagcttgaagaagaacaaacaaagcagctgttcaagtgaatgacagagaag 3120
|||||
DB 3383 TTGCGATTCAGCAAGCTGAAGAAAGCAAAACCAAGCAGCTGTCAAGTGAATGACAGAGAAAG 3442
|||||
QY 3121 ctatctgtgacctgtgacctgtgtcggggatctaagttgtcatctctgataaacccaca 3180
|||||
DB 3443 CTATCTGTGGCCTTGGCCTTGTGCGGGGATCTAAGGTTGCAATTCGATGAACCCACA 3502
|||||
QY 3181 gctgtgtgtgaccttactcccgaggggaatataaggaagctgtcgtcgaataaccgacaa 3240
|||||
DB 3503 GCTGCTGTGGAACCTTATCTCCGAGGGGAATATGGAAGCTGCTGTGAATATCCGACAA 3562
|||||
QY 3241 ggcgcacaactatctctctacacaacacataatgaagcggagcgttccctggggagagag 3300
|||||
DB 3563 GCCCGACACATTAATCTCTCTACACACACATGATGAAGCGAGACGCTCGGGGAGACAG 3622
|||||
QY 3301 attgcacatctctccatlggaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3360
|||||
DB 3623 ATTGCATCATCTCCATGGGAAGCTGTGCTGTGGCTCTCTCTCTCTCTCTCTCTCTCTCT 3682
|||||
QY 3361 cagctgggaagaagctactactgacctgtgtcaagaagaatgtggaatccctccctcagt 3420
|||||
DB 3683 CAGCTGGGAACAGGCTTACTTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3742
|||||
QY 3421 tccctcagaacagtaagtaagcgtgtcatcacttgaacaaaggaagagcagtgcttccag 3480
|||||
DB 3743 TCTCTCAGAAACAGTATGAGACATGTGTCAATCACTGAAAGAAAGAGAGAGAGTGTTCAG 3802
|||||
QY 3481 agcagttctgactgtgacctgtggcagagcaatgaagatgacagcgtgacacatcgtatgtc 3540

Db 3803 AGAGTTCTGATGCTGGCCCTGGGACAGACCATGAGATGACCGCTGACATCGATGTC 3862
QY 3541 tctgtctctccaaacctcaatcaagaagcaltgtcttgaagcccgcttgglygaagacata 3600
Db 3863 TCTGCTATCTCCAAACCTCATCAGGAAGCATGTCTGAAGCCCGCTGTGGAAACATATA 3922
QY 3601 gggcatagcttgaactatgtgtcccatatgaagctgtctlaaagaaggaccccttctgaga 3660
Db 3923 GGGCATAGAGCTGACCTATGTGTGCTGCAATGAAAGCTGTAAAGGAGGAGCGCTTTGTGGA 3982
QY 3661 ccttctcaatagaatgaagaccgctcccaagcttgagcattctcaatgaatgaatcctca 3720
Db 3983 CTCTTCATGAGATGATGACCGGCTCTCAGACCTGGGCACTTCTAGTATGACATCTCA 4042
QY 3721 gaagacaccttgaagaataatctctcaaggtgtgcccgaagagatgggtgtgagtctgag 3780
Db 4043 GAAGACACCTGGAGAAATATCTCAAGGTGGCCGAAGAGAGTGGGTGATGCTGAG 4102
QY 3781 acctcaagatgtaccttgcacgaagaagaagaagcggcgcttggggagacgaagc 3840
Db 4103 ACCTCAGATGATGCTTGTGCGACAAACAAAGAGCGGCGCTTGGGGAACAGAGAGC 4162
QY 3841 tgtcttgcgcccgttcaatgaagaatgaatgtctgtatccaatgaatctgacataagacca 3900
Db 4163 TGTCTTCGCGCCGTTCACTGAAAGATGATGCTGCTGATCCAAATGATTCATCATAGACCA 4222
QY 3901 gaatcaagaagaagaagaactgtctcaatgtgagatgtgagcgaagagtcctaccagttgaa 3960
Db 4223 GAATCCAGAGAGACCAAGATGCTGCTCAATGGGATGAGAGGAGGAGGAGGAGGAGGAGG 4282
QY 3961 ggcctgaagaacttcaacagaagaagaatgtgtgccccttctgtgaagaagaatgttaattg 4020
Db 4283 GCGTGAAGAACTTACACAGCAAGATGTGTGTGCGCTTTTGTGAAGAGACTGCTAATTTGCC 4342
QY 4021 agagcgaagtcgaagaagaatcttctgtcagatgttctgtgcaagctgtgttctgtcalt 4080
Db 4343 AGAGGAGATCGGAAAGATTTTGTCTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4402
QY 4081 ggcctgtgttgaagcctgtgtgtgcccaccccttggcaaglacccagcctgtgaactcaag 4140
Db 4403 GCCCTTGTGTTAGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4462
QY 4141 cccctgaatgtacaagaagaagaatcattgtcgaagaatgtctgtcctgaagaagaagaaga 4200
Db 4463 CCTGATGTACACAGCAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4522
QY 4201 accctggaactttaaagccctcaacgaagaagcctgtgtcctgtggaagccgctgtatgaa 4260
Db 4523 ACCCTGGAAGCTTTAAACCGCTTCAACAAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 4582
QY 4261 ggaaccccaatcccaagaagaagcctgtgcaagaagaagaagaagaagaagaagaagaaga 4320
Db 4583 GGAACCCCAATCCCAAGACAGCGCCCTGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4642
QY 4321 gtccccagaacataatgaagccttccagaatgtggaactgtgacaaatgcagaaccttca 4380
Db 4643 GTTCCCAACACATATGATGATGCTTCCAGAAATGGAACTGGCAATGACAGAACCTTCA 4702
QY 4381 cctgtatgccagttgtagcagcagaagaatcaagaagatgtgcgctgtgtgtcccccaagg 4440
Db 4703 CCTGATGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4762
QY 4441 gcaaggggggtgtcctcctcccaagaagaagaagaagaagaagaagaagaagaagaagaaga 4500
Db 4763 GCAGGGGGGCTGCTCCTCCCAAGAAAGAAACAAACAACTGCAGATATCTCTCAGAGACTG 4822
QY 4501 acaagaagaagaagaatgtgatatctgtgtgaagcgtatgtgcagatcaatgaagcaaaagc 4560
Db 4823 ACAGGAAAGAAACATTTGGATTTATCTGTGTAAGAGCTATGCTGAGATCATATGAGCCAAAAGC 4882
QY 4561 ttaagaagaagaatctgtgtgaatgaatgttagatgagcgttctccctgtgtgtgtagt 4620
Db 4883 TTAAGAAACAGATCTGGGTGAATGATTTAGGATAGGCGGCTTTTCCCTGGGTGCTAGT 4942
QY 4621 aatactcaagaacttctccagatcaagaagttatgaatgcatcaaaacaatgaagaaga 4680
Db 4943 AATACTCAAGCACTTCCCTCCGAGTCAAGAACTTATGATGCGCATCAAAACAAATGAAGAAA 5002
QY 4681 caactcaagaactgtgccaagaagaagatctgcagatcgatattctcaacagcttgggaagttc 4740
Db 5003 CACCTTAAGCTGGCCCAAGAGAGTTCAGATGATGATTTTCAACAGCTGGGGAAGATTT 5062
QY 4741 atgaagagactggacaccagaataatgtcaaggtgtgtgttcaatacaagaaggtgtcat 4800
Db 5063 ATGACAGACTGGACACCAAGAAATATATCTCAAGGTGTGTGTCAATTAACAAAGGCTGGCAT 5122
QY 4801 gcaatcaagcttcttctgaatgtatcaacaatgtccattctcgggccaactgtgcaaaag 4860
Db 5123 GCAATCAAGCTCTTTCCTGTAATGATCAACAAATGCAATTCGCGGCAACCTGCAAAAG 5182
QY 4861 ggaaggaacccctagccatlaatgaatlaactgtctcaataatccctgaaatcccaag 4920
Db 5183 GGAGGAACCCCTAGCCATTAATGAAATTAATGCTTTCAATATATCCCTGAAATCTCACCAAG 5242
QY 4921 cagcagcctcaagaaggtgtcctgtatgaaccaatcaatgtgagatgtcctgtgtccatctgt 4980
Db 5243 CAGCAGCTCTCAGAGTGTGCTGTGATGACCAACATGATGATGATGATGATGATGATGATGAT 5302
QY 4981 gtcatcttgcgaatgtcctgtcctgtccagcagcttgcgtatcctgaatcccaagagcgg 5040
Db 5303 GTCATCTTTCGAATGTCTTCTGCTCCAGCAGCTTGTGCTGATTCCTGATTCAGACGAGCG 5362
QY 5041 gtccgaagaagaagaagaacccctgtcagatcatatgaatgaagaagctgtcatctgtgtc 5100
Db 5363 GTCACCAAGAGAAACACCTGCAATGATCAATGATGATGATGATGATGATGATGATGATGAT 5422
QY 5101 tctaattgtctgtggaatgtgaatgaatgaatgtgtccctgtcccaactgtgcatatcatc 5160
Db 5423 TCTAATTTTGTCTGGATATGTGCAATTAATGATGATGATGATGATGATGATGATGATGATG 5482
QY 5161 ttaactgtcttccagaagaagttcctatgtgtcctcaaccaatctgtgtgtgtgtgtgtgt 5220
Db 5483 TTCATGTCTTCAGACAGAGAGTCTATGTGTCTCCACCAATGCTGCTGCTGCTGCTGCTG 5542
QY 5221 ctacttgtcgt 5280
Db 5543 CTACTTTTGTCTGT 5602
QY 5281 aagatcccaagcagacgtatgt 5340
Db 5603 AAGATCCCAAGACAGCTATGT 5662
QY 5341 ggcagcgtgtgccaacttgt 5400
Db 5663 GCGAGCTGTGCGACCTTGT 5722
QY 5401 galatcctgaagtcgt 5460
Db 5723 GATATCTGGAAGTCCGCTTGT 5782
QY 5461 gacatgtgtgaaaaaacaggaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5520
Db 5783 GACATGTGTGAATAAACAGGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5842
QY 5521 gtgtcaacatcttctgt 5580
Db 5843 GTGTCAACATTAATCTTGT 5902
QY 5581 gtgtgttcttctcaatlaactgt 5640
Db 5903 GT 5962
QY 5641 gtaaatgaagaatctatctctctgtgaatgaatgaatgaatgaatgaatgaatgaatgaat 5700
Db 5963 GTAATGCAAAAGCTATCTCTGTGAATGATGAAGATGAAGATGAAGATGAAGATGAAGATGA 6022

QY 5701 agaattcttgatggtgagggccgaatgacatcttagaataccaagggtgacgaagata 5760
 |||||
 Db 6023 AGAATCTTGATGATGGAGGCCAGAAATGACATCTTGAATATCAAGAGTTGACGAAGATA 6082
 QY 5761 tatagaaggaaggaagacctgtctgtgaagaatttgctgagcaattctctctgtgag 5820
 |||||
 Db 6083 TATAGAAGGAAGGAGGAGGCTGCTGTTGACAGATTTGGGTGGCAATTCCTCTGCTGAG 6142
 QY 5821 tgccttgaggtccctgggaagtaatggggctggaataatcaacttccaagtgttaaca 5880
 |||||
 Db 6143 TGCTTTGGGCTCCTGGGAGTTATGGGGCGGAATAATCATCACTTCAAGATGTTAACA 6202
 QY 5881 ggaagatacaacgtgtaccagaagagatgtcttcttaacaaaaatagtatctataaac 5940
 |||||
 Db 6203 GGAGATACCCCTTACCAAGAGATGCTTCTTACAAAAATAGTATCTTATCAAC 6262
 QY 5941 atccatgaagtaacatgaagcaatgggtacttgccctcaagttgattgcatcacagagctg 6000
 |||||
 Db 6263 ATCCATGAATATACATGAAACATGGGCTACTGCCCTCAGTTTATGCCATCAGAGCTG 6322
 QY 6001 ttgattggagagaaacacgtgagttcttgccttttgaagagagttccagaagaaga 6060
 |||||
 Db 6323 TTGACTGGAGAGAACACGTGAGTTCTTGCCTTTTGAGAGAGATCCAGAGAAAGAA 6382
 QY 6061 gttggcaagttgtgaggtgagctatccgaataacgtgctgtgaagatagagaataaa 6120
 |||||
 Db 6383 GTTGGCAAGGTTGGTGAGTGCGCCATTCGGAAACTGGGCTCTGAGATGTGAGAAATA 6442
 QY 6121 tatgtctgtaactatgattgaggaacaacaagaagctctctcaagccatgagtttgatc 6180
 |||||
 Db 6443 TATGCTGTGATCTATATGAGAGCAACAAAGCAAGCTCTTACAGCATGCGTTTGATC 6502
 QY 6181 ggcgggacctcgtggtgttcttgatgaaccacacagagcatgattcccaaaagccgg 6240
 |||||
 Db 6503 GCGCGGCTCCTGCTGTGCTTCTGATGAACCCACAGGACATGATGCCAAAGCCCGG 6562
 QY 6241 cggctcttgaggaattgcccctaaagttgttcaagagagggagatagtagtcttaca 6300
 |||||
 Db 6563 CGGTTCTTGGGAATTTGCCCTTAAGTGTGTCAAGGAGGAGATAGTAGTCTTACA 6622
 QY 6301 tctaatagtaagaaatgtgaagctcttgcactagaatgagcaatcagtgatcaatgaga 6360
 |||||
 Db 6623 TCTCATGATGATGAAGATGATGAGCTCTTGTGACATGAGATGCAATCATGATGAGA 6682
 QY 6361 aggttcaaggtgcttggcagtggtccagcatctaaataatggttggagatggttataca 6420
 |||||
 Db 6683 AGGTTCAAGGTGCTTGGCAGTGTCCAGCATCTAATAAATAAGTTGAGATGTTATACA 6742
 QY 6421 atagtttaagaatagaaggttccacccggagcttgaagcctgtccaggaatttcttga 6480
 |||||
 Db 6743 ATAGTTGATGATGATGAGGATGATGAGGATGATGAGGATGATGAGGATGATGAGG 6802
 QY 6481 ctgcattctcctggaagtggttctaaagagaacaacccgaatcagtgatcaatcagaact 6540
 |||||
 Db 6803 CTGCAATTTCTGGAAGTGTCTTAAAGAGAAACCGGAACATGCTAATATACCACTT 6862
 QY 6541 ccaatcttaattatcttcttggcagagatatcaagcatctctccagagcaaaaaagga 6600
 |||||
 Db 6863 CCATCTTCATATCTTCTTGGCCAGGATATTCAGCATCTCTCCAGAGCAAAAAACGA 6922
 QY 6601 ctcccaatagaagaactactgtgttctcaagaacaacacttgaacaagtattgttaactt 6660
 |||||
 Db 6923 CTCACATGATGAGACTACTCTGTTTCTAGCAACACACTTGACCAAGTATTTGTAACTT 6982
 QY 6661 gccaaagaccaaagtgtatgatacgaacttaaaagacctctatatacaaaaaacagaca 6720
 |||||
 Db 6983 GCCAAGGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7042
 QY 6721 gtagtggacgttgcagttctcaacttcttcaagagatgagaagatgagaagctat 6780
 |||||
 Db 7043 GTAGTGGACGTTGACGTTCTCAGATCTTCTTACAGGATGAGAAAGTGAAGAAAGCTAT 7102

QY 6781 gtagaagaatccgtgtcatacag 6804
 |||||
 Db 7103 GTATGAGATCTCTTCTATACGG 7126

RESULT 5
 AX060721 10474 bp DNA linear PAT 22-JAN-2001
 LOCUS Sequence 9 from Patent WO0078972.
 DEFINITION AX060721
 ACCESSION AX060721
 VERSION AX060721.1 GI:12406109
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 10474)
 AUTHORS Lawn, R.M., Wade, D. and Garvin, M.
 TITLE Regulation with binding cassette transporter protein abcl
 JOURNAL Patent: WO 0078972-A 9 28-DEC-2000;
 CV THERAPEUTICS, INC. (US)

FEATURES
 source location/Qualifiers
 1..10474 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 2907 a 2304 c 2415 g 2844 t 4 others
 ORIGIN

Query Match 100.0%; Score 6802.4; DB 6; Length 10474;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 6803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atggctgtgtgctcgaagtgagttgctgtgtggaagaacctcttcagaagaaga 60
 |||||
 Db 323 ATGGCTGTGTGGCTCCTAGCTGAGGTTGCTGTGTGGAAGACCTTCTTGAAGAAAGA 382
 QY 61 caaactgcaagctgttacttgaagtgagtgcttcttacttctcctgactgac 120
 |||||
 Db 383 CAAGATGTCAGAGTGTACTGGAAGTGCGCTGCTCTTATCTCTGATCTGATC 442
 QY 121 tctgtcgtgctgagctaccacccctatgaacaacatgaaatgacatttccaaataagcc 180
 |||||
 Db 443 TCTGTTCGGCTGTGACCTACCCACCTATGAACAACATGATGCTTCTTCAATTAAGCC 502
 QY 181 atgcccctcgaagaacacttcttctgttcaagggagatctgttaatgccaacaacccc 240
 |||||
 Db 503 ATGCCCTCTGCAAGAACACTTCTTGGGTTCAGGGATTTATCTGTATGCAACAAACCC 562
 QY 241 tgttccgttaccgactcctctgggagagctcccgaggtgttggaaactttaacaatcc 300
 |||||
 Db 563 TGTTCCGTTACCCGAGCTCCTGGGAGGCTCCGAGTGTGGAAACTTTAAACAAATCC 622
 QY 301 atgtgagctgctgttctcagaatgctcggagagcttcttatacagccagaagaagacac 360
 |||||
 Db 623 ATGTGGCTGCTCCTGTTCTCAGATGCTCGAGGCTCTTTTATACAGCAAGAAAGCACCC 682
 QY 361 agatgaagagacatggcgaagttctgagaacattcaacagacatcaagaatccagctca 420
 |||||
 Db 683 AGCATGAAGACATGGCAGAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA 742
 QY 421 aacttgaagttcaaatctctgttggacaatgaaacctctcgggttctcatalaac 480
 |||||
 Db 743 AACTTGAAGCTTCAAGATTCTCGTGGACAAATGAACCTTCTGCTGGTCCATATCAC 802
 QY 481 aacctctctcccaagctactgttggacaagaatgctgaaggctgagatcattctccac 540
 |||||
 Db 803 AACCTCTCTCCCAAGATGCTACTGTGACAAAGATCTGAGGCTGATGTATCTATCTCAC 862
 QY 541 aaggtattttgcaaggctaccagttacatttgaacagctgtgcaatgataaataca 600
 |||||
 Db 863 AAGGTATTTTGAAGGCTACAGATTATTTGACAAAGTGTGCAATGATCAATAATCA 922

QY 601 gaagagatgatcaacttggtgaccagaagttctgaagcttctggtctacccaagag 660
Db 923 GAAGAGATGATTCACCTGGTGACCAAGAGTTCTGTAGCTTTGTGGCTACCAAGAG 982
QY 661 aaactgctgacagacagcagtaacttgcttccaaatgagacacccctgaagccactgt 720
Db 983 AAACGGCTGACGACGACGACGACTTCGTTCCAACTGACATCTGAAACCAATCTCTG 1042
QY 721 agaacactaaactacatccctccctccgaagagagctgctgtaagccacacaaaca 780
Db 1043 AGAACACTAAACTCTACATCTCCCTCCCGAGAGAGCTGCTGAAGCCACAAAAACA 1102
QY 781 ttgctgataactcttggaactctgcccagagctgttcagcatgagaagctgtgagac 840
Db 1103 TTGCTGACATGCTTGGGACTGTGGCCAGAGGCTGTTCAACATGAAAGCTGAGAGAC 1162
QY 841 atgagacagaggtgacttcttcaaccaatgtaaacagctccacactccctccacccaatc 900
Db 1163 ATGGAGACGAGGATGATGTTCTGACCAATGTGAACAGCTCCAGCTCTCCACCCCAATC 1222
QY 901 taacagagctgtctcgtlatctgtcgggacatcccgagagaggggagctgaagatcaag 960
Db 1223 TACAGAGCTGTGTCTCTGATGTCTGGGGCATCCGAGGGAGGGGGCTGAAGATCAAG 1282
QY 961 tctctcaactgtatgaggaacaacaactacaaagccctcttggaagcaatgagcactgag 1020
Db 1283 TCTCTCAACTGTATGAGGACAACTACAAAGCCCTTGTGAGGCAATGAGCAGCTAG 1342
QY 1021 gaagaatcgaacactctatgaaactctacactccctactgtaagatgtaagatgaag 1080
Db 1343 GAAGATCTGAACCTCTATGACAACTTACAACTCTTACTGCAATGATTTGATGAAG 1402
QY 1081 aattggaagctgaactccctctccgcatatcttggaagacactgaaagccgtctcgt 1140
Db 1403 AATTGAGAGCTGATCTCTTCTCCGATTAATCTGAAAGCTCTGAAGCCGCTGCTCCT 1462
QY 1141 gggagaactcctglatacacttgacactccagccaagagcaggtcatgctgtaagtgaa 1200
Db 1463 GGGAAAGTCTGTATACACTGACACTCCAGCCCAAGGAGGTGATGGCTGAGGTGAAC 1522
QY 1201 aagaacctccagaagactggtgtgttccatgactctggaagcaatgtggaagaaactcag 1260
Db 1523 AAGGCTCTCCAGGAACCTGGCTGTGTCTCATGATCTGAAAGCATGTGGGAGAACTCAG 1582
QY 1261 cccaagaactcctgacactcaggaagaacagcaagaatggaactctgcccagatgctgtg 1320
Db 1583 CCCAAGATCTGACACTTCATGAGAAAGCAAGCAAGAAATGAGACTTCTCCGAGTGTG 1642
QY 1321 gacagcagggacaatgacacactttgggaacagcagttgagtgactagattgagaccc 1380
Db 1643 GACAGCAGGGACAATGACCTTTTGGGAACACACTTGGATGGCTTAATGAGACAGCC 1702
QY 1381 caagaacatcgtggtcttggccaagcaccagagagatgctcaggtccagtaatgctt 1440
Db 1703 CAGACATCTGCTGCTTTTGGCCAAAGCAAGAGATGTCCAGTCCAGTATGTTT 1762
QY 1441 gtttacaactggaagaaacttcaacgagactaaccaagcaatcccgagacatctcag 1500
Db 1763 GTGTACACCTGAGAGAAAGCTTCAACGAGACTAACCCAGGCAATCCGGACATCTCCG 1822
QY 1501 ttcaatgagatgtgtcaacttgaaacaagctagaaaccaatgacaacagaaatctgtgctc 1560
Db 1823 TTATGAGAGTGTCAACCTGAAACAAAGCTAGAAACCATATGCAACAACTCTGGCTCAG 1882
QY 1561 aacaagttcatggaagctgtctgtaaggaagaaatcttgagctgtaatgtgttcaactg 1620
Db 1883 AACCAATCATGAGAGCTGCTGATGAGAGAAAGTTCTGGGCTGTATTTGTTCACATGGA 1942
QY 1621 attactccagagcagcatgtgagctgcccacatcatgtcaagtacaagaatccgaatgag 1680
Db 1943 ATTACTCCAGGAGCAATTAAGCTGCCCATCATGTCATACAAATCCGAATGAGCAATT 2002
QY 1681 gacaatgtgagaggaacaataaatacaagagtggtgtaactggaacctggtcctcgaact 1740

Db 2003 GACAAATGTGAGAGGACAAATAAATCAAGGATGGGTACTGTGGACCTGTCTGAGCT 2062
QY 1741 gaacctttgaggaactgtgtaactgtggtggggtcttcgctacttgcaagatgtgtgt 1800
Db 2063 GACCCCTTGGAGACATGTGTGATGCTGTGGGGGCTTCCCTACTTGCAGATGTGGTG 2122
QY 1801 gaagagcaatcatcagaggtgtctgacggtgacccggaagaagaactgtgtctatgtcaa 1860
Db 2123 GAGCAGGACATCATCAGGGTGTCTGACGGGCAACGAGAAAGAAATGCTGTCTATATGCA 2182
QY 1861 cagatgcccataccctgttaagltgataacatcttctggtggtgtatgagccgtgcaatg 1920
Db 2183 CAGATGCCATATCCCTGATACGTTGATGACATCTTTCTGGGGATGAGCCGGCAATG 2242
QY 1921 cccctctataagctgtgctggttactaagtggtgtgtatcatcaagggatcgtg 1980
Db 2243 CCCCTTATGACGCTGTGGATTTACTGATGCTGTGATATCAAGGGCATGCTG 2302
QY 1981 tatgaagaagagcagcgtgaaagacatgagatcatgagccttgaaacagata 2040
Db 2303 TATGAAGAAGAGGCAAGGCTGAAGAGAACATGGGATCATGGGCTGTGACAAACGATA 2362
QY 2041 ctctgtttagctgtatcaattagtagccatctcctctctgtgagcgtggtcgtcta 2100
Db 2363 CTCTGTTAGCTGTTCATTAATAGCTCATCTCTCTTCTTGTGAGCGCTGGCTGCTA 2422
QY 2101 gtgtatcatcctaaagtgaagacactgtgcccctcaagtgatccaggtgtgtgttc 2160
Db 2423 GTGTATCATCTAAATTAAGAAACCTGCTCCCTTAATCAATGATCCAGGAGTGTGTGTC 2482
QY 2161 ttccgtctcgt 2220
Db 2483 TTCTGTCTCGT 2542
QY 2221 tccagagcaactgagcagcagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2280
Db 2543 TCCAGAGCAACCTGTGACAGCAAGCTGTGGGACATCATCTACTACGCTTACTCTGCC 2602
QY 2281 taagctcgt 2340
Db 2603 TACGTCTGT 2662
QY 2341 ctgctgtcctcgt 2400
Db 2663 CTGCTGTCTCTGT 2722
QY 2401 ggcattgagtgagtgaggaacactgtttgagagctcgtgtgtgtgtgtgtgtgtgt 2460
Db 2723 GGCATTTGAGTGTGAGTGTGAGCAACCTGTTTGAAGTCTCTGTGAGGAAGATGCTTAAT 2782
QY 2461 ctcaacaacttgcacatcgaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2520
Db 2783 CTCACCACTGTGATCTCATGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2842
QY 2521 tacattgagctgt 2580
Db 2843 TACATTTAGGCTGTCTTTCCAGGCCATGACGAATTTCCAGGCCCTGTGTATTTCTTGC 2902
QY 2581 accaagttcactgt 2640
Db 2903 ACCAAGTCTCTACTGT 2662
QY 2641 aagaagatgtcaagaatctgcatgtgaggaagaaaccccaacttgaagctgtggtgtc 2700
Db 2963 AAGGAATGTGAGAAATCTGATGAGAGGAACCCCACTTGAAGCTGTGGCTGTCTC 3022
QY 2701 attcagaacctgtgtaaaagtctacagagatgagatgtggtgtgtgtgtgtgtgtgt 2760
Db 3023 ATTCAAGAACTGTGTAAGATCTACGAGATGGGATGAAGTGGCTGTGTGTGTGTGTGT 3082
QY 2761 ctgaattttatgt 2820

Db	3083	CTGATTTTTATGAGGGCCAGATTCACCTTCCTTGGGACCACAAATGAGACGGGGAAAGAC	3142
Qy	2821	acccecatgtcaatccctgcacccgggtgtgtcccccgaactcggcaacgcgcatacctctg	2880
Db	3143	ACCAACATGTCATTCCTGACCGGGTTGTTCGCCCGAAGCTTGGGACACCGCTCAATCTG	3202
Qy	2881	ggaagaacatctgcctctgaatgtgacacatccggcagaacctgggggtctgtcccaag	2940
Db	3203	GGAAAAACATTTGGCTCTAGATGAGACACATCCGGCGAAACCTGGGGGTCTTCCCCAG	3262
Qy	2941	cataagtgatgtcttgcatagtctgactctgaaagaacacatctgttctctatgtcccttg	3000
Db	3263	CATTAAGTGGTGTGTTGACATGCTGACTGTCGAAGAACAACATCTGGTCTTAATGGCCGCTTG	3322
Qy	3001	aaagggctctctgaagaacgctgaaagcggagatgtgaacagatgtgccctggatgttgt	3060
Db	3323	AAAGGGCTCTCTGAGAAGACGTCGAAGGGGGAGTGAAGACAGATGGCCCTGGATGTTGGT	3382
Qy	3061	ttgcatacaagaagcctgtaaaagcaaaacaaacgcgcgtctaagtggaatgtcagagaag	3120
Db	3383	TTGCATCAACGACGACTGAAAAACAAAACCAACCGTCGTGAGTGGAAATGCAAGAAAG	3442
Qy	3121	ctatctgtggccttggccttgtctggggatctaaagttgtcatctctgtatgtacccaca	3180
Db	3443	CTATCTGTGGCTCTGGGCTTTGTGGGGGATCTAAGATTTGTCATTCGTGATGAACCCACA	3502
Qy	3141	gctgtgtgtgaaccttactctccgcaagggaataitgagagctgcgtcgtgaatlacgcaa	3240
Db	3503	GCTGTGTGGACCCCTTAATCTCCGACAGGGAAATATGGAGCTGCTGTAATACCGACAA	3562
Qy	3241	ggccgacacatattctctctacacacacatggaatgaagcggacgtctctgtgggacag	3300
Db	3563	GGCCGACACATTAATTCCTCTACACACACATGATGAAGCGGAGCGTCCTGGGGACAG	3622
Qy	3301	attgccatcatctcccatgggaagctgtgcctgtgtgggctctccctggtttctgaagaac	3360
Db	3623	ATTGCCATCATCTCCCAATGGGAAGCGTCTGTGGGCTCTCCCTGTTCTGAAGAAC	3682
Qy	3361	cagctgggaacaagctactacccgacctctgtgtcaagaagaatgttgaatctccctcagt	3420
Db	3683	CAGCTGGGAACAGGCTACTACCTGACTTGTCATGGTCAAGAAAGATGTGAAATCCTCCCTCAGT	3742
Qy	3421	tcctgtcagaacagtagtagcactgtgtcatatacctgtgaaaagagagacagtgtttctcag	3480
Db	3743	TCTCTCAGAAAACTACTACTACTGTCATCTGATACCTGAAAAAGAGACAGATGTTTCCAG	3802
Qy	3481	agcaattctgaatgtgcctcgggcagcggccatgaagatgtgaacgcctgacatcagatgtc	3540
Db	3803	AGCAATTCTGATGCTGGCCTGGGAGCGACATGAGAGTGAACCCCTTACCATGGAATGTC	3602
Qy	3541	tctgtcatctcaaaccccatcaggaagacatgtgtctgaagcccgctgtgtggaagacata	3600
Db	3863	TCTGCTATCTCCAAACCTCATCAGAGAGCAATGTCTGAAGCCCGGCTGTGGAAGACATA	3922
Qy	3601	gggcatgtgcgcgaacctatgtgtgcgcataitgaagcgtgcataaagaaaggagcccttgttga	3660
Db	3923	GGGCAATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTTAAGGAAGAGACCTTTGTGGAA	3982
Qy	3661	ccctctcatgtgatgtgaacggctctcagacacttggagatctagttatgtgatctca	3720
Db	3983	CTCTTTCAATGAGATTGATGACCGGCTCTGACCTGGGCAATTCATAGTTATGGCATCA	4042
Qy	3721	gagacgacccctggaagaataatctccctaaggtgtggccgaagagatgtgggtgtgagtgtgag	3780
Db	4043	GAGAGACCCCTGGAGAAATTTCTTAAGGTGGCGGAAGAAAGTGGGTGATGCTGAG	4102
Qy	3781	acctgaagatgtgaccttgcgcagcaagaacgaacggcggcctctcggggacaagaagc	3840
Db	4103	ACCTCAAGATGATGACTTGCACGACGAAGACGAAGACGGCGGCTTGGGGACCAAGACAGAC	4162
Qy	3841	tgctctgcgcgttcaactgaagaatgtatgtctgtatccaaatgtatctgtacatagacca	3900
Db	4163	TGCTCTGGCCGCTTCACTGAAGATGATGCTGCTGATTCCAAATGATTCCTGACTATACACCA	4222

Qy	3901	gaatccagagagacgaactgtcctcagttggatgtagtgagcaaaaggtccctaacagttga	3960
Db	4223	GAATCCAGAGAGACAGACTTGTCTCACTGGGATGGATGGCAAGGGTCTCTACCGAGTAA	4282
Qy	3961	gagctggaacttacaagcaacagtttctgagccctttgttgaagaaagcgtcaattggc	4020
Db	4283	GGCTGGAAACTTACACAGCAACAGTTTGGGCCCTTTGTGTGAAGACATGCTAATTGGC	4342
Qy	4021	agacgagctcgaaagatattttctcgaatctgtctgcagctgtgttctgtcatt	4080
Db	4343	AGACGAGCTCGAAAGATTTTGTGTGATGTGCTTGGCAGCTGTGTGTCTGATTT	4402
Qy	4081	goccttctgttcagccctgacatcgtgtgcaccccttctggcaagtaccacagctggaattccg	4140
Db	4403	GCCCTTGTGTTCACCCCTGATTCGTGGCCACCTTTGGCAAGTACCACCTCTGGAACCTTCAG	4462
Qy	4141	cccttgatgtacaacggaacagtagacacatttgcacgaatagtctccttgagacaagga	4200
Db	4463	CCCTTGAGTGTCAACGACGACAGTACACTTTGTTCACGAAATGATGCTCCGAGACACGGCA	4522
Qy	4201	acccttgaaactcttaaacgcccctaccacaaagacctgtgcttcggagaccgctgtatggaa	4260
Db	4523	ACCCTGGAACCTTTAAAGCCCTCACCAAGAACCTGTGCGACCCGCTGTATGGAA	4582
Qy	4261	ggaaacccaatcccaagacagcccttcgaagcagggaggaagatgtgaccactgtgccca	4320
Db	4583	GGAAACCCCAATCCCAAGACACGCCCTGCCAGCCAGGGGAGAAAGATGACACCTGCCCA	4642
Qy	4321	gtccccaagacatacagagactcttccagaatlyggaacttgacatgacagaaccttca	4380
Db	4643	GTTCCTCCAGACCATCATGAGACTCTTTCAGAAATGGAACTGACATGTCAACAACTCTTCA	4702
Qy	4381	cctgcatacgcaggtgtagcagcgacacaaatcgaagaatgtctgtccgtgtgtccccaagg	4440
Db	4703	CCTGTATCCCAAGTGTAGCAGCGACAAAAATCAACAAATGTCTCCTGTGTGTCCCAAGG	4762
Qy	4441	gcaagggggctgcctcctccacaagaacaacaaactgcagatatccttcaagacctg	4500
Db	4763	GCAGGGGGGCTGCTCCTCCCAACAAAGAAACAAACATGACGATATCTTCCAGGACTTG	4822
Qy	4501	acaaggaagaacatctcagataltctgtgtgaagaagtatgtgcagatacatgcaaaagc	4560
Db	4823	ACAGGAAGAACAATTTCGGATTATCTGCTACAAACCTAATGTCAATATATGCCAATAAGC	4882
Qy	4561	ttaagaacaaagatctgtgtgaatgagtttagttagtggcgcttccctgtgtgcagt	4620
Db	4883	TTTAAGAACAAATCTGGGTGTAATGATTTAGGTATGGCGGCTTTCCCTGGGTGAGT	4942
Qy	4621	aactactcaagcacttctcagagtcagaagatlaatgatgtacatcaacaagaatgaagaa	4680
Db	4943	AATACTCAAGCACTTCTCCAGTCAGAGAAGTTAATGATGCCATCAACAAATGAGAA	5002
Qy	4681	caactaaagctgtgccaagaagaagttcgtgagatctcgtttcctaagcgttggaaagatt	4740
Db	5003	CACCTTAAAGCTGTGCCAAGGAAGTTTGTGCAGATCGATTTTCTCAACAGCTTGGAAAGATT	5062
Qy	4741	atgcacgagcttgacaaccaagaataaatgtcaaggtgtgttcaataaacaaggtctgcac	4800
Db	5063	ATGACAGGACTGTGCACCCAGAAATTAATGTCAAGTGTGTTCAATATACAAAGGCTGCGAT	5122
Qy	4801	gcaactcagctcttcttcgaaigtatcaacaagaatgcatctctccggccaactgtgaaag	4860
Db	5123	GCATATAGCTTTTCTTAATAGTATATACAAATAGCCATTTCTCGGGCCAACTGTCAAAAG	5182
Qy	4861	ggaggaacccctcagcatlatggaattactgtcttcaatcatcccttgatcttcccaag	4920
Db	5183	GGAGGAACCCCTAGGCATTATGGAATTACTGTCTTCAATCATCCCTGATATCTCCAAAG	5242
Qy	4921	cagcagcttctcagaggtggtctctgtatgacaacatcagttgagtgctctgtgtgcacatgt	4980
Db	5243	CACACACTTTCAGAGTGGCTCTATATACAAATCATGGATGATCTCTTGTGTCAATCTGT	5302

QY 4881 gtaacatcttgcgaatgctccctgcctccagcagcttgcgtatctcctgataccagagcgg 5040
|||||
Db 5303 gtcattctttgcaattgctcttgcctccagccagcttgcgtatctcctgataccagagcgg 5362
|||||
QY 5041 gtcagcaagcaaaacacccgcagcttgcgtatctcctgataccagagcgg 5100
|||||
Db 5363 gtcagcaagcaaaacacccgcagcttgcgtatctcctgataccagagcgg 5422
|||||
QY 5101 tctaatcttgcgtatctcctgataccagagcgg 5160
|||||
Db 5423 tctaatcttgcgtatctcctgataccagagcgg 5482
|||||
QY 5161 tctaatcttgcgtatctcctgataccagagcgg 5220
|||||
Db 5483 tctaatcttgcgtatctcctgataccagagcgg 5542
|||||
QY 5221 tctaatcttgcgtatctcctgataccagagcgg 5280
|||||
Db 5543 tctaatcttgcgtatctcctgataccagagcgg 5602
|||||
QY 5281 tctaatcttgcgtatctcctgataccagagcgg 5340
|||||
Db 5603 tctaatcttgcgtatctcctgataccagagcgg 5662
|||||
QY 5341 tctaatcttgcgtatctcctgataccagagcgg 5400
|||||
Db 5663 tctaatcttgcgtatctcctgataccagagcgg 5722
|||||
QY 5401 tctaatcttgcgtatctcctgataccagagcgg 5460
|||||
Db 5723 tctaatcttgcgtatctcctgataccagagcgg 5782
|||||
QY 5461 tctaatcttgcgtatctcctgataccagagcgg 5520
|||||
Db 5783 tctaatcttgcgtatctcctgataccagagcgg 5842
|||||
QY 5521 tctaatcttgcgtatctcctgataccagagcgg 5580
|||||
Db 5843 tctaatcttgcgtatctcctgataccagagcgg 5902
|||||
QY 5581 tctaatcttgcgtatctcctgataccagagcgg 5640
|||||
Db 5903 tctaatcttgcgtatctcctgataccagagcgg 5962
|||||
QY 5641 tctaatcttgcgtatctcctgataccagagcgg 5700
|||||
Db 5963 tctaatcttgcgtatctcctgataccagagcgg 6022
|||||
QY 5701 tctaatcttgcgtatctcctgataccagagcgg 5760
|||||
Db 6023 tctaatcttgcgtatctcctgataccagagcgg 6082
|||||
QY 5761 tctaatcttgcgtatctcctgataccagagcgg 5820
|||||
Db 6083 tctaatcttgcgtatctcctgataccagagcgg 6142
|||||
QY 5821 tctaatcttgcgtatctcctgataccagagcgg 5880
|||||
Db 6143 tctaatcttgcgtatctcctgataccagagcgg 6202
|||||
QY 5881 tctaatcttgcgtatctcctgataccagagcgg 5940
|||||
Db 6203 tctaatcttgcgtatctcctgataccagagcgg 6262
|||||
QY 5941 tctaatcttgcgtatctcctgataccagagcgg 6000
|||||
Db 6263 tctaatcttgcgtatctcctgataccagagcgg 6322
|||||
QY 6001 tctaatcttgcgtatctcctgataccagagcgg 6060
|||||
Db 6323 tctaatcttgcgtatctcctgataccagagcgg 6382
|||||
QY 6061 tctaatcttgcgtatctcctgataccagagcgg 6120
|||||

Db 6383 gttggcagaggttgcgtatctcctgataccagagcgg 6442
|||||
QY 6121 tctaatcttgcgtatctcctgataccagagcgg 6180
|||||
Db 6443 tctaatcttgcgtatctcctgataccagagcgg 6502
|||||
QY 6181 gttggcagaggttgcgtatctcctgataccagagcgg 6240
|||||
Db 6503 gttggcagaggttgcgtatctcctgataccagagcgg 6562
|||||
QY 6241 gttggcagaggttgcgtatctcctgataccagagcgg 6300
|||||
Db 6563 gttggcagaggttgcgtatctcctgataccagagcgg 6622
|||||
QY 6301 tctaatcttgcgtatctcctgataccagagcgg 6360
|||||
Db 6623 tctaatcttgcgtatctcctgataccagagcgg 6682
|||||
QY 6361 gttggcagaggttgcgtatctcctgataccagagcgg 6420
|||||
Db 6683 gttggcagaggttgcgtatctcctgataccagagcgg 6742
|||||
QY 6421 tctaatcttgcgtatctcctgataccagagcgg 6480
|||||
Db 6743 tctaatcttgcgtatctcctgataccagagcgg 6802
|||||
QY 6481 tctaatcttgcgtatctcctgataccagagcgg 6540
|||||
Db 6803 tctaatcttgcgtatctcctgataccagagcgg 6602
|||||
QY 6541 tctaatcttgcgtatctcctgataccagagcgg 6600
|||||
Db 6863 tctaatcttgcgtatctcctgataccagagcgg 6922
|||||
QY 6601 tctaatcttgcgtatctcctgataccagagcgg 6660
|||||
Db 6923 tctaatcttgcgtatctcctgataccagagcgg 6822
|||||
QY 6661 gttggcagaggttgcgtatctcctgataccagagcgg 6720
|||||
Db 6983 gttggcagaggttgcgtatctcctgataccagagcgg 7042
|||||
QY 6721 gttggcagaggttgcgtatctcctgataccagagcgg 6780
|||||
Db 7043 gttggcagaggttgcgtatctcctgataccagagcgg 7102
|||||
QY 6781 gttggcagaggttgcgtatctcctgataccagagcgg 6840
|||||
Db 7103 gttggcagaggttgcgtatctcctgataccagagcgg 7126
|||||
RESULT 6
AX060898
LOCUS AX060898 10474 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 7 from Patent WO0078971.
ACCESSION AX060898
VERSION AX060898.1 GI:12406275
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 10474)
AUTHORS Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
TITLE Atp binding cassette transporter protein abcl polypeptides
JOURNAL Patent: WO 0078971-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source
1..10474
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others

QY	2101	gugygcaccccgaaagtttagaaccgcgcgcctacagtgatcccaagcgtggtgtgtgc	2160
Db	2423	gtggctatcctcgaattttggaAAACCTCCTCCCAAGATCATCCAGCGCTGGTTGTGC	2482
QY	2161	ttccctccgctgtttgcctgtgttagaactccctcaagtcctcgttctgttttagcaacttc	2220
Db	2483	tttcctgtccggttttgcctgtgtgttACAACTCTGCAgtccttctcgtATTAGCAACTCTTC	2542
QY	2221	ttccagagccaactgtgcagcagcctgtgtgtgtgatcatctacttcaagcgtctagctgcc	2280
Db	2543	ttccAAGCCAAcctmGCCAGCGCTGTGGGGCATCATCTTCACTTCAcGCTGTAACCTGGCC	2602
QY	2281	taagctccgcttctgtgtgttagcttagcagactaagtggtgcttaacactaaagctctgcagc	2340
Db	2603	ttAGCTCCTgtgtgtgtgcAGTGGCAAGCACTAGCTGGGCTTCAcACTCAAGATCTTCCCTTAGC	2662
QY	2341	ctgcgtctccctgtgtgccttttggtgttgcgtctgtatcttgccttttagaagaag	2400
Db	2663	ctgctgtccctgtgtgccttttggtgttgcgtctgtatcttgccttttagaagaag	2722
QY	2401	ggcatctgtgaatgcagctgtggacaacctgtttgaagctcctgtgtgaagaatgtgttcaat	2460
Db	2723	ggcATTGGAgtgcAGTGGGAACACTTTTGAAGTCTGTGGAGGAAGATGGCTTCAAT	2782
QY	2461	ctccacactctgcatactccatgatgtgttttagaaccttcccttaagtggtatataccg	2520
Db	2783	ctCACCACTTGAGATCTCAGATATGTCTGTGACACCTTCTCTATAGGGGTATAGCTGG	2842
QY	2521	tacatttgagcgtgtccttccagccagtlacggaatcccaagcccttgatatttccctgc	2580
Db	2843	ttACATTtGAGGCTgtCTTTCAGGCGAGTACGGAAATCCAGAGCCTTGATTTTCTTTC	2902
QY	2581	accaagctccctcctgtgtttgcgaggaagaatgtgaagaagcaccctggttccaaccag	2640
Db	2903	ACCAAGTCTTCTGTGTGTGGCGAGAAAGTGAATGAAGAAAGCAcCCTGTGTTCAACAG	2962
QY	2641	aagaaatgtcaagaatctgcattgtgaggtgaagcccaaccacttgaagctgtgctgtgc	2700
Db	2963	AAGAAATGTCAgAAATCTGATGTGAGAGGAACCAcCACTTGAACCTGGGCTGTCC	3022
QY	2701	attcgaaacctcgtgtaaaagctctaccgaatgtggaatgtgtcgttcgatgtgcctgcga	2760
Db	3023	ATTCAgAAcCTGTGTAAAAAGTCTACCGAAGATGGAGATGAAGTGGCTGTGTGATGGCTGGCA	3082
QY	2761	ctgaattttttagtggtgcagatcacactccctccctgcggccacaaatgtgagcggtgaagc	2820
Db	3083	CTGAATTTTATAGAGGCCCAgATCACCCTCTTCTGTGGCCAAATAGGAGCGGGAAAGC	3142
QY	2821	accacacatgtcaatcctgcagcgggtgtgtcccccagacctgtgtgtgaacgcgtctaatcctg	2880
Db	3143	ACCAcCAATGTCAATCTGAGCCGGGTGTTCcCCCGACCTGGGCAcCGCTTACATCTCG	3202
QY	2881	ggaaaaaaccttgcctctgtgagtgaacaccacccagcagaaacctgtgtgtgtgtcccaag	2940
Db	3203	GGAAAAAGCACTGTGCTGTGAGATGACACCACTTCGGGCAAACTGTGGGGTGTGTCTCCAG	3262
QY	2941	cataagctgtcgttttagacatgcagctgcagatgtgcgaagaacaactgtgttctatagccgcttg	3000
Db	3263	CATAAGCTGTGTTTGTGACATGCTGCAATGTGTCAAGAAACACTGTGTTTATGCCCCGTTG	3322
QY	3001	aaaggtcctctgtgaagaacgttgaagcggagatgtgaagcagatgtgcctgtgaatgtgtgt	3060
Db	3323	AAAAGGCTCTCTAGAGAGCAcGTGAAGGGCGGAGATGTGAGAGATGTGCCCTTGATGTGGT	3382
QY	3061	tttgcacccaagcaagctgtgaaaaacaaanaaacgcagctgttaagttgaaatgcagagaag	3120
Db	3383	TTTGCACTCAAGCAAGCTGAAAAACAAACAAACCAcGCTGTAAAGGTGAATGTCAAGAAAG	3442
QY	3121	ctatcgtgtgccttgacctgtgtcgtgtgtatcaagatgtgtcatctctgtatgaaaccaaa	3180
Db	3443	CTATCTGTGcCTTGTGcCTTGTGTGGGGATCTAAGGTTGTGATCTTGTGATGAACCCACA	3502

QY	3181	gctggtgtgagacccttaaccccgagggagaaatagggagctgtctgtgaataacgacaa	3244
Db	3503	gctggtgtgagacccttactcccgacggggaaataggagctgtctgtgaataacgacaa	3562
QY	3241	ggcgagacattatctctctcaacacacaaatgtaagcggaagtccttggggagcag	3300
Db	3563	ggcgagacattatctctctcaacacacaaatgtaagcggaagtccttggggagcag	3622
QY	3301	attgcacatcatcccatagggaagctgtgctgtgtggccctccctgtcttctgaagac	3360
Db	3623	attgcacatcatcccatagggaagctgtgctgtgtggccctccctgttcttgaagac	3682
QY	3361	cagctgtggaaacagcctactaccctgtgacatgylcaagaagaatgtgaaatcctccctcagt	3420
Db	3683	cagctgtggaaacagcctactaccctgtgacatgylcaagaagaatgtgaaatcctccctcagt	3742
QY	3421	tccctcagaagaacagtaagtagcactgttccacttgaagaagaaggaagatgttcttcag	3480
Db	3743	tccctcagaagaacagtaagtagcactgttccacttgaagaagaagaaggaagatgttcttcag	3802
QY	3481	agcagttctcgaatcgtgctgtggagcgaacaaatgaagatgaaacgctgtgacaacgcgatgtc	3540
Db	3803	agcagttctcgaatcgtgctgtggagcgaacaaatgaagatgaaacgctgtgacaacgcgatgtc	3862
QY	3541	tctgtcatctccaactcatatagaacaaatgtgtctggaagcccgctgtgtgaaagacata	3600
Db	3863	tctgtcatctccaactcatatagaacaaatgtgtctggaagcccgctgtgtgaaagacata	3922
QY	3601	gggcaatgacctcgaactatgtctcctcaatgaagctcgtcaagaaggaagaccccttgtgaa	3660
Db	3923	gggcaatgacctcgaactatgtctcctcaatgaagctcgtcaagaaggaagaccccttgtgaa	3982
QY	3661	cccttcatgtgatgtgatgacccgctctcagaccctgtggacatttcaatgatagtcatcca	3720
Db	3983	cccttcatgtgatgtgatgacccgctctcagaccctgtggacatttcaatgatagtcatcca	4042
QY	3721	ggagcagaccctggagaaataatccctaaggtggccgaagaagatgggtgtgatgtctgag	3780
Db	4043	ggagcagaccctggagaaataatccctaaggtggccgaagaagatgggtgtgatgtctgag	4102
QY	3781	accctagaatgtactctgtccagaagaacgaaacagcgccctctcggggagacaagcagac	3840
Db	4103	accctagaatgtactctgtccagaagaacgaaacagcgccctctcggggagacaagcagac	4162
QY	3841	tgctctggccggttcacttgaagaatgtatgtctgcatccaatgtatcttcgaatagaacca	3900
Db	4163	tgctctggccggttcacttgaagaatgtatgtctgcatccaatgtatcttcgaatagaacca	4222
QY	3901	gaatccaaagagacagactcgtcccaatgtggatgtgaatgtgaagaaggttccaccaggttga	3960
Db	4223	gaatccaaagagacagactcgtcccaatgtggatgtgaatgtgaagaaggttccaccaggttga	4282
QY	3961	ggctgtgaaacttacagaacaacagttgtgtgccccttltgtgaagaagactgtctaattgcc	4020
Db	4283	ggctgtgaaacttacagaacaacagttgtgtgccccttltgtgaagaagactgtctaattgcc	4342
QY	4021	agaacggagctggaaaggaatlttltgtcgaatgtgtcttggccaagctgtgttgtctgcatc	4080
Db	4343	agaacggagctggaaaggaatlttltgtcgaatgtgtcttggccaagctgtgttgtctgcatc	4402
QY	4081	ggccttgtgttcagcctcgtatcgtgcacaaccttltggcaagtaaccacagccttgaacctcag	4140
Db	4403	ggccttgtgttcagcctcgtatcgtgcacaaccttltggcaagtaaccacagccttgaacctcag	4462
QY	4141	cccttgatgttaacaaacgaaacagtaacaaatltgtccagcaatgatgtccttgaagacggga	4200
Db	4463	cccttgatgttaacaaacgaaacagtaacaaatltgtccagcaatgatgtccttgaagacggga	4522
QY	4201	acccttgaacctttaaagcgcctccacaaagaccccttgccttcggaaaccgctgtatggaa	4260
Db	4523	acccttgaacctttaaagcgcctccacaaagaccccttgccttcggaaaccgctgtatggaa	4582
QY	4261	ggaacccaatccagacacgccttgcagagcagggagggagaaagtgtgacaactgtgcca	4320

4583 GGAAGCCATCCAGACAGCCCTGCCAGCGAGGAGAGAGTGGACCACTGCCCA 4642
4321 gtcccccaacatcatatgaactctccagaa tggaaactgagaaatcagaacctca 4380
4643 GTTCCCAACCATCATATGAACTCTTCCGAAATGGGAATGACATGAGAACCTTCA 4702
4381 cctgcatacagatgtagcagcagaacaaatcaagaagaatgctgctgtgtgtcccaagg 4440
4703 CCGCATGCCAGTGTAGCAGCAGCAAAATCAAGAAGATGCTGCTGTGTGTCCAGAGG 4762
4441 gcaaggagctgctcctccacaagaacaaacacgacgatatcctcctaaggacctg 4500
4763 GCGAGGGGCTGCTCTCCACAAAGAAACAAACACTGCGATATCTTGAAGACCTG 4822
4501 acagaagaacatctcgatatactgtagaagcagatgtagaatacagaacaaagc 4560
4823 ACGAGGAAGACATTTGGGATTTATCTGGTGAAGAGTATGTGAGATCATAGCCAAAGC 4882
4561 ttaagaacaagaatctggatgaatgagtttagttagtgagcgtcttcctgggtgtcagt 4620
4883 TTTAAAGAACAGATCTGGGTGATGATTAGGTATGCGGCTTTTCCCTGGGTGCACT 4942
4621 aatactcaagcactcctcccgatcaagaagatgaatgtagcacaacaagaagaaga 4680
4943 AATACTCAAGCACTTCTCCGAGTCAAGAACTTAATGATGCCATCAACAAATGAGAA 5002
4681 caccataagctggcagaagacagttctgcagatcgaattctcaacacgttggaaagatt 4740
5003 CACCTTAAGCTGGCCAAAGACAGTCTGAGATCGATTTCTCAACAGCTTGGGAAGATT 5062
4741 atgacagagctgagacccagaataatgtccaaggtgtagttaaataaaggagctgagat 4800
5063 ATGACAGGAGTGGACACCAAAATATGTCAGGTGTGTTCAATATACAAAGGCTGCAAT 5122
4801 gcaatcaagctcttccctgaatgtagcaacaatgacatctccgggccaacctgcaaaag 4860
5123 GCATCAAGCTCTTCTCGAATGTCATCAACAATGCCATTCTCGGGCCAACTGCAAAAG 5182
4861 ggaagaagaacctagcaatataatgaatgaatgaatgaatgaatgaatgaatgaatga 4920
5183 GGAAGAGAACCTTGAATGAAATTAACGCTTTCAATCATCCCTGAAATTCACCAAG 5242
4921 caacagctcagaggtgagctcgaatgaacacatcagtgatgtctgtgtcactgt 4980
5243 CAGCAGCTCTCAGAGGTGAGCTGTGATGACCACTCACTGATGATGCTGTGTGTGATCTGT 5302
4981 gtaactcttgcaatgtcctcgtcccaagcagcttgtagtctcgtatctcgtatccagaagc 5040
5303 GTCATCTTGTCAATGTCTTGTCTGTCGCCAGCCAGCTTGTCTGATCCGATCCAGAGCG 5362
5041 gtcagcaagaacaaacccctgcagatcgaatgaatgaatgaatgaatgaatgaatgaat 5400
5363 GTTCAGCAAGCAAAACCCCTGCAAGTTCATGATGATGATGATGATGATGATGATGATG 5422
5101 tctaattctgtaggaatgtagcaatgaatgtagtctcgtcccaacatgtagtcaatc 5160
5423 TCTAATTTTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5482
5161 ttaactgtctcgaagcaagctcgaatgtagtctcgtcccaacatgtagtcaatc 5220
5483 TTTCACTGTCTTCCAGCAAGTTCATGATGATGATGATGATGATGATGATGATGATG 5542
5221 ctactctgtgtagtggtagtgaatcaacacccctcgaatgtagtcaatc 5280
5543 CTACTTTTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5602
5281 aagaatcccaagcagaactatgtagtgcacacagcgtgaacgtctcgaatgtagtcaat 5340
5603 AAGATCCCAAGCAGCAGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 5662
5341 ggaagcgtgtagcactctgtgtagtgcgtgtagcgtgtagcgtgtagcgtgtagcgtgtag 5400

5663 GCGAGCGGCGCCACCTTTGTGCTGAGCTGTTCACCGACAAATGAAGTGAATATATCAAT 5722
5401 gatactcgaagctcgtgtctgtatctcccaatcttgcctgggaagaggtcatc 5460
5723 GATATCCGAAAGTCCGTTCTTGTATCTTCCACATTTTGTGCGGAGCAGGCTCATC 5782
5461 gacatgtgaaacaaacagcaatgagctgtagcctgtgaaaggttgggaaatcgtct 5520
5783 GACATGTGAAAAACCAAGCAATGCTGATGCTCCGCAAAAGTGTGGGAAATCGCTTT 5842
5521 gttcaacatatacttggagcttggtagcagaacctctgcacatggtcgtggaagg 5580
5843 GTGTCACCATTTATCTTGGAGCTGTGAGAGCAAACTCTTCCGCAAGCGCTGGAAGGG 5902
5581 gtgtgtctctcccatctacgtctgtagcagaagatctctcagagccagacct 5640
5903 GTGCTTCTTCCCTCATTAACGTTCTGTGATCCAGTACAGATTTCTTCAATGAGCCAGACT 5962
5641 gtaatgcaagctacatcctcgtgaatgaatgaatgaatgaatgaatgaatgaatgaat 5700
5963 GTAATTCGAACGATATCTCTCTGATGATGATGATGATGATGATGATGATGATGATG 6022
5701 agaatcttgaatgtagcagcagaatgaatcctagaatcaagaggtgtagcagaata 5760
6023 AGAATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6082
5761 tataagaagaagcagaacccgtcgttgaagaggttgcgtggacatccctcgtgtgag 5820
6083 TATAGAAGGAAGCGGAACCTGCTGTGTACAGATTTGCGTGGCATTCCTCTGTGTGAG 6142
5821 tgccttggcctccttgagatgaatgaggttgaatgaatgaatgaatgaatgaatgaat 5880
6143 TGCTTTGGGCTCTGAGGATTAATGAGGCTGGAATATCATCACTTCAAGATGTTAA 6202
5881 ggaatatacactgtagcagaagagatgtagtcttccatcaaaataagatcttcaaac 5940
6203 GAGATATACCACTGTTACAGAGAGATGCTTCTTAAACAAATAGATATCTTATCAAC 6262
5941 atccatgaatatacagaacatgagctacagctcagtttagatccatcaacagagctg 6000
6263 ATCCATGAAGTATCATCAGAACATGGGCTACGCTCCTGATTTGATGCCATCAGAGCTG 6322
6001 ttgaactgtagaagaacacagctgtagtcttgcctcttgaagagaggtcccaagagaaga 6060
6323 TTGACTGGGAGAGAACACTGAGATCTTGTGCTTTGAGAGGAGTCCAGAGAAAGAA 6382
6061 gttgcaaggtgtgtgaggtggcgaatcgaacacgtggcctcgtgaagtagtgaagaaga 6120
6383 GTTGCAGAGGTTGTGAGTGGGCGATTCGGAATCTGGGCTGTGAATGAGAAAGAA 6442
6121 tatgctgtagaactatgtaggaagcaacaacgaagctctctacagcagatgtagt 6180
6443 TATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6502
6181 ggcgggctcctgtgtgttcttgatgaatcccaacacgaagatgtagtcccaagccgg 6240
6503 GCGGGGCTCTCTGTGTCTTGTGATGAATCCACACAGCATGAGTGAATCCCAACCCGG 6562
6241 cgtctctgtagaattgtgcccgaatgtgtcgaagagagagtagtcaatgtagtca 6300
6563 CGGTTTGTGAAATGTGCTCAATGTTGCAAGAGAGGAGATGATGATGATGATGATG 6622
6301 tctcatagtagaagaatgtagaagctcttgcacatgaatgtagaagtagtcaatgtag 6360
6623 TCTCATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6682
6361 aggttagtgccttggaggtgtccagcatctaaataaaggttggagatgtagtca 6420
6683 AGGTTACAGGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 6742
6421 atagttgtagaagtagcagaagtagtcaacccggaactggaagcgtgtagcagatctt 6480
6743 ATAGTTGTAGGAATATGACAGGATGATGATGATGATGATGATGATGATGATGATGAT 6802

[illegible]

RESULT	7					
AX060900						
LOCUS	AX060900	10474 bp	DNA	linear	PAT 22-JAN-2001	
DEFINITION	Sequence 9 from Patent WO078971.					
ACCESSION	AX060900					
VERSION	AX060900.1	GI:12406276				
KEYWORDS						
SOURCE	human.					

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	Source
1 (bases 1 to 10474)	Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.	ATP binding cassette transporter protein abcl polypeptides	Patent: WO 0078971-A 9-28-DEC-2000;	CV THERAPEUTICS, INC. (US)	Location/Qualifiers
					1..10474
					/organism="Homo sapiens"
					/db_xref="taxon:9606"
					2907 a 2304 c 2415 g 2844 t 4 others
					BASE COUNT
					ORIGIN

QY	301	atttggtgcgcgcgtcttctcaagatgcctcgagggcttcttttataagccgaagaagacac	360
Db	623	ATTGTGECTCGCCTTTCTCAAGATGCTGGAGGGCTTTCTTTATACAGCCAGAAAGACACC	682
QY	361	agcatgaaggaatgcgcaaaagttctbagaacattacaagaagatacaagaatcacgtca	420
Db	683	AGCATGAAGGACATGCGCAAAAGTTCTGTGAAACATTACAGCATGATCAAGAAATCGACTCA	742
QY	421	aacttgaagcttcaagatttccctggtyggacaatgaaaccttctctggttctctataaac	480
Db	743	AAC TTGAAGCTTCAAGATTTCTCTGTGTGACAATGAAACCTTCTCTGGTTCCTATATATAC	802
QY	481	aacctctctctcccaaaatctactgtygacaagaatgcttgagggctatgttcaatccac	540
Db	803	AACCTCTCTCTCCCAAAAGTACTGTGTGACAAGATGCTGAGGGCTATGTCTATTCTCCAC	862
QY	541	aaggtatttttgcaagctacagattacatttgaaagttctgtgaaatgatatgaatcaatca	600
Db	863	AAGGATTTTGTTCGAAGGCTACCATCTTCAATTTGCAAGTCTGTGCATATGATCAAAATCA	922
QY	601	gaagatgatttcaacttgytgacccaagaagttcttgaagctttgagccttaccacaagag	660
Db	923	GAAAGATGATTTCAACTTGGTGACCAAGAAAGTTTCTGAGCTTTGTGGCTTACCAAAAGAG	982
QY	661	aaactgctgcgaagcagcgagtaacttcgttccaagaatgagacatccatgaagccaatctg	720
Db	983	AAACTGCTGCAGACAGACGCGAGTACTTCTGTTCCAAATGACATCTCTGAAGCCATTCCTG	1042
QY	721	aaaacactaaacttbaatctccctctccgagcaagaagagctgctgtaagcccaaaaaca	780
Db	1043	AAACACTAAACTCTBACTACTCTCCCTTCCGAGCAAGAGAGCTGGCTGAACCCACAAAATCA	1102
QY	781	tgcgtgcatagtctcttggagctctbgycccaagagctgttcaagatgaagcctgaggttac	840
Db	1103	TTCGTGATAGTCTTTGGGAGCTCTGGCCAGAGACTTTCAGATAGAAAGTCGGAGTATAC	1162
QY	841	atggcacagagagtgatgatttctgaccaatgtyaacagcttcaagctcctccaaccaatc	900
Db	1163	ATGCGCACAGGAGGATGATTTCTGTACCAAGTCAACAGCTCCAGCTCTCCACCCAAATTC	1222
QY	901	taccagagctgctctcgtattatgctctgtyggacatcccgagagggggggggtctaaagataag	960
Db	1223	TACCAAGGCTGTGTCGTATTTGTGTGGGGGATCCCGAAGGAGGGGGGCTGAAGATCAAG	1282
QY	961	tctctcaactggtatbgaagacaacatacaaaagccctctttgsgagaatgycactgag	1020
Db	1283	TCTCTCAACTGTGATGAGGACAACACTACAAAGCCCTTTGTGGAGCAATGGCACTGAG	1342
QY	1021	gaagatgcttgaacctctatgaacaactcaacaaccccttactgtaatgatttataagag	1080
Db	1343	GAAAGTGTGAACCTTCTATGACAACACTTACAACTCCTTACTGCAATGATTTGATGAGAG	1402
QY	1081	aatttgaagcttagtctctcttcccgcatlatacttgnaaagctctgaagccgctgcgtt	1140
Db	1403	AATTGTGAGTCTTACTCTCTCTTCCCACTTATCTGAAAGGCTGAAACCCCTGCTGCTGT	1462
QY	1141	ggagaagatcctgataaactgtaacatccagccaagaagcaggtatagtgcgtgaagtgaaac	1200
Db	1463	GGAAGAATCTCTGATATACCTGTGACACTCCAGCCACAGGCAAGCATGTATGGCTGAGGTGAAAC	1522
QY	1201	aagaccttcaaggaactgagctgtgtctcactatgtcgaagagcatbtyggaagaaactcagc	1260
Db	1523	AAGACCTTCCAGGAACGTGGCTGTGTTCCATGATGTGAAAGGATGTGGAGGAAGTCAACTCAGC	1582
QY	1261	cccaagatctggacattcatbgaagaacagccaagaatgagacctgttccgaaatgctgtg	1320
Db	1583	CCCAAGATCTGGACCTTCAATGAGGAACACCAAGAAATGAGACTTGTCCGATCTGCTTGG	1642
QY	1321	gaacgagggagacaatgacaaccttbtggaaacagcagtttggatctttagatcttgaacagcc	1380
Db	1643	GACAGCAGGGACATATGACACTTTTGTGGAAACGACAGTTGGATGGCTTATGATTTGAGCAGCC	1702

Dh 3863 TCTGATCTCCAACTCATGAGGAGAGCATGTGTCTGAGGCCGGCTGTGGAACATA 3922
Qy 3601 ggagatgagctgacctatgtgtcctatagaagctgtctaaaggagagccctgttgaa 3660
Dh 3923 GGGGATGAGCTGACCTATGTGTCTCCATATGAACTGCTAAAGGAGGAGCTTTGTGAA 3982
Qy 3661 cctctcaatgagatgtgacctgacctgacctgacctgacctgacctgacctgacctg 3720
Dh 3983 CTCTTTCATGAGATGTGATGACCGGCTCTCAACCTGAGGATTTCTATGTCATCTCA 4042
Qy 3721 gagaagacctgagaagaataatctcaaggtgagccgaagaagatgaggtgagtgag 3780
Dh 4043 GAGAGGAGCCCTGGAAGAAATATCTCAAGTGGCCGAAGAGAGTGGGTGAGTGGTGA 4102
Qy 3781 acctcaatgtgacctgtgacctgacctgacctgacctgacctgacctgacctgacct 3840
Dh 4103 ACCTCAATGTGATCTGTGACGCAAGCAAGCAAGCGGCGCTTGGGGCAAGAGAGC 4162
Qy 3841 tgtcttgcaccttcaatgagatgagtgctgctgctgctgctgctgctgctgctgct 3900
Dh 4163 TGTCTTGCCCGTTCACTGAGATGATGCTGCTGATCCAAATATCTGATAGACCA 4222
Qy 3901 gaatacgaagaagaagactgtctcagtgagatgagcaagggctcctcagtgagaa 3960
Dh 4223 GAATCCAGAGAGACACTGTCTCAGTGGGATGATGGCAAGGGCTCTACAGTGAAA 4282
Qy 3961 gactggaacttcaacagcaacagttgtgagcccttctgagaagaagactgctaatgc 4020
Dh 4283 GCGTGAATCTTACACGCAACAGTTGTGGCCCTTTGTGGAGAGACGCTAAATGGCC 4342
Qy 4021 agacgagatgagaagaatltttgtcagatgtgtctgacctgtgtgtgtgtgtgtgt 4080
Dh 4343 AGAGGAGTGGAGAAAGATTTTGTCTCAGATGTCTGCGACCTGTTGTGTGTGTGT 4402
Qy 4081 gacctgtgtcagctgt 4140
Dh 4403 GCGCTGT 4462
Qy 4141 cctctgagatgacaagaacagatcatgtgtcagcaatgtgtgtgtgtgtgtgtgtgt 4200
Dh 4463 CCTGT 4522
Qy 4201 acctgtgaaactttaaagccctcacaagaagccctgtgtgtgtgtgtgtgtgtgt 4260
Dh 4523 ACCCTGGAATCTTAAACGGCCCTCACCAAGAACCTGCTGGGACCGCTGTATGAAA 4582
Qy 4261 ggaacccaatcccaagaacagccctgtcagagagggagagaagtgtgacaactgtcc 4320
Dh 4583 GGAATCCCAATCCCAAGACAGCCCTGCCAGCGAGGAGGAGAGAGTGGACCACTGCCCA 4642
Qy 4321 gtctcccaagaacatgaagactcttcagaatgtggaactgtgacaatgtcagaacct 4380
Dh 4643 GTTCCCAAGACCATGTGAGACCTCTTCCAGAAATGGGAATGTGACAAATGACAACTTCA 4702
Qy 4381 cctgtcagtgagtgagagcgaacaaatcgaagaatgtctcgtgtgtgtgtgtgtgt 4440
Dh 4703 CCGCATGCGCATGTGTGAGCGAGCAAAATCAAGAAATGTCTGCTGTGTGTGTGTGT 4762
Qy 4441 gcaagggagctgtcctcctccacaagaanaaacaacactgtcagatatcctcaagact 4500
Dh 4763 GCAAGGGGGCTGCTCTCTCCACAAAGAAAACAAACACTGCAGATATCTCTTAGAGCC 4822
Qy 4501 acagaagaagaacatttggattatctgtgtgaagagatgtgtcgaatcagaacaaagc 4560
Dh 4823 ACAGGAGAGAAATTTGGATTATCTGTGTGGAAGACCTATGTGCAATATATACCAAAAGC 4882
Qy 4561 ttaagaagaagaatctgt 4620
Dh 4883 TTAAGAAGAACATCTGGGTGAATGAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 4942
Qy 4621 aatctctgaagcaactcctcctcagatcaagaagttaatgtgtgtgtgtgtgtgtgt 4680
Dh 4943 AATACTCAAGCACTTCTCTCCGAGTCAAGAAATTAATGATGCATCAACAAATGAAGAA 5002

Qy 4681 caactaaagctgtgcaagaagacagctctcagatcagatcttccaacagctgtggaatlt 4740
Dh 5003 CACCTTAAAGCTGGCCAAAGACAGTTCTGAGATGATTTCTCAACAGCTTGGAAAGATT 5062
Qy 4741 atgaagagctgtgacaacgaagaataatgtcaaggtgtgtgtgtgtgtgtgtgtgtgt 4800
Dh 5063 ATGACAGGAGCTGGAACCAAGAAATATGTCAAGGTGTGTGTGTGTGTGTGTGTGTGT 5122
Qy 4801 gcaatcagctcttccctgt 4860
Dh 5123 GCAATCAGCTCTTCTCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5182
Qy 4861 ggaagaacccctagccatatagtgaatctcgtgtgtgtgtgtgtgtgtgtgtgtgt 4920
Dh 5183 CGAGAGAACCCCTAGCCATATGAGATTAATGATTAATGATTAATGATTAATGATTAAT 5242
Qy 4921 cagaagctctcagaaggt 4980
Dh 5243 CAGCAGCTCTCAGAGGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5302
Qy 4981 gtcacttctgcaatgt 5040
Dh 5303 GTCATCTTGTCAATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5362
Qy 5041 gtcagaagaagaacacccctgcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5100
Dh 5363 GTCAAGCAAGCAACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5422
Qy 5101 tcaatttctgt 5160
Dh 5423 TGTATTTTGT 5482
Qy 5161 ttcactgtctcctcagcagaagtcctatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5220
Dh 5483 TTCATCTGTCTTCCAGCAAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5542
Qy 5221 ctacttctgt 5280
Dh 5543 CTACTTTTGT 5602
Qy 5281 aagatcccaagcagaagcctatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5340
Dh 5603 AAGATCCCAAGCAGCCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5662
Qy 5341 ggcagcgt 5400
Dh 5663 GGCAGCGT 5722
Qy 5401 gatacctgtgaagctgt 5460
Dh 5723 GATATCTGAGATCTCGT 5782
Qy 5461 gacatgtgtgaagaacagcgaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5520
Dh 5783 GACATGTGTGAAGAAACCAAGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5842
Qy 5521 gtlcacaatatactgt 5580
Dh 5843 GTGTACCATATTTTGT 5902
Qy 5581 gtagtgttctcctcactactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5640
Dh 5903 GT 5962
Qy 5641 gtaaatgcaagctatctcctgtgaatgagatgaagatgtgtgtgtgtgtgtgtgtgtgt 5700
Dh 5963 GTAAATCAAGAGCTATCTCTGAATGATGAAGATGAAGATGTGTGTGTGTGTGTGT 6022
Qy 5701 agaatctgt 5760
Dh 6023 AGAATTTGT 6082

QY 5761 tatagaaggaagcggagcctgctgttgcagagatttgcgtgggattctctctgtgtgag 5820
 |||||
 Db 6083 TATAGAGGAAGCGGAAAGCCTGCTTTGACAGAGATTTGCGGGGATTCCTCGGTAG 6142
 QY 5821 tgccttggcctccttggaggttaagggcgtgaataatcacaacttcaagaatga 5880
 |||||
 Db 6143 TCGTTTGGGCTCTCGGAGTTATATGGGCTGGAATAATATCATCACTTTCAAGATGTAA 6202
 QY 5881 ggaatatacactgttaccagagagatgcttctccttaacaaatagatccttacaac 5940
 |||||
 Db 6203 GGAGATACACACTGTTACAGAGAGATGCTTCTTAAACAAAATAGTATCTTATCAAC 6262
 QY 5941 accatgaatgatacagaacatgggtctacacgcttcctggttgcatacagaagt 6000
 |||||
 Db 6263 ATCCATGAAGTACATCAGAACATGGGCTACTCCCTCAGTTGATGCCATCAGAGCTG 6322
 QY 6001 ttgactgtgaagagacacgttgaagcttcttgccttctgaagaggtcccaagagaag 6060
 |||||
 Db 6323 TTGACCTGGGAGAGAACAGCTGAGTTCTTGGCCCTTTTGAGAGGAGTCCAGAGAAAGA 6382
 QY 6061 gttgcaaggttgtgtgagtggcgatctggaaactgggctctgtgaagtatgagaaaaa 6120
 |||||
 Db 6383 GTTGGCAAGTGTGTGAGTGGGCGATTCGGAACCTGGGCTGTGAGATGTGAGAAAAA 6442
 QY 6121 tatgctgttaactatagttgagaggaacaaagcaagctctctacagccatggctttgac 6180
 |||||
 Db 6443 TATGCTGTACTATATGTGGAGGCAACAAACCCAGCTCTTACAGCCATGGCTTTGATC 6502
 QY 6181 ggcgggctcctctgtgtgttcttctgtatgaacccacacagagatgaltcccaagccgg 6240
 |||||
 Db 6503 GGGGGGCTCTCTGTGTGTGTTTCTGATGAACCCACACAGCCTGATGCCAACCCCGG 6562
 QY 6241 cggctcttgtgaatgtgtccttaagtgtgttctcaaggaaggaagatcagtaagtctaa 6300
 |||||
 Db 6563 CGGTTTGTGGAATGTGCTCCCTAACTGTGTCGAAGGAGGAGATCACTAGTGTCTTAA 6622
 QY 6301 tccatagataggaagaagtgaagcttctgaactagatgagcaatctgttcaatga 6360
 |||||
 Db 6623 TCTCATAGTATGGAAGATGTGAGCTTTTGACATAGATGGCAATCATGTGTCATGA 6682
 QY 6361 aggttcaaggtccttggcaggtgtccagacatctaaataaagtttggagaatggttata 6420
 |||||
 Db 6683 AGGTTCAGGTCCTTGAGGTGTCAGCATCTPAAAAATAGTTTGAATGGTTATACA 6742
 QY 6421 atagttgtgaagaaagaggttccaaacccggagcttgaagcgttccagagattcttga 6480
 |||||
 Db 6743 ATAGTTGTAGAAATACAGAGGTCCAAACCGGACCTGAGCTGTCCAGATTTCTTGA 6802
 QY 6481 ctgcaatctcctgaaggtgtctaaagaagaacacccgagacatgtctacaatcacagct 6540
 |||||
 Db 6803 CTTCATTTCTGGAAGTGTCTTAAAGAGAAACACCGGACATGCTTACATATCCAGCTT 6862
 QY 6541 ceatcttcatlactctctcgtgcagagataatcagacatcctctccagagcaaaagca 6600
 |||||
 Db 6863 CCATCTTCAATATCTTCTGCGCAGGATATTCAGCATCTCTCCAGAGCAAAAAGCGCA 6922
 QY 6601 ctccaataaagaactactgttcttcaagaagaacacttgaacaaatatttgaacatt 6660
 |||||
 Db 6923 CTCACATTAAGAACTACTGTGTTCTCAGACAAACCTTGACCAAGATTTTGGAACTTT 6982
 QY 6661 gcaagaagcaaaagtgatgaagcaacttaaaagacctcatatcaacaanaacagaca 6720
 |||||
 Db 6983 GCCAAGAGCAAAAGTATGATGACCACTTAAAGACCTCTCATTTACCAAAAACAGACA 7042
 QY 6721 gtagtgaagttgcaagttctcacaatcttctcagaagatgagaagtgaagaagctat 6780
 |||||
 Db 7043 GTACTGACGCTTGCAAGTTCACATCTTTTCTACAGAGATGAGAAAGTGAAGAAAGCTAT 7102
 QY 6781 gtagaagaatcctgtcatcacg 6804
 |||||
 Db 7103 GTATGAAGAAATCCTGTTCAATACG 7126

RESULT 8
 AX092594 7860 bp DNA linear PAT 21-MAR-2001
 LOCUS Sequence 6 from Patent WO0115676.
 DEFINITION
 ACCESSION AX092594
 VERSION AX092594.1 GI:13444651
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 7860)
 AUTHORS Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M.
 TITLE Compositions and methods for modulating hdl cholesterol and triglyceride levels
 JOURNAL Patent: WO 0115676-A 6 08-MAR-2001;
 University of British Columbia (CA) ; Xenon Genetics Inc. (CA)
 FEATURES
 source location/Qualifiers
 1..7860
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 2014 a 1860 c 2008 g 1978 t
 ORIGIN
 Query Match 99.9%; Score 6796; DB 6; Length 7860;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 6799; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 atgagcttctggcctcagctgaagttgctgtgtgagaagaacctcacttccagaagaaga 60
 |||||
 Db 75 ATGGCTGTGGCCCTCAGACTGAGCTTGCTGTGGAGAAACCTCAGTTCCAGAAAGAA 134
 QY 61 caaatatgacgtgttacttgaagttggcctcgtctattatctccatgacatgac 120
 |||||
 Db 135 CAACATGTACGCTGTACTGGAAGTGGCTTGCCCTCTATTATTAATCTTCATCTGATC 194
 QY 121 tctgtcgcgtgagctacccaccctatgaacaacatgaatgccatttccaataaagcc 180
 |||||
 Db 195 TCTGTGGGTGAGTACCCACACCCATGACACATGATGCCATTTTCCAAATTAAGCC 254
 QY 181 atgcccctgcagaagaacatcctccttgggttcaagggtatctcgttaatgccaacaacccc 240
 |||||
 Db 255 ATGCCCTTGCAAGAACCTTCTTGCGGTTCAGGGGATTAATCTGTAAGGCCAACACCCC 314
 QY 241 tgttcgcttaccgacacccctggggaagctcccgaggtgttggaaacttaacaacatcc 300
 |||||
 Db 315 TGTTCCTGTACCCGACCTCTGGGAGGCTCCCGAGTGTGTGGAACCTTTAACAAATCC 374
 QY 301 attgtgcctgcgttcttctcagatgtctggaagcttcttcttatacagccagaagaacac 360
 |||||
 Db 375 ATTGTGGCTCGCGCTGTCTCAGATGCTCGGAGGCTTTTATACAGCCAAAGACACC 434
 QY 361 agcatgaagagacatgcgcaaaagttcttgaagaacattacagcaagatcaagaatcaagctca 420
 |||||
 Db 435 ACCATGAAGAGCATCGCAAAAGTTCTGCAACATTACAGCAATCAAAATTCACGCTCA 494
 QY 421 aacttgaagcttcaagatcttctgtgtgacaatgaagaacctctctgtgttctcatalaac 480
 |||||
 Db 495 AACCTTGAACCTTCAAGATTTCTGTGTGACATGAACACTTCTGTGGTCTCTGATAC 554
 QY 481 aaactctctcccaaaagctctactgttgacaagaatgtcgaaggtcgtatgtcaatctcac 540
 |||||
 Db 555 AACCTCTCTCTCCCAAAAGCTACTGTGACAAAGATGAGGCTGAGGTGATTCCTCAC 614
 QY 541 aaggtatttttcaagagctcacaagtttaacttgaagaatctctgtgaatgatacaatca 600
 |||||
 Db 615 AAGGTATTTTTCGAAGGCTACCAAGTTTACATTTGACAAAGTCTGTGCAATGGATCAAAATCA 674
 QY 601 gaagatgatacacttgtgacaagaagaagtttctgaagcttctgtgctcctcaagaagag 660
 |||||
 Db 675 GAAAGATGATTAATCACTGTGTGACCAAGAGTTTGTGAGCTTGTGGCTTACCAAGGAG 734

```
QY 661 aaactgctgcagcagacgagtaacttgltcccaatgacatccctgaagccaactctg 720
    |||
Db 735 AAACGTGGCGACAGCAGGAGTACTTTCCTCCAACTGGACATGGACATCTGTAGGCAATCTGT 794
QY 721 agaacactaacctacacccctccctcccgagcaagagctgctggaagcccaaaaaa 780
    |||
Db 795 AGAACCTAAACTCTACATCTCTCCCTTCCGAGCAAGAGAGCTGGCTGMAAGCCCAAAAACA 854
QY 781 ctgtgcatagctcttggaactctgcccagagagctgttcaagcatgaaagctgagtgac 840
    |||
Db 855 TTGCTGCAATAGTCTTGCGGACTGTGGCCCGAGGAGCTGTTGACGATGAAAGCTGGAGTAC 914
QY 841 atgcgacagagagatgtagtcttgaccaaagtgaacaagctccagctccccaactc 900
    |||
Db 915 ATGCGACAGAGAGATGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCCAAAATC 974
QY 901 taccagagctgtctcgtatgtctgcgggcatcccgagagagaggggctgaaatcaag 960
    |||
Db 975 TACAGAGGCTGTGTCGTATGTGTGCGGAGATCCCGAGAGGGGGGCTGAAGATCAAG 1034
QY 961 tctctcaactgtatgagagacaaactacaaagccctcttgagagcaatgagcctgag 1020
    |||
Db 1035 TCTCTCACTGGATGATGAGGACAAACAACAAAGCCCTCTTGGAGGCAATGGCACTAG 1094
QY 1021 gaagatgctgaaacctctctatgacaactctacactcccttactgcaatgattgaaag 1080
    |||
Db 1095 GAAGATGCTGAACCTTATATGACAACCTCTACACTCCTTACTGCAATGATTGATGAAG 1154
QY 1081 aatttggagctagctcctctctcccgcatlactggaagagctctgaagccgctgctgct 1140
    |||
Db 1155 AATTGGAGTGAATGCTCTCTTCCGCAATATCTGMAAGCTCTGAAGCCGCTGCTGCTT 1214
QY 1141 gggagatcctgtatatacactgacactccagcccaagcagagtgatgctgagtgagac 1200
    |||
Db 1215 GGGAGATCCTGTATATACNCTTACACTCCAGCCACAAGGAGATGATGCTGATGAGTGAAC 1274
QY 1201 aagacctcccaagaaactgctgtgtlccatgactctggaagagcatgtggagagaaactcagc 1260
    |||
Db 1275 AAGACCTTCCAGGAACCTGGCTGTGTCCATGATGGAAGGATGTGGAGAGAACTCAGC 1334
QY 1261 cccaagatctgacactctatgagaacagcccaagaatgagactgtctcgatgtgtgtg 1320
    |||
Db 1335 CCCAAGATGTGACCTTCTATGAGAGAACAGCCAAATATGACCTTGTCCGATGCTGTG 1394
QY 1321 gacagcaagaggaacatgacaactcttggaagacagcagctgagtgcttgaatggaagcc 1380
    |||
Db 1395 GACACAGAGGACATGACCACTTTGGGAACAGCAGTTGATGATGAGACAGCC 1454
QY 1381 caagacatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
    |||
Db 1455 CAAGACATCGTGGCTTTTGTGGCCAAAGCACCAGAGATGTCCACTGCAATATGCTTCT 1514
QY 1441 ggtacacactggaagaagctcttcaacagacttaacaggagcaatccgagacatatctgc 1500
    |||
Db 1515 GGTACACTGTGAGAGAGAGCTTTCACAGAGACTAACAGGCAATCCGAGCATATCTGCC 1574
QY 1501 ttcatgagtggtgttcaacctgaaagctagaaacccatagaaacagaagctgtgtctac 1560
    |||
Db 1575 TTCAATGGAGTGTACACTGAAACAGCTAGAACCAATAGCAACAGAGCTGGGCTGATC 1634
QY 1561 aacaagatcagagagctctgcatgtagaggaagatcttgagctgtgtgtgtgtgtgt 1620
    |||
Db 1635 AACAGATCCATGAGAGCTGCTGATGAGAGAGAAATTCGGGTGATTTGTTCACGTGA 1694
QY 1621 attactccagcagcagctgagctgcccacatgtaacagtaacagatccgagatgacatt 1680
    |||
Db 1695 ATTACTCCAGGAGAGATGTAGCTGCCCATCATGTCAAGTACAAAGATCCGAATGACATT 1754
QY 1681 gacaaatgtggagaggaacaataaataaagatggttactgaggaacccctgtcctcgagct 1740
    |||
Db 1755 GACAAATGTGGAGAGACAAATAAATCAAGAGATGAGTACTGGACCCCTGCTCGAGACT 1814
QY 1741 gacctcttgagagacatgctgtagctgtggtgggggcttcgactctgcaagatgtgtgt 1800
    |||

QY 1815 GACCCCTTTGAGGACATGCGGTACGTGTGGGGGGCTTCCCTACCTTGCAGAGATGTGCTG 1874
    |||
Db 1801 gacgagcaatcatcagagtggtctgacgggacccgaagaagaactggtctatgaa 1860
    |||
Db 1875 GAGAGGCAATCATCAGAGTGTCTACGGGCAACGAGAAAGAAACTGTGTCTATATGCAA 1934
QY 1861 caatgcccataccctgttcaogttagatcatcctctcgggtgtgtgtgtgtgtgtgtgt 1920
    |||
Db 1935 CAGATGCCCTATCCCTGTACGTGATGATGATCATCTTCTGCGGGTGTATGACCCGGTCAATG 1994
QY 1921 cccctcttcaagcagcagctgagctgatttactgagtgagtgatgaaagcattctgt 1980
    |||
Db 1995 CCCCCTTTCATGAGCTGTGCTGATTTACTCAAGTGGCTGTGATCATCAAGGAGCATGTG 2054
QY 1981 tatgagaagagagcagcagctgaaagagacatgcatgatactgagcctggaacaacagcata 2040
    |||
Db 2055 TATGAGAAGGAGGACGCTGMAAAGACCATGGGATCATGGGGCTGCAACACGATC 2114
QY 2041 ctctgtttagctgtgtcatatagctcatcctctctctgtgtgtgtgtgtgtgtgtgt 2100
    |||
Db 2115 CTCTGTGTAGCTGTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2174
QY 2101 gtgtgcatcctgaaagtgagaaacctgtcccttaacagtgatccagcgtgtgtgtgtgt 2160
    |||
Db 2175 GTGTCATTCCTGAAGTATGAGAAACCTGTGCTCCCTACAGTATCCAGCGTGTGTGTG 2234
QY 2161 ttcctgtcagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2220
    |||
Db 2235 TTCTGTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2294
QY 2221 tccagagccaacctgagagagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2280
    |||
Db 2295 TCCAGAGCCAACTGCGAGAGAGCTGTGGGGGATCATCTACTTCAAGCTGTACCTGTGCC 2354
QY 2281 taagtcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2340
    |||
Db 2355 TACCTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2414
QY 2341 ctgtgtctcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2400
    |||
Db 2415 CTGCTGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2474
QY 2401 ggcattggaatgagtgaggaacaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2460
    |||
Db 2475 GGCATTGAGAGTGAAGTGTGAGCAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2534
QY 2461 ctcaaccaactcgtatccatgtagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2520
    |||
Db 2535 CTCACCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2594
QY 2521 tacatgaagctgtctcttccagccagtaacaggaatcccaagccctgtatcttctctg 2580
    |||
Db 2595 TACATTGAGCTGTCTTCCAGGCCAGTACGGAATTCACGAGCCCTGTGTATTTCTCTTGC 2654
QY 2581 accaagtcctactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2640
    |||
Db 2655 ACCAAGTCTTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2714
QY 2641 aagaagatgtcaaaatctgtcatgtagaggaagcccaaccaacttgaagctgtgtgt 2700
    |||
Db 2715 AAGAAGATATCAAAAATCTGATGAGAGAGAAACCCACCCACTTGAAGCTGGGCGTGTCC 2774
QY 2701 attcaagacctgtttaaagactcaacagagatgagatgaagtgctgtgtgtgtgtgtgt 2760
    |||
Db 2775 ATTCAAGACTGTGTAAGTCTACCGAGATGGGATGAAGTGTGTGTGTGTGTGTGTGT 2834
QY 2761 ctgaattttatagggccagatcacctctctctgtgtgtgtgtgtgtgtgtgtgtgtgt 2820
    |||
Db 2835 CTGAATTTTATAGGGGAGGACGATCACCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2894
QY 2821 accacatgtcaatccttgagcagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2880
    |||
```


Query Match 99.8%: Score 6788; DB 6; Length 7260;
Best Local Similarity 99.9%: Pred. No. 0;
Matches 6794; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 atgagctgttgccctcagcaggtgtgctgtgtgaagaacctcactcttcagaagaaga 60
DB 321 ATGGCTTGTGGCCCTCACACTGAGGTTGCTGTGGAAGAAACCTCACTTTCAGAGAAGA 380
QY 61 caaatactcagcgtgttacttgaagtgccctgacctattactctccgatctgac 120
DB 381 CAACACATGTCAGCTGTACTGTGAATGGCTGCGCTCATTTATTTACTTCATCTGATC 440
QY 121 tctgttcggtgagctacccacctatgaacaatgaatgcaatttcacaataaagcc 180
DB 441 TCTGTTGGCTGAGCTACCCACCCATGACACATGAAATGCCATTTTCCAAATAAGCC 500
QY 181 atgaccttgcaagaacacctctcgttgatcaggagatattctgtatgtccacaacccc 240
DB 501 ATGCCCTTGCAAGAACACTTCTGGGTTCAGGGGATTAATCTTAATGCCAACACCC 560
QY 241 tcttcctgtacccagctcctgaggagctcccgaggtgtgtgaaaccttaacaalc 300
DB 561 TGTTCCTGTTACCCGACCTCTGGGAGGCTCCGGAGTTGTGTGAACCTTTAAACAAATCC 620
QY 301 attgtgctgcgctgttctcagaatgcgagagcttcttatacagccagaagaacc 360
DB 621 ATTGTGGCTGCGCTGTTCAGATGCTGGAGGCTTCTTTATACGCCCAAGAACACCC 680
QY 361 agcatgaagaacatgagcaagttctgaagaattacagcagatcaagaataacagctca 420
DB 681 AGCATGAAGAACATGGCAAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA 740
QY 421 aactgaagcttcaagaatttccctgtgtgaaacaaatgaacctctcctgttccatatac 480
DB 741 AACTTGAGCTTCAGATTTCCGGTGACATGAACACTTCTGCGGTCTGATATCAC 800
QY 481 aacctctctcccaagctactctgtgagcaagatgctgagagctgagatctatctcac 540
DB 801 AACCTCTCTCCCAAGTCTACTGTGACAGATGCTGAGGGCTGATGTCTTTCCAC 860
QY 541 aaggtattttgcaaggtaccagatatactgaacagctgtgtcaatgatacaaatca 600
DB 861 AAGGTATTTTGGCAAGGCTACAGATTGACATTTGACAAAGCTGTGCAATGGATCAAAATCA 920
QY 601 gaagagatgatacaactgtgtgaccaaagaatttctgagcttctgtgcttaccacaagag 660
DB 921 GAAGAGATGATCACTGTGTGACCAAGAAATTTGAGCTTGTGGCTTACCAAGGGAG 980
QY 661 aaactgctcagcagagagagactctgttccaacatgacatcctgaagccaactctg 720
DB 981 AAATGCTGCTCAGACAGGACAGTACTTCTTCCACATGAGACATCTGAAAGCAATCTCTG 1040
QY 721 agaacataaactatactcctctcccgagcaagagctgctgtgaagccacaataaaca 780
DB 1041 AGAACACTAAACTACATCTCCCTTCCGACCAAGAGACTGGCCGCAACCCCAAAATTA 1100
QY 781 ttgtctgatatgttggagactctgcccagagagctgttaagatgaagaagctggagtaac 840
DB 1101 TTGCTGATGATGTGGGACTGTGGCCCAAGAGCTGTTCAGCATGGAAGCTGTGAGTGC 1160
QY 841 atgagcagagagatgatttctgaacaatgtgaacagctccagctccctcacccaatac 900
DB 1161 ATGGGACAGAGAGTGTGTTCTGACCAATGTGAACAGCTCCAGCTCTCCACCCAAATC 1220
QY 901 taccagagctgtgtctgtatgtctgcgggcatcccgagggaggggctgtgaatcaag 960
DB 1221 TACCAGCTGTGTCTGTATTTGCTGTGGGCAATCCGAGGAGGGGGCTGAAGATCAAG 1280
QY 961 tcttcaactgtgtatgaggaacaactataaagccctcttgaggaatgacatgac 1020
DB 1281 TCTCTCAACTGTGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTTGAG 1340

QY 1021 gaagatgtctgaacaccttctatgacaactctacaactccttactgtcaatgtatgaaag 1080
DB 1341 GAAGATGTGAAACCTTGTATGACAACTTACAACTCTTACTGCAATGATTTGATGAAG 1400
QY 1081 aattctgagcttagtctcctcttcccgatatactgaaagctctgaagccgctgtcgtt 1140
DB 1401 AATTTGGAGTCTAGTCCCTTTCCGGATTTATCTGAAAGCTGTGAAGCCGCTGCTGTT 1460
QY 1141 ggaagaatcctglatalacaactgaacctccagccacaaggaagatgcatggtgaggaac 1200
DB 1461 GGAAGATCTCTGTATACACTGACACTCCACCAAGGAGGTCATGCTGAGGTGAAC 1520
QY 1201 aagaccttccaggaacttgctgtgtccatgatatctggaagagcatgtggaagaaactcag 1260
DB 1521 AAGACTTCCAGGAACCTGCTGTGTTCATGATCTGGAAGGACATGTGGAGAACTCAGC 1580
QY 1261 cccaagatctggaaccttcaatggaagacccaagaanaatggaacttgcggaatgctgt 1320
DB 1581 CCCAAGATCTGAGACCTTCATGAGAACAGCCAAAGATGACCTTGTCCGATCTGTTG 1640
QY 1321 gacagcaggaagaatgacaccttggaggaagcagatggtgctgaattggaagcc 1380
DB 1641 GACAGCAGGACAAATGACACTTTTGGAGACAGCATTTGATGGCTTAGATGAGACGCC 1700
QY 1381 caagacatgctgtgttcttggccaagcaccagaagatgtccagttccagtaatgttct 1440
DB 1701 CAAGACATGTGGCGCTTTTGGCCAAGCACCCAGAGATGTCCAGTCAATATGTTCT 1760
QY 1441 ggttacacctgagagaagcttcaacgagactaaccaagcaatccggagccatatctcgc 1500
DB 1761 GTGTACACTGTGAGAAACCTTCAACGAGACTTAACAGGCAATCCGACCATATCTGC 1820
QY 1501 ttcatgaaatgtgttaaaccttgacaagcttagaaccttagacaagaaatgtgtcctatc 1560
DB 1821 TTCTATGAGTGTGTCACTGTAACCTGAACCAAGCTAGAACCCATAGCAAGAGTGTGCTATC 1880
QY 1561 aacaagttcaatgagctgtgtgatagagaagaatctgtgctgtgtatgtgttcaatgga 1620
DB 1881 AACAACTCATGAGTGTGCTGATGAGAGAAATCTCTGGCTGTGATTTGTTCACTGGA 1940
QY 1621 attaccctcaggaagattagctgtgcccatactgcaagtaacaatccgaatgacat 1680
DB 1941 ATTACTCCAGGACGATGAGAGCTGCCCCATCTATGTCMACTACAAATCCGAATGACATT 2000
QY 1681 gacaatgtgagagagacaataataatacaagaatgagatgagacctgtgtcctgagct 1740
DB 2001 GACAACTGTGAGAGGACAAATATAATCAAGATGGGTACTGGAGCCCTGCTCGAGCT 2060
QY 1741 gaaccttgaaggaatgagatgagatgctgtgaggggcttgcctacttgcaagatgtgt 1800
DB 2061 GACCCCTTTGAGGACATGCGGTACGTTGGGGGGCTTGGCTTGTGAGGATGTGGTG 2120
QY 1801 gagagagcaatcaatcagaggtgtgacgggcaaccgagaagaacatggtgtctatagaa 1860
DB 2121 GAGCAGGCAATCATCAGAGGTGCTGACGGGACCGAGAAATAAAGTGTCTATATGCAA 2180
QY 1861 cagatgcccataccctgtttagttagtgaatcttctgcgggtgataagacgggtcaatg 1920
DB 2181 CAGATGCCCTATCCCTGTACGTTGATGACATCTTCTCGGGTGTATGAGCCGGTCAATG 2240
QY 1921 cccctctcaatgagcgtgagctgtatctactcagtgctgtgatactcaaggaactgtg 1980
DB 2241 CCCCTTTTCATGACGCTGGGCTGTGATTTACTAGTGGCTGTATCAAGGGCATCTGTG 2300
QY 1981 tatgagaagagagcagcgtggaagaagaccatgctgataatgagccttgacaacagcata 2040
DB 2301 TATGAGAAGAGAGGAGCGCTGAAGAAGACCATCGGATCATGGCCCTGGAACAGCATC 2360
QY 2041 ctctgtttagctgtgtcatatgataagctcaatctcctctctgtgtgagcgtgtcgtcta 2100
DB 2361 CTCTGTTTACCTGTTCATTAGTACCTCATTCCTCTTGTGTGAGCCCTGCTGCTGA 2420
QY 2101 gtgtatcctcgaagattaggaacactgtgcctacagatgataccagcgtgtgtgttc 2160

```
Db 2421 GTGGTCATCTGTAAGTTAGAAACCTGCTGCCCTACAGATGCCAGCTGGTGTGTC 2480
Qy 2161 ttcctgctccgltgttctgtgtgtgacaaatcctgcagtgcttccctgattagacacactctc 2220
Db 2481 TTCCTGTCCGTGTGGTGTGTAACAAATCTGCAGTGGCTTCTGATTAAGCACACCTTC 2540
Qy 2221 tccagagcaacctgacacacacacacacacacacacacacacacacacacacacacacacac 2280
Db 2541 TCCAGAGCCAACTGGACAGACCTGTGGGGCATCATCTACTTACGCTGACCTGCC 2600
Qy 2281 tacctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2340
Db 2601 TAGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2660
Qy 2341 ctgctgtctccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2400
Db 2661 CTGCTGTCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2720
Qy 2401 ggcattgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 2460
Db 2721 GGCATTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAG 2780
Qy 2461 ctacacactctgactcactcactcactcactcactcactcactcactcactcactcactcactc 2520
Db 2781 CTCACCACTTCCGTCTCCATGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2840
Qy 2521 taccattgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2580
Db 2841 TACATTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAG 2900
Qy 2581 accaagctctactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2640
Db 2901 ACCAAGTCTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2960
Qy 2641 aagagaatgtcagaatcctgcatagtgagagagagagagagagagagagagagagagagagag 2700
Db 2961 AAGAGAATATCAGAAATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3020
Qy 2701 attcgaacacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2760
Db 3021 ATTGCAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3080
Qy 2761 ctgaattttatagagagagagagagagagagagagagagagagagagagagagagagagagag 2820
Db 3081 CTGAATTTTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3140
Qy 2821 accacatgtcaatcctcactcactcactcactcactcactcactcactcactcactcactcact 2880
Db 3141 ACCACATGTCAATCTCAACCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3200
Qy 2881 ggaagaacatctgctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 2940
Db 3201 GGAAGAACATCTGCTGTGATGAGCACCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3260
Qy 2941 cataagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3000
Db 3261 CATAAGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3320
Qy 3001 aaagagctctctgtgaagacagtgagagagagagagagagagagagagagagagagagagagag 3060
Db 3321 AAAGAGCTCTGTGAGAGACAGTGAAGCGGAGATGAGACAGATGAGCTTGGATGTGTGTGTGTGT 3380
Qy 3061 ttgcacatcaagacagtgagagacagacagacagacagacagacagacagacagacagacagacag 3120
Db 3381 TTGCACATCAACAGTGAGAAAGCAAAAGCAGCTGTGAGTGTGAGATGAGAGAGAGAGAGAGAGAG 3440
Qy 3121 ctacatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3180
Db 3441 CTACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3500
Qy 3181 gctgtgtgtgacaccttactcccgagagagagagagagagagagagagagagagagagagagag 3240
Db 3501 GCTGTGTGTGACACCTTACTCCCGAGGGAGATGAGAGCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 3560
Qy 3241 ggcgcacacatlatctctctctacacacacacacacacacacacacacacacacacacacacac 3300
Db 3561 GGCGCACACATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3360
Qy 3301 attgcatcatctcccatgtggagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3360
Db 3621 ATTGCAATCATCTCCATGTGGAAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3680
Qy 3361 cagctgtggaacagctactcactcactcactcactcactcactcactcactcactcactcactc 3420
Db 3681 CAGCTGGGAACAGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 3740
Qy 3421 tctgtcagaacacagtagtagcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3480
Db 3741 TCTGCAGAAACAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 3800
Qy 3481 agcagctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3540
Db 3801 AGCAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3860
Qy 3541 tctgtcactcccaacccatcagaagacagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3600
Db 3861 TCTGTCTATCTCCAACTCATCAGAGAACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3920
Qy 3601 gggcagtagcctgtgactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3660
Db 3921 GGGCAGTAGCCTGTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3980
Qy 3661 ctctctatagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3720
Db 3981 CTCTTATATAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4040
Qy 3721 gagaagacccctgtgaagaataatctcctcaagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3780
Db 4041 GAGAGACCCCTGTGAAGAAATATCTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4100
Qy 3781 acctcagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3840
Db 4101 ACCCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4160
Qy 3841 tgtcttcgcccgtctcactgtgaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3900
Db 4161 TGTCTTCGCCCGTTCACTGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4220
Qy 3901 gaatcagaagacagactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3960
Db 4221 GAATCCAGAGAGACAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4280
Qy 3961 ggtctggaacatctacagagaacaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4020
Db 4281 GGTCTGGAACATTAACAGACAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4340
Qy 4021 agacgagatcgaagaagatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4080
Db 4341 AGACGAGATCGGAAAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4400
Qy 4081 ggcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4140
Db 4401 GGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4460
Qy 4141 cccctgtagtatacaagcaagtagacatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4200
Db 4461 CCTGTGATGTACAGCAAGTAGTACATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4520
Qy 4201 accctgtgaactcttaagcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 4260
Db 4521 ACCCTGTGAACCTTTAAAGCCCTCAACAAAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4580
Qy 4261 ggaacacacacacacacacacacacacacacacacacacacacacacacacacacacacacac 4320
Db 4581 GGAACACCAATCCCAAGACAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4640
```

[illegible]

Qy	5401	gattctctgaagcgcgtctcttcttgattctcccaatttttccttgaggaagagggctcacc	5460
Db	5721	gattatcttgaaagccgcgtgttcttgatcttccacattttttcccttgagacagggctcattc	5780
Qy	5461	gacattgtagaaaaaccaggcaatggtctatgctccctcggaagaagtttggggaatcgctt	5520
Db	5781	gacattggtgaaaaaacaggcaatggcgctgatgccttgaaagaagtttggggaaattgccttt	5840
Qy	5521	gtgtccaccattactctgggaacttggttgggaagcaaacctctcgccatggscgtgggaagg	5580
Db	5841	gttgccaccattattcttgggagcttgggtggagcaaaaaccttctggccatggccgtggagaagg	5900
Qy	5581	gtgtgtctctcccatiactgtcttgacacgaagacagatcttcatcaggccagacct	5640
Db	5901	gtgtgtcttcttcccatiactgtcttgacacgaagacagatcttcatcaggccagacct	5960
Qy	5641	gtaaaagcaaaagctactcctctctgaatgtgaatgaatgtgagggcggaagaagag	5700
Db	5961	gtaaatgcacaaagcattctcctctgaattgtwgaagatgtgaagatgtgaaggcggaagacag	6020
Qy	5701	agaaattctgatgtgtagagccagaatgaatgacattagaatcaagagattgacgaagata	5760
Db	6021	agaaattctgatgtgtagagccagaatgacattagaatcaagagattgacgaagata	6080
Qy	5761	fatagaaggaagcggaagcctgtctltgaagagatttgctggggcatctcctcgtgtgag	5820
Db	6081	tatagaagaagccggaagcctgcctgtttgacagagatttggctggcgatctccctcggtgag	6140
Qy	5821	tgcttttggtccctcggaagatltatgggcttggaagaatcaaaccttcaaatgtltaca	5880
Db	6141	tgcttttggtccctcggaagatltatgggcttggaagaatcaaaccttcaaatgtttmaca	6200
Qy	5881	ggagataccacctgttaccagaagagatgtcttcccttaacaaaaatagatattcaaac	5940
Db	6201	ggagatataccacctgtttaccagaagagatgtcttcccttaacaaaaatagatattcaaac	6260
Qy	5941	atccatgaagaacatcgaaacatgggctactgcctccagatttgatagcatcacagactg	6000
Db	6261	atccatgaagaacatcgaaacatgggctactgcctccagatttgatagcatcacagactg	6320
Qy	6001	ttgacttggaagagaacacagtgagacttcttgcacctttagagagagttcccaagagaagaa	6060
Db	6321	ttgacttggaagagaacacagtgagacttcttgcacctttagagagagttcccaagagaagaa	6380
Qy	6061	gttgcgaaggtttgtgtgagtggtgcgatttcggaacatggtgcctgtbaatbatgggaaaaa	6120
Db	6381	gttgcgaaggtttgtgtgagtggtgcgatttcggaacatggtgcctgtbaatbatgggaaaaa	6440
Qy	6121	tatgtctgttaactatgtaggaagcaacaaacgaactctctacagcatagctcttgatc	6180
Db	6441	tatgtctgttaactatgtaggaagcaacaaacgaactctctacagcatagctcttgatc	6500
Qy	6181	ggcgggacctctgtgtgttcttgatgtaaacccacacacgaagcatgtatcccaagcccg	6240
Db	6501	ggcgggacctctctgtgtgttcttgatgtaaacccacacacgaagcatgtatcccaagcccg	6560
Qy	6241	cggtctctgttgaaattgttgcctcaagtggttgttaaggaaggagagatcaagtatgttaca	6300
Db	6561	cggtctctgttgaaattgttgcctcaagtggttgttaaggaaggagagatcaagtatgttaca	6620
Qy	6301	tctcatatgtagaagaatgtgaaagctcttgcacatagaatgtgcaatcatgtgtcaatgga	6360
Db	6621	tctcatatgtagaagaatgtgaaagctcttgcacatagaatgtgcaatcatgtgtcaatgga	6680
Qy	6361	aggttcaggtgacctgtgcagtgttcagcatctaaaaaataggtttggagatgtgttataca	6420
Db	6681	aggttcaggtgacctgtgtgcagtgttcagcatctaaaaaataggtttggagatgtgttataca	6740
Qy	6421	ataagtttaagaaatagaaggtttcaaacccggagacttaagccgttccaaagattcttggga	6480
Db	6741	ataagtttaagaaatagaaggtttcaaacccggagacttaagccgttccaaagattcttggga	6800
Qy	6481	cttgcattctctggaagtgttcttaaaagagaacacccggagaatgctataacaccagctt	6540

Db 6801 CTTGCAATTCCTGGAAGGTTCCAAAGAGAAACCGGAAACGCTACATACCATCTT 6860
QY 6541 ccatttcattatctctctgagcagatatctcagcatctctccagagcaaaagcga 6600
Db 6861 CCATCTTCATATCTTCTCTGGCCAGATATTCAGCATCTCTCCGAGACAAAAGCGA 6920
QY 6601 ctccacatagaagactactctgtttctcagaacaacacttgacaagatattggaactt 6660
Db 6921 CTCACATAGAGAACTACTCTGTTTTCAGACAAACCTTGACCAATATTGTGAATCTT 6980
QY 6661 gccaaagaccaaagttagatgtagaccacttaaaagacctcattacacaaacagcaga 6720
Db 6981 GCCAAGAGCAAAAGTATGATGACCACTTAAGAACCTTCATATACAAAGACAGACA 7040
QY 6721 gtagtgagcttgagcttctcacaactcttctcagaagatgagaagatgagaagactat 6780
Db 7041 GTAGTGAGCGTTGCAATCTTCTTCTACAGATGAGAAAGTGAAGAAAGCTAT 7100
QY 6781 gtagaagaatccgttcatagag 6804
Db 7101 GTATGAGAAATCCTGTTCAATACG 7124

RESULT 10
AX127830 9741 bp DNA linear PAT 15-MAY-2001
LOCUS AX127830
DEFINITION Sequence 69 from Patent WO0130848.
ACCESSION AX127830
VERSION AX127830.1 GI:14134477
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 9741)
AUTHORS Denelle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duvergier,N., Jaje,M., Searfoss,G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
TITLE Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
JOURNAL Patent: WO 0130848-A 69 03-MAY-2001;
Aventis Pharma S.A. (FR)
FEATURES
source Location/Qualifiers
1..9741
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2650 a 2180 c 2290 g 2620 t 1 others
ORIGIN

Query Match 99.7%; Score 6784.8; DB 6; Length 9741;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6792; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 atgagctgttgtagctagctgagtgctgctgctgtagaagaacacttccagaagaaga 60
Db 185 ATGAGCTGTGAGCTAGCTGAGAGGTTGCTGTGTGAAAGAACCTCACTTTCAGAGAAAGA 244
QY 61 caaacaatgcagctgttactggaagtgagcctgagcctctattctctcctgagctgac 120
Db 245 CAAACATGTCAGCTGCTGTGGAAGTGGCTGGCTCTTATATCTCTCTGATCTGATC 304
QY 121 tctgttcgagctgagctaccacccatgaaacaatgaaatgcaatttccaaataagcc 180
Db 305 TCTGTTCGCTGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC 364
QY 181 atggccttcgaggaacacttcttggttgagggagatattatctgtaaatgcaacaacccc 240
Db 365 ATGGCCTTCGAGGAACACTTCTCTGGGTTCAAGGGATTATCTGTAATGCCAAACACCC 424
QY 241 tcttcctgtaaccactcttgaggagagctccggagatgttggaacttaacaatcc 300
|||||

Db 425 TGTTTCGTTTACCCGACTCTCTGGGAGGCTCCCGAGTGTGTGAACCTTAACAAATCC 484
QY 301 attgagctcgagctgttctcagatgctcggagagctcttttataagccaaagaaccc 360
Db 485 ATTGAGCTCGGCTGTCTTCTCAGATCTCGAGGCTTCTTTATATAGCCAGAAAGACACC 544
QY 361 agcatgaaggaatgagcaagttctggaacattacagcagatcaagaatccagctca 420
Db 545 AGCATGAAGCATGCGCAAAAGTTCTGAGAACATTACAGCAGATCAAGAAATTCACGCTCA 604
QY 421 aactgaagcttcaagatctctgtgtgacaatgaaacctctctggtttccatatac 480
Db 605 AACTGAACCTTCAAGATTTCCTGGTGGAACAATGAACCTTCTCGGGTTCCTGATCAC 664
QY 481 aacctctctcccaagcttactgtgacaagatgctggaagctgagctatctccac 540
Db 665 AACCTCTCTCTCCCAAGTACTCTGTGACAAAGATGCTGAGGGCTGATGCTATCTCCAC 724
QY 541 aagtaattttgcaagctgacagtlacatttgacaagctgtgcaatgaaatca 600
Db 725 AAGTATTTTTCGAAGCTACAGCTACAGTTACATTTGACAACTCTGTGCAATGATCAAAATCA 784
QY 601 gaagagatgattcaactgtgtgacaagaagttcttgagcttctggtctacccaagag 660
Db 785 GAAGAGATGATTCAACTTGTGTGACCAAGATTTCTGAGCTTTGTGGCTTACCAAGGAG 844
QY 661 aaactgctgcaagcagagcagtaactctgtccacaatgacatcctgaaagccaatcctg 720
Db 845 AAACCTGCTGACGACGACGAGCTACTCTGCTTCCAAATGACATCTGAAACCAATCTCG 904
QY 721 agaactcaactcaactcaactcccttcccgagcaagagctggttgaaagccaaataca 780
Db 905 AGAACAATAAATCTTACATCTCTCCCTCCGAGCAAGAGGCTGAGCAAGCAAAATCA 964
QY 781 ttgctgcaatgcttgagactctgcccagagagctgttcagcatgaaagctgagtgac 840
Db 965 TTGCTGCAATGCTTGGAGCTCTGGCCAGAGAGCTTTACAGATGAGAGCTGAGAGTAC 1024
QY 841 atggcagagaggggtgagtttctgacaaatgtagaagctccagctccccaacaaatc 900
Db 1025 ATGCGACAGAGGCTGATGTTCTGACCAATGTGAACAGCTCCACTCCACCAATATC 1084
QY 901 taccagctgtgctcgtatgtctgtcgagacatccagaggaagggctgaaatcaag 960
Db 1085 TACCAAGCTGTGCTCGATTTGTCTCGCGGATCTCCAGAGGAGGGGCTGAAGATCAAG 1144
QY 961 tctctcaactggtatgaggaacaactacaaagccctcttggaggaatgagcagtgag 1020
Db 1145 TCTCTCAACTGTGTATGAGGACAACTACAAACCTCTTTGGAGGCAATGACATGAG 1204
QY 1021 gaagatgtgaacctctctatgacaactctacaactcttactgcaatgattgataag 1080
Db 1205 GAAGATGTGAACCTTCTGTATGACAACCTCTTACTGCAATGATTTGATGAAAG 1264
QY 1081 aattggaagctagctctcttcccgatatactgaaagctcgtgaagccgctgtcgt 1140
Db 1265 AATTGGAAGCTAGCTCTCTTTCCGATATATCGAAACCTCGAAGCCGCTGCTGCTT 1324
QY 1141 gggaagatctctgtatatacactggaactccagcccaaggaagtgatagtgagagac 1200
Db 1325 GGGAGATCTCTGTATACACTGTGACACTCGACCAAGAGGCAAGGCTAGGTGAGGTAAAC 1384
QY 1201 aagaccttccaggaactgctgtgtlccatgatactggaagagcatgtgaggaactcagc 1260
Db 1385 AAGACCTTCCAGGAACGTGGCTGTGTTCCATGATCTGGAAGGCAATGAGGAGCAACTCAG 1444
QY 1261 cccaagatctggaactctcatgaggaacagccaagaatggaacctgtccgagatgtgtg 1320
Db 1445 CCCAAGATCTGAGACTTCATGGAAGAACAGCAAGAAATGAGACCTTTCGCGATGCTGTG 1504
QY 1321 gacagcaggaacaatgacaacttltgggaacagcaatgtgataatgagagagc 1380
Db 1505 GACAGCAGGACAAATGACCACTTTTGGGAAACAGCAGTTGATGAGTTCAGACGCC 1564
|||||


```
OY 1381 caaagacacgctgggttttttggccaagaccccaagagatgtccagtcagtaagtctt 1440
    |||
    |||
    |||
Db 1565 CAAGACATCGTGGCGTTTGGCCAAAGACCCAGAGATGTCACATCGAATGAAGTCT 1624
OY 1441 ggtacaccttgagagaagcttcaacagagataaccaggaatccgagacatctcgc 1500
    |||
    |||
    |||
Db 1625 GTGTACACTGGAGAGAAAGCTTTCACAGAGACTAACAGGCAATCCGAGACCATCTCGC 1684
OY 1501 ttcaatggagtgttcaacctgaacaagctagaaccataagacaagaagctgtgctatc 1560
    |||
    |||
    |||
Db 1685 TTCATGAGATGTGTACACTGAACCTGAACAGCTAGAACCCATAGCAAGAGTCTGGCTCATTC 1744
OY 1561 aacaagatcatagaaactgtgtatagaaggaagttctggcgtgattgtgttcaatga 1620
    |||
    |||
    |||
Db 1745 AACCAATCCATGAGCTGCTGGATGAGAGAAAGTTCTGGGCTGTGATTGTCTCACTGGA 1804
OY 1621 attactcagagcagcatatagcttgcgccatcatgtcaagtaagaatccgaatgagacat 1680
    |||
    |||
    |||
Db 1805 ATTACTCCGAGCAGCATTTAGCTGCCCATCATGTCAAGTACAAATCCGAATCGAATGACATT 1864
OY 1681 gacaatgtgagagaggaacaataaatacaaggaatgggtactggagccctgttctgaagt 1740
    |||
    |||
    |||
Db 1865 GACAAATGTGAGAGAGCAAAATAAAATCAAGAGATGGGTACTGGGACCTGTCTCTGAGCT 1924
OY 1741 gaccccttgaagagacatgagtgtaagtcttggggggcttgcctacttggagatgtgtg 1800
    |||
    |||
    |||
Db 1925 GACCCCTTTGAGAGACATGCGGTACGTCTGGGGGCTTCTGCTACTTGCAGATGTGGTG 1984
OY 1801 gagcaagcaatcatcagagggtctgaacgggacacgaagaagaactgtgtctatatgcaa 1860
    |||
    |||
    |||
Db 1985 GAGCAGGCAATCATCGAGGTGCTGAGAGGCGACGAGAAAGAAATCGTGTATATGCA 2044
OY 1861 cagaatgacctatccctgttaagttatgatacattcttgcgggtgtagagccggttcaatg 1920
    |||
    |||
    |||
Db 2045 CAGATCCCTATCCCTGTACGTGATGACATCTTCTCGGGGTGATGAGCGCGCTCAAGT 2104
OY 1921 ccccttcatagacgtctgacctgagattactcaagtgctgtatcatcaaggacatcgtg 1980
    |||
    |||
    |||
Db 2105 CCCCCTTTCATGACCTGGCCCTGATTTACTAGTGGCTGTGATCATCAAGGCGCATCGTG 2164
OY 1981 tatgaagaagagacagcgtctgaagaagacatgctgagatcagggccttggacaacagcata 2040
    |||
    |||
    |||
Db 2165 TATGAGAGAGGAGCGGCTGAAAGAGACCATCGGATCATGGGCTGTGACAAACAGCATTC 2224
OY 2041 ctctggtttagctgtgtcatatagtaacctcatcttcttcttctgttggagcgttgcctga 2100
    |||
    |||
    |||
Db 2225 CTCTGTTTGTAGCTGTTCATATTAGCTCATCTCATCTCTTCTTGTGAGCGCTGGCCGTGA 2284
OY 2101 gtgttcatcctgaagttaagaagaacgtctgacctacagatgataccagcgtgtgttctgc 2160
    |||
    |||
    |||
Db 2285 GTGGTATCTCTGAAGTTAGAAACCTGTGCTCCTACAGATGATCCAGCGCTGGTGTGTTC 2344
OY 2161 ttctctgtcgtgttctgtctgtgtgtgaacatctcgtcaatgtcttcttgaatgaacatcttc 2220
    |||
    |||
    |||
Db 2345 TTCTCTGTGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2404
OY 2221 tccaagagcaacctgtgacagcagcctgttggggacatcatctacttcaacgtgtacccccc 2280
    |||
    |||
    |||
Db 2405 TCCAGAGCCCAACCTGGGAGAGGCTGTGGGGGATCATCTACTTACGCGTGTACCTGCC 2464
OY 2281 taagtctgtgtgtgtgaatgagcagactagtggtcttcaacatcaagaatcttgcgtatgc 2340
    |||
    |||
    |||
Db 2465 TACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2524
OY 2341 ctgctgtctcctctgtgtcttcttgggttggctgtgaatcttgccttcttgaagagcag 2400
    |||
    |||
    |||
Db 2525 CTGCTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2584
OY 2401 ggaatgtgagtgtgagtgagacaactgttggagagctcttggaggaagtggtcttcaat 2460
    |||
    |||
    |||
Db 2585 GGCATTGAGTGTGAGTGTGAGCAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2644
```

Db 3725 TGTGCTATCTCCACCTTCATCAGGAAGCATGTGTGAAGCCCGCTGTGGAAACATA 3784
OY 3601 gggcatgagctgacctatgtgtccatatagaagctgaagggagcccttctgga 3660
Db 3785 GGGCATAGAGCTGACATATGTGTGCTCATATGAAGCTGCTTAAGAGGAGGACCTTTGTGGAA 3844
OY 3661 cctcttcatagagatgataagcggctctcaagacctgggcatcttaagtaagcatc 3720
Db 3845 CTCTTTCATATGATGATGATGACCGGCTCTCAGACCTGGGATTTCTAGTTATGCACTCA 3904
OY 3721 gagaacacctggaagaataatctcctcaaggtggcgaagaagaagtgagtgatgtgag 3780
Db 3905 GAACACACCTTGGAAATAATATTCCTCAAGTGCGCCGAAGAGAGTGGGTGATGCTGAG 3964
OY 3781 acctcagatgtaacctgtccagaagaagaagcgggacctcggggagaagaagcagagc 3840
Db 3965 ACCCTGATGTGTACCTTGGCAGCAAGCAAGAGCGGCGCTTGGGAGCAAGCAGAC 4024
OY 3841 tgtcttcggcccttcaactgaagatgagtctgtatccaaatgattctgaatagacc 3900
Db 4025 TGTCTTGGCCGCTTCACTGAAGATGCTGCTGATCCAAATGATTTGACATGAACCCA 4084
OY 3901 gaatccagaagaagacagactgtcagtgagatgagatgagcaaaaggtccatacagatga 3960
Db 4085 GAATCCAGAGAGACAGACTTGTCTAGTGGATGATGCGCAAGGGGTCTACAGGTGAAA 4144
OY 3961 ggctggaacttaacagaagaacagttgtgcccccttctggaagaagactgtcaatgcc 4020
Db 4145 GGTGTGAACCTTACACGACACAGTTGTGGCCCTTTGTGGAAGAAGCTGCTAATTTGCC 4204
OY 4021 agacgagtcggaagaagatttctgtcagatgtcttcagcagctgtgttctgcact 4080
Db 4205 AGACGAGTCGGAAGAGATTTTGTGTGATGTGCTTGTCCAGCTGTGTGTTTCTGCATT 4264
OY 4081 ggccttgttcaagctgtatgtgtccaccccttggcaagtlacccagccttgaaactcag 4140
Db 4265 GGCCTTGTGTGAGCTGTGATGTGTGACACCTTTGGCAAGTACCCAGCTGGAACCTTTCAG 4324
OY 4141 ccctgagtgtacaacgaagaagacacattgttcagcaatgagtcctcgaagaagcggga 4200
Db 4325 CCCTGATGTACACGACAGATACATTTGTTCACCAATGATGCTCTGTAGACACGGGA 4384
OY 4201 accttggaaactttaaagccctccaaagaacccctggcttcgggaacccgtgtatggaa 4260
Db 4385 ACCCTGGAACTCTTAACCCCTCTCACAAAGACCTGTGGAGACCCGCTGTATGAA 4444
OY 4261 ggaaccccaatcccaagaacgcccgtccaaggaagggaagaagtgaaacatggccca 4320
Db 4445 GGAACCCCATCCACAGACAGCCCTGCGCAGGAGGAGAGATGACCACTGCCCA 4504
OY 4321 gtctcccaagaacatataagacctcttcagaatggaaactggacaatgcaagaacccctca 4380
Db 4505 GTTCCCCAGACCATCATGAGACCTTTCAGAAATGGAATGGAACATGCAAGCAACCTTCA 4564
OY 4381 cctgcatccagtgtagaagagacaaatacaagaagatgctgcctgtgtgtccccaagg 4440
Db 4565 CCTGTATGCCAGTGTAGAGGACCAAAATCAAGAAAGATGTGCTGTGTGCCCAAGG 4624
OY 4441 gcaagggggtgctcctcccaaaagaagaacaaacactlgcaatatccttcagaagctg 4500
Db 4625 GCAGGGGGGTGCTCCTCCACCAAGAAACAAACACTTGCAAGATATCTTTCAGGACCTG 4684
OY 4501 acaggaagaacatctggatctatctgttgaagcgtatgtgcagatcatatagccaagc 4560
Db 4685 ACAGGAAGAAACATTTCCGATTATCTGTGTAAGAGATGTGCAATCATAGCCAAAAGC 4744
OY 4561 cttaagaagaagaatctgggttaagttaagttaagttaagttaagttaagttaagttaagt 4620
Db 4745 TTTAAAGAACAGATCTGGGTAAATGATTTAGGTATGGCGGCTTTTCCGTGGGTGTAGT 4804
OY 4621 aatctcaagacttccctccagatcaagaagttaatgcatcaacaataagaaga 4860
|||||

Db 4805 AATACTCAAGCACTTCTCCAGTCAAGAGATTATGATGCCACCAACAAATGAGAAA 4864
OY 4681 caactaaagctggccaagaagacagttctgcaatgattcttcaacacacttgggaagttc 4740
Db 4865 CACCTAAAGCTGGCCAAAGACAGTTCTGCAATGATGATTTTCAACACCTTGGGAAATTT 4924
OY 4741 algaagaagcttgaacacaaataatgtaaggttgttgttcaataaagaaggtctgcat 4800
Db 4925 ATGACAGAGATGAGAACAGAAATATGTCAGAGTGTGTTCAATTAACAAAGCGCTGGCAT 4984
OY 4801 gcaatcagcttcttccctggaatgcatcaacaatgcatctccggcccaacttgaagaag 4860
Db 4985 GCAATCAGCTCTTCTTCTGAATGTCATCAACATTCATTCCTCCGGGCCAACCTGCAAAAG 5044
OY 4861 ggaagaaccccttaagcaatataagattacgtcttcaatcaatcccttgaatcccaag 4920
Db 5045 GGAGAGAACCTTACGACATTAATGAAATTAAGTACTTCAATCATCCCTGGAATTCACCAAG 5104
OY 4921 cagcagctctcagaaggtgtgcttgaagaacaacatcagtgagtgctgtgtccatctgt 4980
Db 5105 CAGCAGCTCTAGAGTGGGTCCGATGACCAATCACTGATGTGCTTGTGCTCATCTGT 5164
OY 4981 gtcactcttgaatgtctctctgtccagcagcttctgtatctctgatacgaagcgg 5040
Db 5165 GTCAATCTTGAATGTCTCTGTCCAGCAGCTTGTCTATTTCTGATCCAGAGCGG 5224
OY 5041 gtcaagaaagcaaaacaccttgacgtlcatcaagtgagtgagtgagcgtgtcatctgtctc 5100
Db 5225 GTCAGCAAAAGCAAAACACCTGCAATTCATGATGAGTGAAGCTGTGATCTACTGCTC 5284
OY 5101 tcaatttctgtgagatgagatgagatgagatgagatgagatgagatgagatgagatgag 5160
Db 5285 TCTATTTTGTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5344
OY 5161 tcaatctgtctcagcagaaggtccatgtgttccctcccaaatctgtcgtgtcagccct 5220
Db 5345 TTCAATGTCTTCCAGCAGAGATGCTTATGTGCTTCCACCAATCTGCTGTGTGATGCTT 5404
OY 5221 ctacttctgtgtatgt 5280
Db 5405 CTACTTGT 5464
OY 5281 aagatcccaagcagcagcctatgtgtgtcaccagcgttgaacacttctcatatgaat 5340
Db 5465 AAGATCCCAAGCAGACAGCTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5524
OY 5341 ggcagcgtgtgcccacttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5400
Db 5525 GGCAGCTGTGACACCTTGT 5584
OY 5401 gatacctgaagtcgt 5460
Db 5585 GATATCTGTAAGTCCGT 5644
OY 5461 gcaatggtgaaacaaacaggaatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5520
Db 5645 GACATGTGTGAAAAACAGAGCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5704
OY 5521 gtgtcaacatctctgt 5580
Db 5705 GTGTACCAATTAATCTTGT 5764
OY 5581 gtgtgttctctcctcaactgt 5640
Db 5765 GT 5824
OY 5641 gtaaatgcaaaagctatctcctcctgtgaatgtaagatgtaagatgtaagcgtggaagacag 5700
Db 5825 GTAAATGCAAAAGCTATCTCTCTGATGTGAATGATGAAGATGATGAGCGGGAAGACAG 5884
OY 5701 agaatcttgatgt 5760
Db 5885 AGAATCTTGT 5944

QY	5761	tataagaaggaaggaaggaagctgctgctgttgaacgaatttgcgttgggaattccctccctgctgag	5820
Db	5945	TATGAAGAAGGGAAGCCTGCTGTTTGACAGGATTTGGGAGGATTCCTCTGGGAG	6004
QY	5821	tgcttggagctctgggaagttaa'ttgaggatctggaaaaatcaaacacttccaagtltlaa	5880
Db	6005	TGCTTTGGGCTCCGGGAGTTATGGGCGCTGGAAATCATCAACTTTCAAGTGTTAACA	6064
QY	5881	ggagaataccactgttaaccagaagagatgcttcttccttaacaaaatagatattalcaaac	5940
Db	6065	GGAGATACCACTGTTACCAAGAGAGATGCTTTCTTAACAGAAATGATCTTATCAAC	6124
QY	5941	atcaataaataacatacaagaacatgggactactgtccctcaagtcttgatggcatcaagagctg	6000
Db	6125	ATCCATAGATACATACAGAACATGGGCTACTGCGCTCAGTTTGATGCCATCACAGAGCTG	6184
QY	6001	ttgacttggagagaacacgyltgagatcttcttgcccttltgagagagatcccaagaagaag	6060
Db	6185	TTGACTGGAGAGAACACGTTGGAGTTCTTTGGCCCTTTTGAAGAGAGTCCCAAGCAAGAA	6244
QY	6061	gttggcaaggttggatggatgtgggagatctggaaacttgggacttggatgaatgagagaanaa	6120
Db	6245	GTTTGGCAAGGTGGGTGATGGGAGATTCGAAACTGGGCGCTGTAAGATGAGACAAAAA	6304
QY	6121	tatgttgtaactaataatgtaggacaacaacgaagctctctacaagcaatgtgcttgaac	6180
Db	6305	TATGCTGGTAACTATATGTGAGGCAACAAACGAACCTCTTACAGCCATGGCTTTGATC	6364
QY	6181	ggaggagccctctgtgtgttcttgatagaaccacacagcaatgatacccaagcccg	6240
Db	6365	GGCGGGCCTCCTGTGGGTGTTCTTGATGAACCCACACAGGATGATGATCCCAACCCCGG	6424
QY	6241	cggtctcttggagaattgtgtgccctaagtgtgtgaagaaggagagatcagtaagtgttaca	6300
Db	6425	CGGTTCTTGTGGAATTGTGCCCTTAAGTGTGTGTAAAGAGGAGATCACTACTGCTTACA	6488
QY	6301	tctatagtatlgagaagaatgltgaagctcttgcactagaatgagcaatcaatgtlcaatgga	6360
Db	6485	TCTCATAGTATGAGAAATGTGAAGCTCTTTGCATAGATGGCAATCATGGCTCAATGGA	6544
QY	6361	aggttcagggtgtcccttggcagltgtccagaatcttaaaaataglttggagaatgttataca	6422
Db	6545	AGGTTCAAGTCCCTTGGACAGTGTCCACACTTAATAAATAAGTTTGGAGATGGTATACA	6604
QY	6421	atagtgtgaagaatagaagaaggttccaacccggagactgaagcctgtgccagaattctlttga	6480
Db	6605	ATAGTTGACGAATAGCAGGGTCCAAACCGGACCTGAAGCTGTCCAGGATTTCTTTGGA	6666
QY	6481	cttgcaattctctggaagtgttcttaaaagagaacacccggaacatgtctacaataccaagctt	6544
Db	6665	CTTGCAATTTCTCGAAGAGTGTTCACAAAAGAAACACCGGACACTGCTACAAATACACAGCTT	6724
QY	6541	ccatctcaatatctctctcggccaagagatactcaagacccctccccaagagcaaaaagcga	6600
Db	6725	CCATCTTCATTATCTCTCTCTGCGCAGGATTTTACGATCCTCTCCCAAGCAAAAAAGGA	6788
QY	6601	ctccaacatagaagactactctgttcttcagaacaacacttgaaccaaglatitggaactt	6666
Db	6785	CTCCACATAGAAAGACTACTCTGTTTCTCAACACAAACTGTGACCACMACTATTTTGAACTTT	6844
QY	6661	gccaaaggacaaagtgaatgaatgaccaccttaaaagacctctcatcaacaaaacagaca	6722
Db	6845	GCCAAAGACCAAAGTGAATGATGACCACTTTAAAAGACTCTCATTTACACAAAAACAGANA	6900
QY	6721	gtagtggacgttggacgttctacactcttcttacaagatagaagaagtgaagaanaagctat	6788
Db	6905	GTAGTGGACGTTGGACGTTCTCACATCTTTTCTACAGATGAGAAAGTGAAGAAACTAT	6966
QY	6781	gfatgaagaatccgtttcatatcg	6804
Db	6965	GATGAGAAATCTGTTTATACGG	6988

AX139817	RESULT 11			
LOCUS	AX139817			
DEFINITION	Sequence 69 from Patent EP1096012.	9741 bp	DNA	linear
ACCESSION	AX139817			
VERSION	AX139817.1	GI:14275399		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 9741)			
TITLE	Deneffe, P., Rosier-Montus, M.F., Arnold-Reguigne, I., Prades, C., Naudin, L., Lemouine, C., Duvergier, N., Jaye, M., seaross II, G.H., Remaley, A., Brewer, H.B. and Dean, M.			
JOURNAL	Nucleic acids of the human abcl gene and their therapeutic and diagnostic application			
FEATURES	Patent: EP 1096012-A 69 02-MAY-2001;			
source	Aventis Pharma S.A. (FR)			
	Location/Qualifiers			
	1..9741			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
BASE COUNT	2650 a 2180 c 2230 g 2620 t			1 others
ORIGIN				

Query Match	99.7%;	Score 6784.8;	DB 6;	Length 9741;
Best Local Similarity	99.8%;	Pred. NO. 0;		
Matches 6792; Conservative	0;	Mismatches 12;	Indels 0;	Gaps 0;

OY	1	atgctctgttgccctacgcttgagttctctctgtggaagaacctactctcagaagaaga	60
Db	185	ATGGCTGTGTGGCCCTCACCTAAGGTGCTGTGTGGAGAAACCTCACTTTCACAAAGAC	244
OY	61	caaacatgtcagctgttactctgtaagtgagctcgagctctattctctccgactccgata	120
Db	245	CAAACATGTCAAGCTGCTGCTGTGAAGTGGCCGTGGCTCTATTACTCTCGATCTGATC	304
OY	121	tctgttcgcttgagcttaccacacactatagaacaatgagccatttccaataaagcc	180
Db	305	TCTGTTCGGCTGAGCTACCCACCCCTATGAAACATGAATAGCCATTTTCCAAATTAAGCC	364
OY	181	atgcctcttgaggaagaaccttcttggtttgaaggagattatcttatagcacaacccc	240
Db	365	ATGCCCTTGCAAGGAACCTTCTTGGTGTGAAGGATTAATCTTAATGCCCAACACCC	424
OY	241	tgtttccgtttaccgaactccctcgggagagctcccgagtttgttggaaactttaacaatcc	300
Db	425	TGTTTCGTTACCGGACCTCTTGGTGTGAAGGAGCTCCGAGTGTGTGAACCTTAACAATTC	484
OY	301	attgttgctgcgcgttctcagaatgcttggaagctctttatagaccgaagaagacc	360
Db	485	ATTGTGGCTCGCCTTCTTCAGATGCTCGAGAGCTTCTTTATTCACCCAGAAAGACACC	544
OY	361	agcatgaagaagacatgcgcaaatgttcgtgaacatlaagcagcatcaagaataccagctca	420
Db	545	AGCATGAAGACATGCGCAAAAGTTTGTGAACATTACAGCAGATCAAGAAATCCAGCTCA	604
OY	421	aacttgaagcttcaagattctctgtgtgacaatgaaacctctctcgtggttccatalcac	480
Db	605	AACTTGAACCTTCAAGATTTCTCGTGTGACAAATGAACCTTCTCGGTGCTCTGTATCAC	664
OY	481	aaactctctctccaaagtctactctgtggaagaagatgcgtgaagagctgtgtgcatctccac	540
Db	665	AACCTTCTCTCCCAAGTCTACTGTGACAAGATGCTGAAGGGCTGATGTATTTCTCCAC	724
OY	541	aaggtatcttllgcaagctacacagcttacaatllgacaagtctgtgtcaatllgatacaaatca	600
Db	725	AAGCTATTTTTCGAAGGCTACACAGTTTACATTTTGAACAAGTGTGCATATGATCAAAATCA	784
OY	601	gaagagatgataccaacttgggtgaaccaagaagttctcgaagcttltgtgacctacaagaagag	660

QY 2821 accacacgtcaatccctgaacgggtgtgtcccccagactgggagccgcttaactctg 2880
|||||
DB 3005 ACCACCATGTCAATCCTGACCGGCTGTGTCCCGACCTGGGACCGCCCTACATCTCG 3064
QY 2881 ggaagagacattcgctctgagatgagccacatccgagacacttgggggtgtcccccag 2940
|||||
DB 3065 GGAAGAGACATTGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCGAG 3124
QY 2941 cataacgtgtctgttgaacatgtgactgtcgagaacacatctgtgttctatgtcccgcttg 3000
|||||
DB 3125 CATTAAGTGTCTTTGACATGCTGACTGTGCAAGAACACATCTGGTTCATGCCGCTTG 3184
QY 3001 aaagggctctctgagaagacagtgaaagcgagatgtggagcagaatggcccttgatgtgt 3060
|||||
DB 3185 AAAGGGCTCTCTGAGAAAGCAGCTGAAAGCGGAGATGGAGACAGATGGCCCTGATGTGGT 3244
QY 3061 ttggccatcaagcaagcttgaagaagcaaaacagccagctgtcaggtggaatgagaagaag 3120
|||||
DB 3245 TTGGCCATCAAGCAAGCTGAAAAAGCAAAACACAGCTGTCCAGTGGATGCAAGAAAG 3304
QY 3121 ctatctgtgtgctgtgctgtgttcggggatctaaaggtgtcatctctgtgatacccca 3180
|||||
DB 3305 CATATGTGGCCCTTGCCCTTTGCGGGGATCTAAGGTGTCTATCTGTGATGAACCCACA 3364
QY 3181 gctgtgtgtgaccccttaactcccgccaggggaatatgtggagctgtctgtaataaccgaca 3240
|||||
DB 3365 GCTGTGTGTGACCCCTTACTCCGCGACAGGGAATATGGAGCTCTCTGAAATACGACACA 3424
QY 3241 ggcgcgaccattatctctctcaacacacatgtagagcgagctcctgtggggagag 3300
|||||
DB 3425 GGGCGACCATTAATTTCTCTCTACACACACATGAGTAGAAGCGAGAGTCCCTGGGGGACAG 3484
QY 3301 attgcacatcctcccatgtgggaagctgtgtgtgtgtccctccctgttcttgaagaac 3360
|||||
DB 3485 ATTGCCATATCTCCCATGGGAAGCTGTGTGTGTGGCTCTCTCTCTTTCTGAAAGAC 3544
QY 3361 cagctgtggaacagagcttactaactgactgtgtgtcaagaagaatgttgaatcccccag 3420
|||||
DB 3545 CAGCTGGAGAACGGCTACTACTGACCTTGTGTCAAGAAAGATGTGAATCCTCCCTCAAT 3604
QY 3421 tctctgagaacacagtagtagcaactgtgtcatccttgaaaaagaggacagtgcttctcag 3480
|||||
DB 3605 TCTTGCAAGAAACAGTAGTAGCACTGTGTCACTACCTGAAAAAGAGAGACAGTGTCTCAG 3664
QY 3481 agcaagttctgaatgt 3540
|||||
DB 3665 AGCAGTTCATGATCTGTGGCTGGGACGACGACATGAGAGATGACACGCTGACCATCGATGTC 3724
QY 3541 tctgtcatctcaacactcaatcaagcaagcatgtgtgtgaagcccggtgtgtgtgaagacata 3600
|||||
DB 3725 TCTGTCTATCTCAAACTCATACAGAAAGCATGTGTCTGAACCCGCGCTGTGTGAAGACATA 3784
QY 3601 gggcatalgagctgaactatgtgtgtcatatgaagctgtctlaagaggaggagccttgtgaa 3660
|||||
DB 3785 GGGCATGAGCTGACATATGTGTGTCTCATATGAGCTGTCTAAGAGAGGAGGAGCTTTGTGAA 3844
QY 3661 ctctttcatgagatgt 3720
|||||
DB 3845 CTCTTTCATAGATGTGATGACCGGCTCTCAGACCTGGGCAATTCATGATTATGACATCTCA 3904
QY 3721 gagaagcccttggaagaataatctcctcaaggtgtgcgaagaagagtggtgtgtgtgtgtgt 3780
|||||
DB 3905 GAGAGCAGCCTTGAGAGAAATATTCCTCAAGCTGGCGCAAGAGAGTGGGTGTGTGAG 3964
QY 3781 acctcagaatgtacctgtgcagcagaagaagaacagcggtgtgtgtgtgtgtgtgtgtgtgt 3840
|||||
DB 3965 ACCCTCAAGATGTATCTTGCAGCAGCAAGCAAGGAGGAGGAGCTTCCGGGCAAGAGAGAGC 4024
QY 3841 tgtcttgcccggttcaactgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3900
|||||
DB 4025 TGTCTTGCCCGGTCACTGAGATGATGCTGTGATCCAAATGATTTCTGACATAGACCA 4084

QY 3901 gaatccagagagacagactgtgtcagtggaatgtgcaagaaggttccactcaagtgtaaa 3960
|||||
DB 4085 GAATCCAGAGAGACAGACTTGTCTAGTGGATGATGGCAAGGCTCTTCCAGAGTGAA 4144
QY 3961 ggtctgaacttacacagcaacagltgtgtcccttgtgtgaagagactgtcaattgtcc 4020
|||||
DB 4145 GGTGTGAACCTTACACAGCAACAGATTGTGGCCCTTTGTGTGAAGAGACATGATTAATGGCC 4204
QY 4021 agaagagatgtgaaagatlttltgtccagatgtgtctgtccagctgtgtgtgtgtgtgt 4080
|||||
DB 4205 AGACGGAGTGGAAAGATTTTGTCTCAATGTGTGTGCAAGTGTGTGTGTGTGTGTGTGT 4264
QY 4081 ggcctgtgttcagcccgatcgtgtccaccccttgtgcaagtaaccacagcctgtgaactcag 4140
|||||
DB 4265 GCCCTTGTGTTCACCTGTATGTGTCCACCTTGTGGAAAGTACCCACCTGTGAATCTCAG 4324
QY 4141 cctctgataltaacaagcaatgatacatgtgtcagcaatgtatgtctctgtgagacagga 4200
|||||
DB 4325 CCTGTGATGTACAAAGCAACATGATACATTTGTGTGCAATGTGTCTCTGTGAGGACCGGA 4384
QY 4201 acctgtgagacttaaacgcctcaccaagaacccctgtgtgtgtgtgtgtgtgtgtgtgtgt 4260
|||||
DB 4385 ACCCTGGAATCTTAAACGCTTCACCAAGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 4444
QY 4261 ggaaccccaatcccaagacagccctgtccagcgagggaggaagatgtgaacctgtccca 4320
|||||
DB 4445 GGAAMCCCAATCCAGACAGCCCTGTCCAGGACGGAGGAGAGTGTGACACCTGCCCA 4504
QY 4321 gtcccaagaccatcatgagactcttccagaaatgtggaactgtgaaatgtcgaagacctca 4380
|||||
DB 4505 GTTCCCCAGACCATATGATGACCTTCTCCAGATGTGTGCAATGTGTGCAAAACCTTTCA 4564
QY 4381 cctgtatcagatgt 4440
|||||
DB 4565 CCGTGTATCCAGT 4624
QY 4441 gcaagggggt 4500
|||||
DB 4625 GCAGGGGGGCTGCTCTCCACAAAGAAACAAACATGTGAGATATCTTCCAGGACTGTG 4684
QY 4501 acaggaagaacatttctgtatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4560
|||||
DB 4685 ACAGGAAGAAACATTTGCGATTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4744
QY 4561 ttaagaagaacagatctgt 4620
|||||
DB 4745 TTAAGGAACAGATCTGT 4804
QY 4621 aatactcaagcaactcctcccgatgcaagaagltlaatgtagtccatcaacaataagaaga 4680
|||||
DB 4805 AATFACTCAAGCACTTCTCCGAGTCAGAAAGTTATGTATGTCCACCAAAACAATCAAGAAA 4864
QY 4681 caactcaagctgt 4740
|||||
DB 4865 CACCTTAAGCTGTGCAAGAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4924
QY 4741 atgcaagagctgtgacacagaaataatgtcaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4800
|||||
DB 4925 ATGACAGGAGCTGTGACCCAGAAATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4984
QY 4801 gcaatcagctcttccctgtgaatgtcatcaacaalgtccatcttcccggtccaactgtgaag 4860
|||||
DB 4985 GCAATCAGCTCTTCTGT 5044
QY 4861 ggaagaaaccttagcatatgaaatgaattactgtcttcaatcaatccctgtatctcaag 4920
|||||
DB 5045 GAGAGAACCTTAGCATATGTGAATTTACTGTCTTCAATCAATCCCTGTGAATCTCCAGAG 5104
QY 4921 cagcagctctcagaggt 4980
|||||
DB 5105 CAGCAGCTCTCAGAGGT 5164
QY 4981 gtaatcttgcgaatgt 5040

Db 5165 GTCATCTTGCATATGCTTCCTCCAGCAGCTTTGCTGATCTTCATGCCAGAGCGG 5224
Qy 5041 gtcagcaagaacaaacctgcagtcacagtgagtgaggaagcgtgcaactgacgtc 5100
Db 5225 GTCAGCAAGCAAAACACCTGCAATCATCATGAGTGAAGCCGCTCATCTACGCGCTC 5284
Qy 5101 tctaatcttgctggagatgtagcaatgacgtgaccccgcaactgagtcactc 5160
Db 5285 TCTAATTTGCTGGATATGCAATTAAGTGTGCTCCGCACTGGTCAATTAATC 5344
Qy 5161 ttcactgctcccaagaagaagctcactgctgctcccaacccactgctgtagccct 5220
Db 5345 TTCATCTGCTCCAGCAAGATGCTATGTCCTCCACCAATCGCTGTAGCCCTT 5404
Qy 5221 ctactcttgctgtagtggtgctcaatcaactcctcaagtaccagctccttgctc 5280
Db 5405 CTACCTTTGCTGATGGGGTCAATCACACCTCATATGACCCCTCTTGTGCTTC 5464
Qy 5281 aagatcccaagcacaagcctatggtgctcacaagcgtgaacctctcactgacat 5340
Db 5465 AAGATCCCAAGCAAGCCATATGCTGCTCACCAAGCTGAACCTCTTCAATGGCATTAAT 5524
Qy 5341 ggcagcgtggccacacttgctgtagagctgtcaccagaataaagctgaataataat 5400
Db 5525 GGCAGCGTGGCCACTTTGTGCTGGAGCTGTCCACGACAAATAGCTGATTAATCAAT 5584
Qy 5401 gatattccgaagtcgtgctgctgctgctcccaactttgctgctgagcagagctc 5460
Db 5585 GATATCTTAAGATGCTGTTGATCTTCCACATTTTGTGCTGGAGGAGGCTCATC 5644
Qy 5461 gacatgtagtaaaacacagcaatgctgtagtgccctggaaaggttgggagagatcgctt 5520
Db 5645 GACATGTAAGAAACACAGGCAATGCTGATGCTGCAAGATGGTGGGAGATGCTTT 5704
Qy 5521 ggtgcaactatcttgtagaacttgtaggagaaacactctcgcagtaggcgtgagag 5580
Db 5705 GGTGCAACATATCTTGGGAGCTTGGGAGCAAAACCTTTCGCCATGGCCCTGGAAGG 5764
Qy 5581 gtagtctctcctcaactgctgctgctgctgctgctgctgctgctgctgctgctgct 5640
Db 5765 GTGCTTTCTTCTCTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5824
Qy 5641 gtaaatgcaaaagctatcctcctgtagatgaagaagaatgtagagctgtagagcaag 5700
Db 5825 GTAAATGCAAAAGCTATCTCTCTGATGATGAATGAAGATGAGGAGGAGGAGACAG 5884
Qy 5701 agaattctgtagtggtgtaggagcagaatgacatccttaagaatgaagtagtgagag 5760
Db 5885 AGAATTTCTGATGAGTGGAGGCAAGATGACATCTTAAGAAATCAAGCTGACGAAGATA 5944
Qy 5761 tatagaagaagcaggaagcctgctgctgcaagatgctgctgtagcctcctcctgtag 5820
Db 5945 TATAGAGAGCAAGGAGAGCTGCTGCTGATGACAGATTTGGTGGGATTCCTCTGCTGAG 6004
Qy 5821 tgccttgtagcctcctgtaggagtagtgtaggagcagaaatcaactcctaagaatglaa 5880
Db 6005 TGCCTTGGGCTCTCTGGAGTTATGCGGCTGGAATAATCATCAACTTTCAGATGTTACA 6064
Qy 5881 ggaagataccactgtagcagaagagatgcttctcctaacaataaagratcttcaaac 5940
Db 6065 GGAAGATACCACTGTTACCAAGAGAGATGCTTCTTAACAGAAATAGATCTTATCAAC 6124
Qy 5941 atccatgaagtagcagaacatgtagcctgctgctcctcctgtagtgcatacagagctg 6000
Db 6125 ATCCATGAAGTACATGACAGATGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6184
Qy 6001 ttgactgtagagagaacagtgtaggtctcttgccctcttgagaagagagctccagaagaag 6060
Db 6185 TTGACTGGAGAGAACAGTGGAGTTCTTGGCTTTTGAAGAGGCTCCAGAGAAAGAA 6244
Qy 6061 gtagcagaagtgtagtagtgagcgaatcggaactggcctcgtagtagtagaagaa 6120

Db 6245 GTTGCAAGGTTGGTGAAGTGGGCGATTGGAACCTGGCCCTCGTGAAGTATGAGAAAA 6304
Qy 6121 tagctgtagtaactatagtgtaggagcaacaacgcaagctctctcagccatgcttgatc 6180
Db 6305 TATGCTGTAATCTATGATGAGGAGCAACAAACGCAAGCTCTCTACAGCATGCTTTGATC 6364
Qy 6181 ggcgggctcctctgtagtctcctgtagaagcacaacacagagtagtagtccaaagccgg 6240
Db 6365 GCGCGGCTCTGCTGCTGCTTCTGATGAACCCACCAAGCATGATCCCAAGCCCG 6424
Qy 6241 cgttcttgtagaattgtagcctaagtgtgtagaagagggagatcagtagtcttaca 6300
Db 6425 CGTTCTTGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6484
Qy 6301 tctcatgtagtagaagatgtagaagctcttgtagtagtagtagtagtagtagtagtag 6360
Db 6485 TCTCATAGTATGAGAAATGAGAAAGCTTGTGACATGAGATGCAATGAGCAATGGA 6544
Qy 6361 aggtcagtagccttgtagcagtagtagtagtagtagtagtagtagtagtagtagtag 6420
Db 6545 AGGTTCAGGTGCTTGGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6604
Qy 6421 atagtgtagaagtagcagagtagtagtagtagtagtagtagtagtagtagtagtagtag 6480
Db 6605 ATAGTTGATGATGAGCAAGGATGCAACCCGAGCTGCAAGCTGCTGCAAGCTTTTGA 6664
Qy 6481 ctgcatctctgtagaagtgtcttaaaagaaacacggagaaatgctacatccagctt 6540
Db 6665 CTTCATTTCTCTGGAAGTGTGCTCAAAAGAGAAACACCGGAGCAATGCTACATACAGCTT 6724
Qy 6541 ccatctcatalatctctcctgtagcagagatctcagacatctcctcagagcaaaagcga 6600
Db 6725 CCATCTCATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6784
Qy 6601 ctccacatagaagactactctgttctcagacaacacttgaaccaagtattgtgaactt 6660
Db 6785 CTCACATAGAAAGCTCTCTGTTTCTCAAGACAAACCTTACCAAGATTTTGAACCTT 6844
Qy 6661 gccaaagcaaaagttagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 6720
Db 6845 GCCAAGAGCAAAATGATGATGACCACTTAAAGACCTCTCATTTACACAAAAACGAGA 6904
Qy 6721 gtagtagcagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 6780
Db 6905 GTAGTGACAGTGTGCAAGTCTTACATCTTTCTACAGATGAGAAAGTGAAGAACTAT 6964
Qy 6781 gtagtagaagatcctgttctcagag 6804
Db 6965 GTATGAAGAAATCTGTTCAATACG 6988

RESULT 12
AX351038
LOCUS AX351038 9741 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 10 from Patent WO0183746.
ACCESSION AX351038
VERSION AX351038.1 GI:18616393
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (sites)
AUTHORS Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Deneffe, P.,
Brewer, B., Duverger, N., Remaley, A., and Santamarina-Fojo, S.
TITLE Regulatory nucleic acid sequences of the abcl gene
JOURNAL Patent: WO 0183746-A 10 08-NOV-2001;
Aventis Pharma S.A. (FR)
FEATURES
source location/Qualifiers
1..9741
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2650 a 2180 c 2290 g 2620 t 1 others

ORIGIN

Query Match 99.7%; Score 6784.8; DB 6; Length 9741;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6792; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 atgagctgttggccctcagctgaagttgtctgtctgtggaagaacctcatttcagaaga 60
DB 185 ATGGCTTTGGCTTCAGCTGAGGTTGCTGTGGAAGAACCTTCAGGAAGAA 244
QY 61 caaacatgcagctgttacttggaaagtgagcccttattcttctcgtatcctgagc 120
DB 245 CAACATGTCAGCTGCTGCTGGAAGTGGCTTCTTTATCTCTGATCTGATC 304
QY 121 tctgttcgctgagctaccaccctatgaaacaatgaaatgcaatcttccaaataagcc 180
DB 305 TCTGTTCGGCTGAGTACCCTATGAAACAATGAATGCCATTTTCCAAATAAAGCC 364
QY 181 atgacctcgcaggaacacttcttctgttgcagggatattctgtaatgcaacaacccc 240
DB 365 ATGCCCTTCGAGGAACCTTCCTTGGGTTCAGGGATTTATCTGATTCACCAACCCC 424
QY 241 tgttccgttaccagactcctg99gagctcccgagttgttggaaacttacaacatcc 300
DB 425 TGTTCCTGTAACCGACTCTCGGGAGGCTCCCGAGTTGTTGGAACCTTTAAACAATCC 484
QY 301 attgtgctgcgctgttctcagaatgctgagagctcttattacaagcagaagaaccc 360
DB 485 ATTGTGGCTCGCTGTCTCAGATGCTCGAGGCTCTTTTATACAGCCAGAAAGCACCC 544
QY 361 agaatgaagacatgagcgaagttctgagaacatcacagaacaaatcaagaatccagctca 420
DB 545 AGATGAGAGACATGGGCAGAAAGTTTGAAGACTTACAGCAGATCAAGAAATCCAGCTCA 604
QY 421 aacttgaagcttcaagaattctctgtgtgacaatgaaaccttctgtgttccatac 480
DB 605 AACTTGAAGCTTCAGATTTCTGTGTGACAAATGAACCTTCTGTGGTCTCTGATAC 664
QY 481 aacctctctcccaagagctactgttggacaagaatgctgaaggctgatatcttccac 540
DB 665 AACCTCTCTCCCAAGTCTACTGTGACAAAGATGCTGAGGCTATGATTCATTTCCAC 724
QY 541 aaggtatttttgcagagctaccagttacatttgacaagctgtgcaatgagatcaaaatca 600
DB 725 AAGGTATTTTGCAGAGCTACAGTTACATTTGACAAAGTGTGCAATGATGATCAAAATCA 784
QY 601 gaagagatgattcaacttggatgacaaagaagttctgaagcttgtgtgcttaccagaagag 660
DB 785 GAAGAGATGATTCAACTTGTGACCAAGAGTTTGTGAGCTTGTGGCTACCAAGGAG 844
QY 661 aaactgtctcagagagagagagacttcttccaacaatgaaacttccgaagccaatccg 720
DB 845 AAATGTGCTCAGAGAGAGGAGTACTTGTTCACCAATGACATCCCGAAGCCAAATCTCTG 904
QY 721 agaacataactatcatcttccctcccgcaagagagctgtgtaagccacaacaa 780
DB 905 AGAACATTAACACTTACATCTCCCTTCCGACGAGAGAGCTGGCCGACCAAAAAACA 964
QY 781 ttgtcatagcttcttggagctctgcccagagctgttccagcatgagaagctgtgagatgac 840
DB 965 TTGTGATGATGCTTGGAGACTTGGCCAGAGAGCTGTTCAGCATGAGAACTGAGAGTAC 1024
QY 841 atgcagacagagatgattgttctgacaatgtaaacagctccagctctccacccaatc 900
DB 1025 ATGCGACAGAGAGTGTGTTTGTGACCAATGTGAACAGCTCCAGCTCTCCACCAATC 1084
QY 901 taccagctgtatctgtattgttctgtgagcatcccgagagagagagagctgtgaagatcaag 960
DB 1085 TACAGAGCTGTGCTGTGATTTGTGCGGCAATCCGAGGAGAGGAGGCTGAAAGATTAAG 1144
QY 961 tctctcaactgtgtaagagacaacatacaagccctcttggagagcaatgtgactgag 1020
|||||

DB 1145 TCTCTCAACTGATGAGGACACMACACTACAAAGCCCTTTTGGAGGCAATGGCACTGAG 1204
QY 1021 gaagatgctgaacaccttctatagacaactcttaccatgcaatgattgataag 1080
DB 1205 GAAGATGCTGAACCTTCTATGACAACTTCAACCTCTTATCTGCAATGATTAAG 1264
QY 1081 aatttgagctagcttctcttcccgatattctggaagctctgaaagccgtgctgt 1140
DB 1265 AATTGGAGTCTAGTCTCTTCTCCGCAATTAATGGAAGCTGTGAAGCCGCTGCTGTT 1224
QY 1141 ggaagatcctgtatacaactgacaactccagcaaggaagtcagtgtgagtgagac 1200
DB 1325 GGAAGATCTGTATACCTGACATCCAGCCCAAGAGCGAGTCATGGCTGAGGTCGTAAC 1384
QY 1201 aagacctccagagactgagctgttccatgatttgaagagcatgtggaggaactcagc 1260
DB 1385 AAGACTTCCAGGAACCTGCTGTGTTCATGATTTGGAAGGCAATGTGGAGGAACCTAGC 1444
QY 1261 cccaagatctgaccttcatggaagacagccaagaatggaactgttccgagatgtgtg 1320
DB 1445 CCAAGATCTGAGCTTTCATGAGAACAGCCAAAGAAATGACCTTGTCCGATGCTGTTG 1504
QY 1321 gacagagagacaatgacacttcttggaaacagcaatgttgagcttagatggacagcc 1380
DB 1505 GACACAGGAGCAATGACACTTTTGGAGACAGAGTTGGATGCTTGAATGACAGCC 1564
QY 1381 caagacatcgtgtgttcttggccaagcaccagaagatgtgtccagtcagatgttct 1440
DB 1565 CAGACATCTGTGCTTTTGGCCAGACCCAGAGATGTCAGTCCAGTAATGTTCT 1624
QY 1441 gtlacaccttggagagaaacttcaacagagactaaccaagcaatccggaatccatctgc 1500
DB 1625 GGTACACTCGAGAGAGACTTTCAACGAGACTAACCGCAATCCGACCATATCTGCG 1684
QY 1501 ttcatgagatgtgttaacctgaacagatgaacccatagaacagaagatctgtctatc 1560
DB 1685 TTCAATGAGTGTGTACCTGMAAGCTGAAAGCCATGACAGCAAGAGTCTGGCTCAATC 1744
QY 1561 aacaagctcagagctgtgtatgagagagagttctgtgtgtatgttctacatgga 1620
DB 1745 AACCAAGTCAATGAGACTGCTGTGATGAGAGAACTTCTGGCTGTATGTCTTCACTGGA 1804
QY 1621 attactcagagcagatgtgagctgcccatcatgttcaagtacaagatccgaatggacatt 1680
DB 1805 ATTACTCCAGCAGACTGAGCTGCCCATCATGCAATGCAATCCGAATGAGACATT 1864
QY 1681 gacatgtgagagagaaataaatacaagatgtgtactgtgagccctgtgtccagct 1740
DB 1865 GACAAATGTGAGAGACAAATTAATAATCAAGATGTGACTGTGGACCTGTGCTCGAGCT 1924
QY 1741 gacaccttggagacatgtgtgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1800
DB 1925 GACCCCTTTGAGGACATGCGGTACGTGTGGGGGCTTCGCTACTTGCAGATGTGCTG 1984
QY 1801 gacagagcaatcatcaaggtgtgtgagcagcagcagcagcagcagcagcagcagcagc 1860
DB 1985 GAGCAGGCAATCATGAGGCTGTGACGGGACCGAAGAAACATGCTATATGGA 2044
QY 1861 cagatgacctatccctgttagatgtatgacatcttctgtgtgtgtgtgtgtgtgtgt 1920
DB 2045 CAGATGCCCTATCCCTGTAGCTTGTGACATCTTGTGCGGATATGACCGGCAATG 2104
QY 1921 cccctctcatagcctgtgcccgtgtattctcagtgagctgtatcatcaagagcagctg 1980
DB 2105 CCCCTTTATAGCTGTGGCTGTGATTAATCAAGTGTGTATATCAAGGCAATGCTG 2164
QY 1981 tatgaaagagagcagcgttgaagagacatgtgagatcatgtgagcctgtgacaacagcata 2040
DB 2165 TATGAAGAGAGGACAGGCTGAAAGAGACATCGGATCATGAGGCTGACAAACAGCATC 2224
QY 2041 ctctgttagctgttcatgttagctcatctctctctgtgtgtgtgtgtgtgtgtgtgt 2100
DB 2225 CTTGTGTTAGCTGTGATTAATGATGACCTCATCTTCTTGTGAGGCTGTGCTGCTA 2284
|||||

[illegible][illegible]

D	4445	GGAAACCCAAATCCGACACACCCCTGCGACGACAGGGAGAAAGTGGACACTGCCCCA	4504
O	4321	gttcccaagaccatcatagagaccctctccagaatggagacgtggaaccccttca	4380
D	4505	GTTCCCCAGACCATCATGAGACCTTTCCAGATGCGGAACCTGGCAATGCGAACCCTTCA	4564
O	4381	ccctgcatgacagtgtagaagcgacaaatcaagaagaatgctgcctgtgtgttccccaggg	4440
D	4565	CCTGCATCCAGTGTAGAGCGACCAAAATCAGAAAGATGCTGCTGTGTGCCCAAGGG	4624
O	4441	gcaagggggagcgcctcctcccaagaagaacaacaactgcagatatcctccagaccctg	4500
D	4625	GCAAGGGGGGCTGCTCCTCCCAAGAAACAAACATCGAGATATCCTTCAGAGACCTG	4684
O	4501	acaaggaagaacatcttcggatlatcggtagaagcgtatgtgcagatcatagccaagc	4560
D	4685	ACAGGAAACAAATTTGCGATTAATCTGGTGAAGACGTATGCGAGATCATAGCCAAAAGC	4744
O	4561	ttaagaagaacaagatctgggtgaatgagtttagtgaatgacgccttccctggggtgcagt	4620
D	4745	TTAAAGAAACAAGATGTGGGTGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTCAGT	4804
O	4621	aatactcaagacactccctccagctcaagaagttaatgtagccatcaacaatgaaagaa	4680
D	4805	AATACTCAAGACCTTCTCCGAGTCAAGAGTAATGATGCGACCAAAACAATGAAAGAA	4864
O	4681	caactaagcttggccaaggaagctctgagatctgattctccaagcttgggaagttc	4740
D	4865	CACCTAAAGCTGGCCAAAGACAGATTCTGCAGATCGATTTCCAACACTTGGGAAAGATT	4924
O	4741	atgaaagagactggaacacgaagaataatgtoaagttgtgttcaataaagaaggttcgat	4800
D	4925	ATGACACGAGACTGGAACCCAGAAATATCTCAAGGTGTGTTCAATACAAAGGCTGGCAT	4984
O	4801	gcaatcagctcttccctgaatgtcaacaatgccaatctccgggccaacctgcaaaag	4860
D	4985	GCAAATCAGCTTTCTCTGAATGTCTATCAACAATGCCATTCTCCGGGCCAACCTTCAAAAG	5044
O	4861	ggaaggaacccatgaacatattagaaatctgcttccaatcaatccctgaaatctcaacag	4920
D	5045	GGAGAACCCCTAGCCATTATGGAATTACTGCTTTCATCATCCCTGGAATCTCACCAAG	5104
O	4921	caagcagctctcagaggtgtgctctgaigaacaatcaagtggatgtccctgtgtccaatgtc	4980
D	5105	CAGCACTCTCAGAGGTGGCTCCGATGACCAACATCAGTGAATGTCCTTGTGTCCATCTGT	5164
O	4981	gtcatcttggcaatgtcctgtgtcccaagcagccttftgcfatcttcbaatcaagaaggg	5040
D	5165	GTCATCTTTGGCAATGTCTGTCCAGCCAGCTTTGTGTGATTTCTCATCAGAGAGCGG	5224
O	5041	gtcaagcaagaacaaacctgcagttcatcaatggagtggaagcctgtcatctactgtctc	5100
D	5225	GTCAGAAAGCAAAACACTGCAATTCATCATGAGTGAAGCCGTGATCATCGAGCTC	5284
O	5101	tcctaatctgtctgggaatgtgtgcaaatgaagttgtccctgcgcaacatggtcatatactc	5160
D	5285	TCTAAATTTTGTCTGGGATGTGTGCAATTAAGTTGTCCCTGCGCACACTGTCATTATATC	5344
O	5161	ttcatctgcttccaagagaagctcctaigtgtctccaacaatctgcctgtgtgtaacccct	5220
D	5345	TTTATCTGCTTCCAGCAAGAAAGTCTATGTGTCTCCACCAATCTGCTGTGTACCCCTT	5404
O	5221	ctactcttgctglataggtgtgatoaalcaacactcctaattgatacagaacgcctctgtgttc	5280
D	5405	CTACTTTTGTCTGATGTGGTGGTCAATCAACACTTCATGTATACCCAGCCCTCTTTGTATTC	5464
O	5281	aaatctcccaagacacataatgtgtgtccacagaagtgaaccttcaatgagcaat	5340
D	5465	AAGATCCCAAGCACAGCCTTATGTGTGTCTACCAAGGTGAACCTCTTCAATTGGCAATTAA	5524
O	5341	ggagcgtgtgacaccttctgtctgagcgtttcaaccgacaataaagctgaataatacaat	5400
D	5525	GGCAGCGTGGCCACCTTTGTCTGTGAGCTGTTCACCAATTAAGCTAATATATCAAT	5584
O	5401	gatalcctgaagtcocgtgtcttctgactctccacatcttggcctggagacgaagctcatc	5460
D	5585	GATATCTCGAAGTCCGCTTTTATGTATCTCCCAATTTTGTCCGGGACAGAGGCTCATC	5644
O	5461	gacatgtgtgaaaaacacgaagcatgtgcatagtcccttgaaaggtttgggagaaatgcctt	5520
D	5645	GACATGTGTAAAAACGACAGCAATGGCTCATGCCCTGGAAGGTTTGGGGAATTCGCTTT	5704
O	5521	gtgtcacattatcttggagacttgggtggagcgaacctcttcgcaatgcccgtggaaagg	5580
D	5705	GTTGCACATTATCTTTGGGACTTGTGTGGAGAAACCTTTGCGCATGGCCGTGGAGGG	5764
O	5581	gtgtgtcttctccataactaacgcttcgtgtacccagtaacagatcttcatcaagcccagact	5640
D	5765	GTGTGTTCTTCTCTATTACTTACTTGTGTGATCCAGTACAGATTCTTCATCAGGCCAGACT	5824
O	5641	gtaaatgcaaaactatctctctctgaaatgaatgaatgaatgtgtgagcgggaaagacag	5700
D	5825	GTAAATGCAAAAGCTATCTCCCTGTGAATATAGATGAAGATGTGAGCCGGGAAAGACAG	5884
O	5701	agaattcttgatgtgtgagggccaagaatgactcttagaataccaagaggttgaagaagata	5760
D	5885	AGAAATTTGATGTGTGGAGGCCAGATACATCTTAGAAATCAAGAGCTTACCAAGATA	5944
O	5761	tataagaagaacggaagcctgtctgttacaggaatttgcgtgggcattcctcctgtgtgag	5820
D	5945	TATAGAGGAACCGGAAGCTCTGTGACAGGATTTGCGTGGCATTCCTCGGTGAG	6004
O	5821	tgcttggcctccctgggagttaaatgggctgtgaaatcaatcaacttcaagatgttaaca	5880
D	6005	TGCTTTGGCTCTCTGGAGATTATGCGGCTGGAAATATCAACTTTCMAATGTATTAA	6064
O	5881	ggaagatacacglttaacgaagagatgcttcccttaacaaatagatcttcaaac	5940
D	6065	GGAGATACCACTTTRACGAGAGAGATGCTTTCCTTAACAGAAATAGTATTTATCAAC	6124
O	5941	atccatgaaglatcatagaacaatgggctactgtccctcagttgatgtcatcaagagctg	6000
D	6125	ATCCAGAAAGTACATAGAGAACATGGGCTACTCCCTCGATTGTGAGCCATACAGAGCTG	6184
O	6001	ttgactgggaaggaacaagatgaatcttctgccttcttgagaaggtcccaagaagaagaa	6060
D	6185	TTTACTGGGAGAACACGTGAGATTCTTGGCCCTTTTGAAGAGAGTCCAGAGAAAGAA	6244
O	6061	gttcgcaaggttggtagtgagtgagatctcggaaactgggacctgtgaaglatagagaagaa	6120
D	6245	GTTTGGCAAGTTGTGATGGGCGATTTCGAAACATGGGCTCTGTGAATGAGAGAAAAA	6304
O	6121	tatgtctgttactatagtgagggcaacaaacgaagctctcaagccatgagcttggatc	6180
D	6305	TATGCTGTGAATCTATGTGTGAGGCAACAAACGAAAGCTCTACAGCCATGTGCTTGTATC	6364
O	6181	ggcgggcctcctgtgtgttcttcgatagaaccacacagagatgagatcccaaaagcccgg	6240
D	6365	GGCGGGCTCTCTGTGCTGTTCGTGATGAACCAACACAGCATGATGATCCCAAAACCCGG	6424
O	6241	cggctctgtgaaatgtgcacctgaagtgtctcaagggagggagatcagtagtgttca	6300
D	6425		


```
|||||
Db 1618 GACAGAGGACCAATACCACTTTTGGAAACAGCACTTGGATGGCTTAATTGGACAGCC 1677
|||||
Qy 1381 caagacatcgttgcgttcttctgccaagcaoccagagatgctcagtcgaatggtct 1440
|||||
Db 1678 CAAGACATGCTGGCTTTTGGCCAAGCACCCAGAGAGATGCTCAGTCCAGTAAATGGTTCT 1737
|||||
Qy 1441 gttacacatctggaagaagcttccaacgactaaccaagcaatccgagccatctgc 1500
|||||
Db 1738 GGTGTACCTGGAGAAACCTTTCAACGAGACTAACCCAGCAATCCGGACCAATCTCC 1797
|||||
Qy 1501 ttcatgagtggtgtcaacctgaaacagctagaaccatagcaacagaaqcttgcctatc 1560
|||||
Db 1798 TTTATGAGAGGTGTCAACTGGAACAGCTAGAACCCATGCAACAGAAATCTGGCTCATC 1857
|||||
Qy 1561 aacaatccatgagagctgtctgatagagagaagttctggcgtgtatgtgtcactgga 1620
|||||
Db 1858 AACAGTCCATGGAGCTGTGATGAGAGAAAGTTCTGGGCTGGTATGTGTCACTGGA 1917
|||||
Qy 1621 attactccagagcaattgagctgcccctcatgtcaagtacaaatccgaatgagcatt 1680
|||||
Db 1918 ATTACTCCAGGACGACTTGGAGCTGCCCATCATGTCAAGTACAAAGATCCGAATGGACATT 1977
|||||
Qy 1681 gacaatgtgagagaggaacaaataaatacaagatggtgtactgagacctgttccctgagct 1740
|||||
Db 1978 GACAAATGTGAGAGAGCAAAATAAATCAAGAGATGGGTACTGGGACCCTGGTCTCCAGCT 2037
|||||
Qy 1741 gaacctctttagagacatgcgttactgtctggtggggtctgcgctactctgcaagatgtgtg 1800
|||||
Db 2038 GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGCTTCGCCCTACTTGGAGATGTGGTGC 2097
|||||
Qy 1801 gagcagagcaatcatcagagtggtgtcgtgaagggacccgagaagaactggtgtctatgcaa 1860
|||||
Db 2098 GAGAGGCAATTCATCAAGGTGCTGACGGGACCGAGAGAAACTGGTGTATATGACAA 2157
|||||
Qy 1861 cagatgcccctacccgtcttcaatgtatgacatcttctcgggtgtatgaaacggttaagt 1920
|||||
Db 2158 CAGATGCCCATATCCCTTTACGTGTGATGACATCTTTCTGGGGTGAATGACCCGCTCAAG 2217
|||||
Qy 1921 cccctctcatgacgtgcgttgatattactcagtgagctgtatcatcaagagcatcgtg 1980
|||||
Db 2218 CCCCTTTCATGAGCGCTGGCTGTGATTTACTCAGTGGCTGTGATCATCAAGGGCATCTGTC 2277
|||||
Qy 1981 taibaagaagagagcagcagctgaaagaacacatcgagatcagtcagggccctggacaacagata 2040
|||||
Db 2278 TATAGAGAGGAGCGACGGCTGAAAGAGAACATGGGATCTAGGGCCCTGGACAACAGATC 2337
|||||
Qy 2041 cctcgtgttagcgtgtcatattagctcatctcctctctctgttgaagcgttgcgtgcta 2100
|||||
Db 2338 CTCTGTTTTAGCTGTTCATTAGTAGCTCATTCCTCTCTTGTGAGCGCTGGCCTGCTCA 2397
|||||
Qy 2101 gttgtcatcctgaagtagaagaacctgcgtccctacagtgatccccagcgtgtgtgtgtc 2160
|||||
Db 2398 GTGTGTCAATCCGAAAGTTAGAGAAACCTGCTCCCTACAGTATCCCAACGAGTGGTGTGTC 2457
|||||
Qy 2161 ttctcgtccgtgtgtgtgtgtgtgtgtgaacatcctcgtcagtgctcctgatatgacaacttc 2220
|||||
Db 2458 TTCTGTGCGGTGTGCTGTGTGTGTACAAATCCTGTGAGTGTCTCTGATTAACACACTTTC 2517
|||||
Qy 2221 tccagaaagcaaacctgagcagcactgtggtgggagcatcatctactcagcgttaccctgccc 2280
|||||
Db 2518 TCCAGAGCCAACTGGCAGAGAGCTGTGGGGGCAATCACTACTACAGCTGATCACTGCC 2577
|||||
Qy 2281 taagtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2340
|||||
Db 2578 TACGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2637
|||||
Qy 2341 ctgtgtctcctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2400
|||||
Db 2638 CTGCTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2697
|||||
Qy 2401 ggcattgagatgagcagtgaggacaacctgtttagagagctcgttgaagaagatggtcctaact 2460
|||||
```

QY 3541 tctgcatctccaacctcatcaggagcatgtctcgaagcccgctgtgtgaagacata 3600
Db 3838 tctgcatctccaacctcatcaggagcatgtctcgaagcccgctgtgtgaagacata 3897
QY 3601 gggcatagcttgacatactgctgcacatagagctgcacaggaagagacattgtgga 3660
Db 3898 gggcatagcttgacatactgctgcacatagagctgcacaggaagagacattgtgga 3957
QY 3661 ctcttcataagatctgtagccgctctcagaccctgggcatcttcagttatgacatca 3720
Db 3958 ctcttcataagatctgtagccgctctcagaccctgggcatcttcagttatgacatca 4017
QY 3721 gagacacaccttgagaagaatattcctcaaggtgtgcgaagagagtggtgtgattgtg 3780
Db 4018 gagacacaccttgagaagaatattcctcaaggtgtgcgaagagagtggtgtgattgtg 4077
QY 3781 acctcagatgtagctctgcagcaagacgaagcggccttcggggagacaagcagagc 3840
Db 4078 acctcagatgtagctctgcagcaagacgaagcggccttcggggagacaagcagagc 4137
QY 3841 tgccttcgcccgtctcagtagaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3900
Db 4138 tgccttcgcccgtctcagtagaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4197
QY 3901 gaatccagaagacagactgtcagtgagatgtagtgcacaaaggtctcaccagtgtaa 3960
Db 4198 gaatccagaagacagactgtcagtgagatgtagtgcacaaaggtctcaccagtgtaa 4257
QY 3961 ggcctggaacttaacagcaacagatltgtgcctctgttggaagaagactgtcattgac 4020
Db 4258 ggcctggaacttaacagcaacagatltgtgcctctgttggaagaagactgtcattgac 4317
QY 4021 agacggaagtcggaagaagatttctgcagattgtctgcagcgtgtgtgtgtgtgtgt 4080
Db 4318 agacggaagtcggaagaagatttctgcagattgtctgcagcgtgtgtgtgtgtgtgt 4377
QY 4081 ggcctgtgtctcagcctgtgtgtgcacaccttgcgaagtagccagcagctgaactcag 4140
Db 4378 ggcctgtgtctcagcctgtgtgtgcacaccttgcgaagtagccagcagctgaactcag 4437
QY 4141 cctctgtagtacaagaagaagatcaacatttgcagcaatgtagtctcctgaagacagga 4200
Db 4438 cctctgtagtacaagaagaagatcaacatttgcagcaatgtagtctcctgaagacagga 4497
QY 4201 accttgaaactcttaaacgacctcaacaaagacacctgtgtgtgcgaagccgctgtatga 4260
Db 4498 accttgaaactcttaaacgacctcaacaaagacacctgtgtgtgcgaagccgctgtatga 4557
QY 4261 ggaacccaatcccaagacagcctgtgcagcagggaggaagatgtgaacacatgcacca 4320
Db 4558 ggaacccaatcccaagacagcctgtgcagcagggaggaagatgtgaacacatgcacca 4617
QY 4321 gttccccaagacatagactcttccagaatgtggaactgtgacaatgcagaaaccttca 4380
Db 4618 gttccccaagacatagactcttccagaatgtggaactgtgacaatgcagaaaccttca 4677
QY 4381 cctgtagtccagtgtagcagcagaacaatcaagaagatgtgcctgtgtgtgtgtgtgtgt 4440
Db 4678 cctgtagtccagtgtagcagcagaacaatcaagaagatgtgcctgtgtgtgtgtgtgtgt 4737
QY 4441 gcaagggggcgtgcctcctccacaagaacaaacactgtgacatctcctcagagctg 4500
Db 4738 gcaagggggcgtgcctcctccacaagaacaaacactgtgacatctcctcagagctg 4797
QY 4501 acaggaagaacatttgatattatgtgtgaagagatgtgtgcagatcatatgacaaagc 4560
Db 4798 acaggaagaacatttgatattatgtgtgaagagatgtgtgcagatcatatgacaaagc 4857
QY 4561 ttaagaagaacagatctgtgtgaatagtttagtgaagcgtcttccctgagtgtagt 4620
Db 4858 ttaagaagaacagatctgtgtgaatagtttagtgaagcgtcttccctgagtgtagt 4917

QY 4621 aatactcaagaacttccctcagtagtcaagaagttatagtagtgcacatcaacaaatgaagaa 4680
Db 4918 aatactcaagaacttccctcagtagtcaagaagttatagtagtgcacacaaatgaagaa 4977
QY 4681 caactaagcttgcccaagagacagttctcgaatagattctcacaacagcttggaagattc 4740
Db 4978 caactaagcttgcccaagagacagttctcgaatagattctcacaacagcttggaagattc 5037
QY 4741 atgacagacttggaacacagaataatgtcaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4800
Db 5038 atgacagacttggaacacagaataatgtcaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5097
QY 4801 gcaatcagcttctcctgaatgtcaatcaaaatgcaatctcctcgggccaactgtcaaaag 4860
Db 5098 gcaatcagcttctcctgaatgtcaatcaaaatgcaatctcctcgggccaactgtcaaaag 5157
QY 4861 ggaaggaacacctgaacatattaggaattactgtcttcacatctccctcgaatctcaaga 4920
Db 5158 ggaaggaacacctgaacatattaggaattactgtcttcacatctccctcgaatctcaaga 5217
QY 4921 cagaagctcacaaggt 4980
Db 5218 cagaagctcacaaggt 5277
QY 4981 gtcacatttgcaatgtctctgt 5040
Db 5278 gtcacatttgcaatgtctctgt 5337
QY 5041 gtcagaagaagaacacacgtcagttcatcagttgagtgaaagctgtcactcactgtc 5100
Db 5338 gtcagaagaagaacacacgtcagttcatcagttgagtgaaagctgtcactcactgtc 5397
QY 5101 tctaatcttctgt 5160
Db 5398 tctaatcttctgt 5457
QY 5161 ttcactgtctcagaagaagttcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5220
Db 5458 ttcactgtctcagaagaagttcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5517
QY 5221 ctacttctgt 5280
Db 5518 ctacttctgt 5577
QY 5281 aagatccccaagacagctatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5340
Db 5578 aagatccccaagacagctatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5637
QY 5341 ggcagcgtgcacaccttgcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5400
Db 5638 ggcagcgtgcacaccttgcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5697
QY 5401 gatacctgaagtcgt 5460
Db 5698 gatacctgaagtcgt 5757
QY 5461 gacatgtgaaacaaacaggaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5520
Db 5758 gacatgtgaaacaaacaggaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5817
QY 5521 gttcacaatattcttgagcctgt 5580
Db 5818 gttcacaatattcttgagcctgt 5877
QY 5581 gt 5640
Db 5878 gt 5937
QY 5641 gtaaatgcaagctatctcctcgtgaatgtgaatgtgaatgtgaatgtgaatgtgaatgtga 5700
Db 5938 gtaaatgcaagctatctcctcgtgaatgtgaatgtgaatgtgaatgtgaatgtgaatgtga 5997
QY 5701 agaattcttgatgt 5760

Db	5998	AGAAATTCCTATGCTGATGGAGCCAGAAATGACATCTTAGAAATCAAGAGATTGACGAATATA	6057
Qy	5761	tataagaagaagaagcagccctgcgttgacaggaattgcgtgaggcaattcctcctcgtltag	5820
Db	6058	TATGAAAGGAAGCGGAAGCCTGCTGTTGACAGATTTCCGTGGGCATTTCCTCCGTGGTAG	6117
Qy	5821	tgcttgggctctcctggagattaaatgggctctggaataatcaacttcaaatgattaa	5880
Db	6118	TGCTTTGGCTCTCGGAGATTAAATGGGCTGGAAAAATATATCACTTTCAGATGTTAA	6177
Qy	5881	ggagataccacctgttaccagagagatgctttcccttaacaaataglatcttaacaac	5940
Db	6178	GGAGATATCCACTGTTACCGAGAGATGCTTCTTAAACAGAAATAGTATCTTATCAAC	6237
Qy	5941	atccatgaagtacatcagaacaatgggctactgcctcaagtttgatgcatacagaactg	6000
Db	6238	ATCCATGAATACATATCAGAAACATGGGCTATCCCTCATGTTGATGCATATCAGACCTG	6297
Qy	6001	ttgactggagagaacaacgtggagttccttgccctttgagagagttccagagaaagaa	6060
Db	6298	TTTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAAGAGAGTCCACGAAAA	6357
Qy	6061	gttgcaagaagttggtagtggcgaatcggaaactgggctcgtgaagta.tgsgaaaaa	6120
Db	6358	GTTTGGCAAGTGTGGTGAAGTGGCGATTTCGAAACTGGGCTCTGTGAATATGAGCAAAA	6417
Qy	6121	tatctgttaactatagttgagggcaacaagcaagctctcaagsgaatgctttatc	6180
Db	6418	TATCTGTGTACTATATGTGAGGCAACAAACGAACTCTACAGCCATGGCTTTGATC	6477
Qy	6181	ggcgggctccctgtgtgttctctgga.tgaaccacacacaggaatgga.tcccaaaagcccg	6240
Db	6478	GGCGGGCTCCTGCGTGTTCGTGATGAACCCACACAGCATGATGCCAAAGCCCGG	6537
Qy	6241	cggttcttgaggaaatgtgtgcacctaatgtttgcaagagggagagatagtagtcttaa	6300
Db	6538	CGGTTCTTGTGGAAATTTGCTCCCTTAAGTGTGTGTAAGAGAGGAGATCGATGCTTAC	6597
Qy	6301	tctcatagtatgagaagaatg.tgaagctctcttgcactagga.tgga.tcaat.tg.tcaatgga	6360
Db	6598	TCTCATAGTATGGAAGAATGTGAAGCTCTTTCGACTAGATGGCAATCATGTGATATGA	6657
Qy	6361	aggttcagggtgccttgccatgtgcgaagatctaaaaaatagtttggagatggttatca	6420
Db	6658	AGGTTCAAGTCCCTTGGCAATGTGCCAATCTTAATAAATAGGTTTGGAGATGATTATCA	6717
Qy	6421	atagtttgaacaatagaaggttcacaaccccgagacctgaagcctgttccagatctcttga	6480
Db	6718	ATAGTTTGAACAATAGCAGGGTCCAAACCGGACCTTAACACCTGTCCAGGATTTCTTGG	6777
Qy	6481	cttgcatcttcctggaag.tg.tlct.ttaaaagagaacacccggaacatgctatacacagctt	6540
Db	6778	CTTGCAATTCCTCGAAGATGTGCCAAAAAGAGAAACACCGGAACATGCTATCAATTCACGCTT	6837
Qy	6541	ccatcttcataatctcttcggccaagatat.tgaagatcctctccacagagcaaaaagga	6600
Db	6838	CCATCTTCATATATCTTCTCTGGCAGGATTTATGAGATCTCTCCACAGCAAAAAAGCA	6897
Qy	6601	cttccacatagaagaactaactcgtttcttcagagaacaacacttgaccgaattat.ttg.aactt	6660
Db	6898	CTTCCATAGAGAAGCACTACTGTTCTTCAGACAAACTTGACCAAGTATTTGTGAACCTTT	6955
Qy	6661	gccaaagcccaaatgatatgatagcacacttaaaagactctcattaaacaaaacaagca	6720
Db	6958	GCCAAAGGACCAAGTATGATGAGACACTTAAAGACCTCTCATTTACAAAAACCAAGCA	7017
Qy	6721	gttagtgagcgttggagttctcaactcttctcacaagat.tgagaag.tgaaagaagaactat	6780
Db	7018	GTAAGTGAACGTTGCAGTCTTCAACTCTTTTCTACAGSATTAGAAAGTGAAGAAAGCTAT	7077
Qy	6781	gta.tgaaagatcct.tg.tlctaa.cgg 6804	

DB	7078	GTMATGAGAAATCGTTCATACGG	7101
RESULT	14		
AXI39818		9854 bp	DNA
LOCUS	AXI39818		Linear
DEFINITION	Sequence 70 from Patent EP1096012.		PAT 30-MAY-2001
ACCESSION	AXI39818		
VERSION	AXI39818.1	GI:14275400	
KEYWORDS	.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 9854)		
AUTHORS	Deinfield,P., Roslier-Montus,M.F., Arnold-Reguigne,I., Prades,C., Naudin,L., Lemouine,C., Duvergier,N., Jaye,M., searloss II,G.H., Remaley,A., Brewer,H.B. and Dean.M. Nucleic acids of the human abcl gene and their therapeutic and diagnostic application Patent: EP 1096012-A 70 02-MAY-2001;		
JOURNAL	Aventis Pharma S.A. (FR)		
FEATURES	Location/Qualifiers		
source	1..9854		
BASE COUNT	2665 a 2219 c 2334 g 2635 t	1 others	
ORIGIN			
Query Match	99.7%; Score 6784.8; DB 6; Length 9854;		
Best Local Similarity	99.8%; Pred. No. 0;		
Matches 6792; Conservative	0; Mismatches 12; Indels 0; Gaps 0;		
OY	1 atgctgttgtagcctaagtcgaatgttgcgtctgtggaagaacctcacattcagaagaaga	60	
Db	298 ATGGCTGTGTTGGCCTCAGCGAGAGTGTCGTGTGAAGAAGACTCACTTCCAGAACAGA	357	
OY	61 caaacatgtaagctgttaactggaagtggccgtgctctattatctctcgatccgatc	120	
Db	358 CAACAATGTACAGTGTGCTGTGGTAAGTGCGCTGCCTCATATTATCTCGATCCGTGATC	417	
OY	121 tcgtgtcggtgtagtaccacacaccttgaaacaacatgaatgccatttccaataaaggc	180	
Db	418 TCTGTTGGCTGAGTACCACCCTTATGAAACAATGATGCCATTTCCAATAAAGCC	477	
OY	181 atgcccctlcaagaacaactlctcttggtltcaagggaattatctgtlaatgccaacacccc	240	
Db	478 ATGCCCTTCAGAGAACACTCTTGGGTCAAGGGGATTTATCTGTATGCAACACACCCC	537	
OY	241 tgttccgttacccagcactcctggggagagctccggagtggttggaaactttaacaatcc	300	
Db	538 TGTTTTCCGTTACCCGACTCTCGGGGAGGCTCCCGGAGTGTGGAAACTTTAAACAATCC	597	
OY	301 attgttgtctgcctgttctctagaatgctcggagagctctttaaaggccgaagaagacc	360	
Db	598 ATTGTGGCTTGCCTGTTCTGATGATGCTGGAGGCTTTCTTTATPACGCCAGAAAGCACCC	657	
OY	361 agcatgaagacatgcgaagtctcagaacatllacagcagatcagaagaatccagctca	420	
Db	658 AGCATGAAGACATGCCCAAAGTTCTGAGAACATTNAGACAGATCAAGAAATCCAGTGCA	717	
OY	421 aaactgaagcttcaagaatlctcctgtgtgagacaigaacacttctcgtgttcctatatcac	480	
Db	718 AACTTGAAGCTTCAAGATTCTGTGTGAGAACATGAACCTTCTGTGGTTCCTGTATCAC	777	
OY	481 aaactctctctcccaagcttactgttggaaaagaatgttggggctgaatgcatcttccac	540	
Db	778 AACCTCTCTCTCCCAAGTACTAGTGTGAGAACAGATGCTGAGGCTGATGTCTATTCAC	837	
OY	541 aaagtatttttgaagaagctaccagttacatttgaacaagcttggacaatgatacaaatca	600	
Db	838 AAGGATTTTTTGCAGAGCTACAGTTCATTTATGACAAGTCTGTGCATATGATCAAAAATCA	897	

QY 601 gaagagatgatacttgtagcaagaagtcttgagcttgtagcttaccacaagag 660
| | | | |
Db 898 GAAGAGATGATTAACCTTGAGTGAACAGAAAGTTTGAGCTTTGGCCCTACCAAGGAG 957
QY 661 aaactggtcgaagagagagactcgttccacaatgacatctggaagccaacccg 720
| | | | |
Db 958 AAAGTGGCTGCAGAGAGGAGTACCTTCCTCCACATGAGACTCTGAAAGCAATCCG 1017
QY 721 agaacactaaactacatcctccctcccgagaagagctggcgaagccaacaaaca 780
| | | | |
Db 1018 AGAACACTAAACCTACATCTCCCTCCGAGCAGACAGCTGGCCGAAACCAAAAAACA 1077
QY 781 ttgctgatagtcttgagactcgtgcccagagagcttgtagaatgagaagctggagtagc 840
| | | | |
Db 1078 TTGCTGATAGTCTTGAGACTCTGGCCAGAGAGCTGTCAAGCTGAGAGCTGAGTGTAG 1137
QY 841 atgcgaagagagtgatgttcttccacaatgttaacagctccagctccccaacccaac 900
| | | | |
Db 1138 ATGCGAGAGAGAGTGATGTTTCTGACCAANTGTAAACAGCTCCAGCTCCCAACCAATC 1197
QY 901 taccagagctgtgtctcgtatgtctgcgggacatcccgagagaggggagctgaagatcaag 960
| | | | |
Db 1198 TACCAGAGCTGTGTCTGTGATTTGTCTGCGGCAATCCGAGGAGAGGGGCTGAAGATCAAG 1257
QY 961 tctctcaactggtatgaggaacaacatacaagccctcttggaggaatggagtag 1020
| | | | |
Db 1258 TCTCTAAGCTGGATGATGAGGACAACTACAAAGCCCTTTGGAGGCAATGGCACTGAG 1317
QY 1021 gaagatgctgaacactctctacacactacacactcctactgacatgatttgaag 1080
| | | | |
Db 1318 GAAGATGCTGAACCTTCTATATGACACTCTACACTCTTACTGCAATATTTGATGAAG 1377
QY 1081 aattggagatcagttccctctcccgacatctctggaagagctctgaagcgtctgctgt 1140
| | | | |
Db 1378 AATTTGGAGTCTAGTCTCTCTTCCGCAATTTCTGGAAGAGCTGTGAAGCCGCTGCTGAT 1437
QY 1141 gggagaatcctctatcacctcgaactcagccacaagcaagtagtctgaagtagaac 1200
| | | | |
Db 1438 GGGAAATCTCTGATACCTGACCTGACCTGACGACAAAGAGGATGCTGAGGTGAAC 1497
QY 1201 aagacctcgaagaaactgctgttccatgatactctggaagagcttggaagaaactcagc 1260
| | | | |
Db 1498 AAGACTCTCCAGGAAGCTGCTGTTCATGATCTGGAAGGATGAGGAGCAACTCAAC 1557
QY 1261 cccaagatcttgagcctcctatggaagacagccaagaatgagactgtccgagatgctgtg 1320
| | | | |
Db 1558 CCCAAGATCTGACCTTCATGAGAAACAGCCAAAGATGAGACCTTGTCCGAGTCTGTG 1617
QY 1321 gacagcagaagaatgacaactcttggaagacagagttgagtgattgattggaagc 1380
| | | | |
Db 1618 GACAGCAGGAGCAATGACCACTTTTGGAGACAGCAGTTGATGCTTGAATTTGGACACCC 1677
QY 1381 caagacatcgtgtgttcttgccaagcaccagagagatgctcagttccagtaattgtct 1440
| | | | |
Db 1678 CAAGACATCTGCTGCTTTTGGCCAAGCAACAGAGATGTCATTCAGATTAATGTTCT 1737
QY 1441 ggtgtaacctggaagagagcttcaagagactaaaccaagcaatccggaacatctcgc 1500
| | | | |
Db 1738 GGTGTACCTGGAGAGAGCTTTCAAGAGAGACTAACAGGCAATCCGAGCATATATCTGCC 1797
QY 1501 ttcaaggaggtgtacaactgacaagcttagaacatagacaacagagctctggtatc 1560
| | | | |
Db 1798 TTCAATGGAGTGTGTCAACTGACAAAGCTAGAACCTATGACAAAGAGTCTGGCTCAATC 1857
QY 1561 aacaagatcagatgagctgtgataagagaagttcttggtgtgtatgtgttccatgga 1620
| | | | |
Db 1858 AACAGATCTCAATGAGAGCTGCTGATGAGAGAGAGTCTGGCGGATATGTGTTCACACTGA 1917
QY 1621 attactcagcagagatgagagctgcccacatcatgtccaagtacaagatccgaatggaatt 1680
| | | | |
Db 1918 ATTACTTCAGGAGAGATGAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1977

QY 1681 gacaaatgtgagagagagacaaataaatacaagatggtgtaactgagacccgtgtcctgagct 1740
| | | | |
Db 1978 GACAAATGTGAGAGAGCAAAATTAATCAAGATGAGTACTGGAGCCCTGCTGAGACT 2037
QY 1741 gaccccttggaagacatcgtgtacgtctctgagggagcttcgactactggaagatggtg 1800
| | | | |
Db 2038 GACCCCTTTGAGAGACATCGGTACGTCTGGGGGGGCTTCGCTTACTTGCAGAGATGTGTG 2097
QY 1801 gacagcaatcaatcaaggtgtcgtacgggacagagaanaaatggtgtatatacaaa 1860
| | | | |
Db 2098 GAGCAGGCAATCATCAGGGTCTGTGACGGGCAACGAGAAAGAAATGAGTGTATATCAAA 2157
QY 1861 cagatgccatccctcgttcaagttgagaacatcttctgaggtgtatgagccggtcaatg 1920
| | | | |
Db 2158 CAGATGCCCTATCCCTGTATGATGACATCTTTCTGGGGGAGAGAGCCGCTCAATG 2217
QY 1921 cccctctcagacgtcgtgctgatttactcagttgctgtgatacatcaagagagatgtg 1980
| | | | |
Db 2218 CCCCTTTCATGACGCTGGCTGGATTTACTCACTGCTGTGATCATCAAGGAGCATGTG 2277
QY 1981 tatgaaagagagcagcgtcgaagagacaaatgcaatcatalgagcctggaacaacata 2040
| | | | |
Db 2278 TATGAGAGAGAGAGAGAGGCTGAAGAGAGCAATGCGATCATGGGCTGGAACAGCATC 2337
QY 2041 ctctggtttagctgtgtcattagtaagcctatccctctctgtgagcgtgtgcgtgta 2100
| | | | |
Db 2338 CTCTGTTTACTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2397
QY 2101 gtgttcaatccctgaagattgagaacactctgcccagaagtagatcccaagctgtgtgtg 2160
| | | | |
Db 2398 GTGCTCATCTCTGAAGTTTGAAGAACTCTGCTTACAGTGTATCCACAGGAGTGTGTGTC 2457
QY 2161 ttccgttccgt 2220
| | | | |
Db 2458 TTCTGTGCTGCTGT 2517
QY 2221 tccaagagcaactcgtcgaagagcctgtgagggaatcaatcacttcaagcgtgtgtgtgt 2280
| | | | |
Db 2518 TCCAGAGGCAACCTGTGAGAGAGAGCTGTGGGGGCAATCTTCACTTCAAGCTGTACCTGCC 2577
QY 2281 taagctcgt 2340
| | | | |
Db 2578 TACCTCTGCTGT 2637
QY 2341 ctgctgtcctcgt 2400
| | | | |
Db 2638 CTGCTGTCTCTGCTGT 2697
QY 2401 ggcattgagatgagctgtggaagacactgttggagagctcgtgtgtgtgtgtgtgtgtgt 2460
| | | | |
Db 2698 GGCATTGGAGTGCAGTGGGCAACCTGTGTGAGAGTCTGTGAGAGAGAGTGTCTCAAT 2757
QY 2461 ctcaacactcgaatcctcagatgagctgttggacacactcctctataggggtgagagctgtg 2520
| | | | |
Db 2758 CTGACCACTCTGCTGT 2817
QY 2521 taactgaagcgtgtccttccagccagtagcgaattcccaagccctgtgtatcttccctg 2580
| | | | |
Db 2818 TACATTGAGGCTGTCTTCCAGGCGCAGTACGAAATCCAGGCGCTGTGTATTTCTCTTC 2877
QY 2581 accaagctcctactggttttgagagagagatgataagagaagccaacccgtgttccacag 2640
| | | | |
Db 2878 ACCAAGTCTTACTGT 2937
QY 2641 aagaagatgcagaatctcagatgagagagagagagagagagagagagagagagagagagag 2700
| | | | |
Db 2938 AAGAGAAATATCAAAATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2997
QY 2701 attcagaacctgtgtaaaagctcagagatgagatgagatgagatgagatgagatgagatgag 2760
| | | | |
Db 2998 ATTACAGAACTGTGTAAGAGCTACCGAGATGGATGAAGTGTGATGATGATGATGATGATGAT 3057
QY 2761 ctgaattttatgagggcagatcaccctcctcgtggccaatgagcggggaagagc 2820

|||||
Db 3058 CTGAATTTTATGAGGCCAGATCACCCTCCTCGGGCCACAAATGAGGGGAGAGG 3117
Oy 2821 accaccatgcaatcccgacgggttgctcccccaccccggaacgcgcacacccg 2880
Db 3118 ACCACCTGTCATCTCGACCGGGTGTTCGCCGACCTCGGGGACCGCGTCATCTCG 3177
Oy 2881 ggaagaacacatcgctcgtgatgagacacatccggcaaacctgggggtctgccccg 2940
Db 3178 GGAATAACATCTGCTGTGATGAGACCATCCGGCAGAACCTGGGGGTCTGTCCCGAG 3237
Oy 2941 cataagtgctgttgacatgctgactgctgaaagaacacatcgtgtctatggccgtg 3000
Db 3238 CATACGTCGTGTGACATGCTGACTGTGAAAGACACATGCTGTATGCCCCGCTTG 3297
Oy 3001 aaaggtcctctgagaagcagctgaagcgagatacgagacagatggccccgtgctgtgt 3060
Db 3298 AAAGGCTCTCTGAGAGACAGTGAAGCGGAGATGAGACGATGGCCCTTGATGTGGT 3357
Oy 3061 ttgcatcaagcaagctgaagaagaacaaagcagctgtcaggttggaatgcagagaag 3120
Db 3358 TTGCGATCAAGCAAGCTGAAAAGCAAAAGCCAGCTGTGAGGTGGAATGCAGAGAAAG 3417
Oy 3121 ctatctgtgacctgacctgtgtcggggagatctaaaggtgcaatctctgagtgaaacaca 3180
Db 3418 CTATCTGTGCTTGCTGGCTTTGTGGGGGATCTAAGTTGTCTGATGTAACCCACA 3477
Oy 3181 gctgtgttgagacccttaactcccgcaagggaatagggagctgtctgtcgaataaccgaca 3240
Db 3478 GCTGTGTGAGCCCTTACTCCCGCAGGGGAATATGGAGCTGTGTAATATCCGACAA 3537
Oy 3241 ggccgcaacatattctctcacaacacacatgataagcgagcgcctcgaggagagag 3300
Db 3538 GGGCGACCATATTATCTCTCTACACACACATGATGAAGGAGCGTCTGGGGAGAGG 3597
Oy 3301 atigccatcactcccatgaggaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3360
Db 3598 ATTCGCATCATCTCCATCGGAGAGCTGTGTGTGGGCTCTCCCTGTTCTGTAACAC 3657
Oy 3361 cagctgggaacaggtactactcctgtgctcaagaagaatgtggaatcctccctcagt 3420
Db 3658 CAGCTGGGAAACAGGCTACTACTCTGCTCAAGAAATGTGGAAATCTCCCTCAGT 3717
Oy 3421 tctcgcaagaacagtagtagactgtgtcactcgtgaagaagagagagagagagagagag 3480
Db 3718 TCCTGCAAAACAGTAGACACTGTGTCTAATCTGAAAAAGGAGAGAGTGTTCAG 3777
Oy 3481 agcagttctgattgctgacctgagcagacatgagagtgacaagctgacatcgtatgtc 3540
Db 3778 AGCAATTCATGCTGGCTGGCGGACGACATGAGAGTGAACGCTGACATGATGTC 3837
Oy 3541 tctgctatcctcaactcactcaagaagcagtgtctgaagccggctgtgtggaacata 3600
Db 3838 TCTGCTATCTCCAACTCATCAGGAAGCATGTCTGMAAGCCCGGCTGTGGAAGACTA 3897
Oy 3601 gggatagagctgacatagctgtctgcatagaagctgctaagagagagagagagagagag 3660
Db 3898 GGGCATGAGCTGACCTATGCTGTGCATATGAAGTGTCTAAGAGAGAGAGCTTTGTGAA 3957
Oy 3661 ctcttctagatgatagacagcgctcagacagctggagcatcttctagttatgacatca 3720
Db 3958 CTCTTTCATGAGATGATGATGACCGGCTCTCAGACCTGGGCAATTTCTAGTTATGCA 4017
Oy 3721 gagacagacctggagaataatctcctaagtgccgaagagagtgggtgtgagtgag 3780
Db 4018 GAGAGAGACCTTGAGAAATATTTCTCAAGGTGGCCGAAGAGAGGGGTGGAATGTAG 4077
Oy 3781 acctagatgttactcctcagaacagacagaaacagcgagccttgaggaaacagagagc 3840
Db 4078 ACCTAGATGTACCTTGTGCAAGACGAAGAAACAGCGGCGCTTGGGGACAGACAGAGC 4137
Oy 3841 tgtctcccgcttactgaagaatgagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3900
|||||

Db 4138 TGTCTTGGCCCTTCATGAGATGATGCTGTGATTCCAAAATGATTTGACATGACCCA 4197
Oy 3901 gaatccagaagacagactgtctcagtgaggatgagtgcaagggctcctaccagtgaa 3960
Db 4198 GAATCCAGAGACAGACTTGTCTCAGTGGAGTGTGCAAAAGGCTCTTACAGGTGAAA 4257
Oy 3961 ggtctgaaacttacaagaacagattgtgaccttgtgtgaagaagactgaattgc 4020
Db 4258 GGTGTGAACCTTACACAGACAGATTTGTGGCCCTTTTGTGMAAGAGACTGTAATGCC 4317
Oy 4021 aagcagagtcggaagaagatttctcagatgtgtctgtcagcgtgtgtgtgtgtgtgt 4080
Db 4318 AGCGGAGTCGGAAGAGATTTTGTGCTGATGTTGCTGCCAGCTGTGTGTGTGTGTGTGT 4377
Oy 4081 ggcctgtgttaagctgt 4140
Db 4378 GGCCTGT 4437
Oy 4141 cctgtgattgacaagaacagatgacatctgtcagaatgagatgagctgtgagagacagga 4200
Db 4438 CCTGTGATGTACAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 4497
Oy 4201 acccttgaaactcttaagccctcacaagaacctgtgtctcggaacccgtgtatgaa 4260
Db 4498 ACCCTGGAACCTTAAACCCCTCACCAAAAGACCTGTGCGGACCGCTGTATGAA 4557
Oy 4261 ggaatacccaatcccaagacgcctgtcgagagagagagagagagagagagagagagag 4320
Db 4558 GGAACCCATCCCAACACAGCCCTGTGCAAGAGGGAGAGAGATGACACTGCCCCA 4617
Oy 4321 gtccccagaacacatcagagactcttcagaaatggaactgtgacaaatgcaaaccttca 4380
Db 4618 GTTCCCAAGACATCATGTGAGACCTCTTCCAGAAATGGAATGGAATGGAATGGAATGGA 4677
Oy 4381 cctgtatgcagtgtatgacagcgacaacaaatcagaagaatgtcctgtgtgtgtgtgtgt 4440
Db 4678 CTTGCATGTCCAGATGTGAGCAGCAGCAAAATCAAAATATCTGCTGTGTGTGTGTGTGT 4737
Oy 4441 gcaaggagggt 4500
Db 4738 GCAGGGGGGTGCTCTCTCCACAAAGAAACAAACACACAGATATCTTCCAGAGCTGT 4797
Oy 4501 acagaagaacatctcagatctcgtgtgaagaaglatgtgcagatcagatcagaagc 4560
Db 4798 ACAGGAAGAAACATTTGCGATTTATCTGTGTAAGACCTATGTGAGATCAAGCAAAAC 4857
Oy 4561 ttaagaagaagaatctgt 4620
Db 4858 TTTAAAGAAACAGATGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATG 4917
Oy 4621 aatactcaagcacttctcagagtcagaagaatgagatgagatgagatgagatgagatgag 4680
Db 4918 AATTAATCAACACTTCTCTCGAGTCAAGAAATTAATGATGCCCAACAAATGAAGAAA 4977
Oy 4681 caactaaagctgtgcaagaagcttctcagatcagatcttctcaacagcttggagaatt 4740
Db 4978 CACTTAAGCTGGCAAGGACAGCTTGCAGATCGATTTCTCAACAGCTTGGGAAGATT 5037
Oy 4741 atgaacagactgtgaacacaaataatgtcaagtggtgtgtgtgtgtgtgtgtgtgtgtgt 4800
Db 5038 ATGACAGAGCTGTGACACCAAAATTAATGTAAGGTGTGTGTGTGTGTGTGTGTGTGTGT 5097
Oy 4801 gcaatcagccttctcagatgt 4860
Db 5098 GCAATTCAGCTTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5157
Oy 4861 ggaagaacacctgacatlttgaaatgactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4920
Db 5158 GGAAGAAACCTTACCATATATGAAATACGTTTCAATCATCCCTGATTCACCAAG 5217
Oy 4921 cagcagctctcagaagtggt 4980
Db 5218 CAGCAGCTTCTCAGAGGTGCTCCGATGACCAATCAAGTGTGTGTGTGTGTGTGTGTGTGTGT 5277
|||||

[illegible]

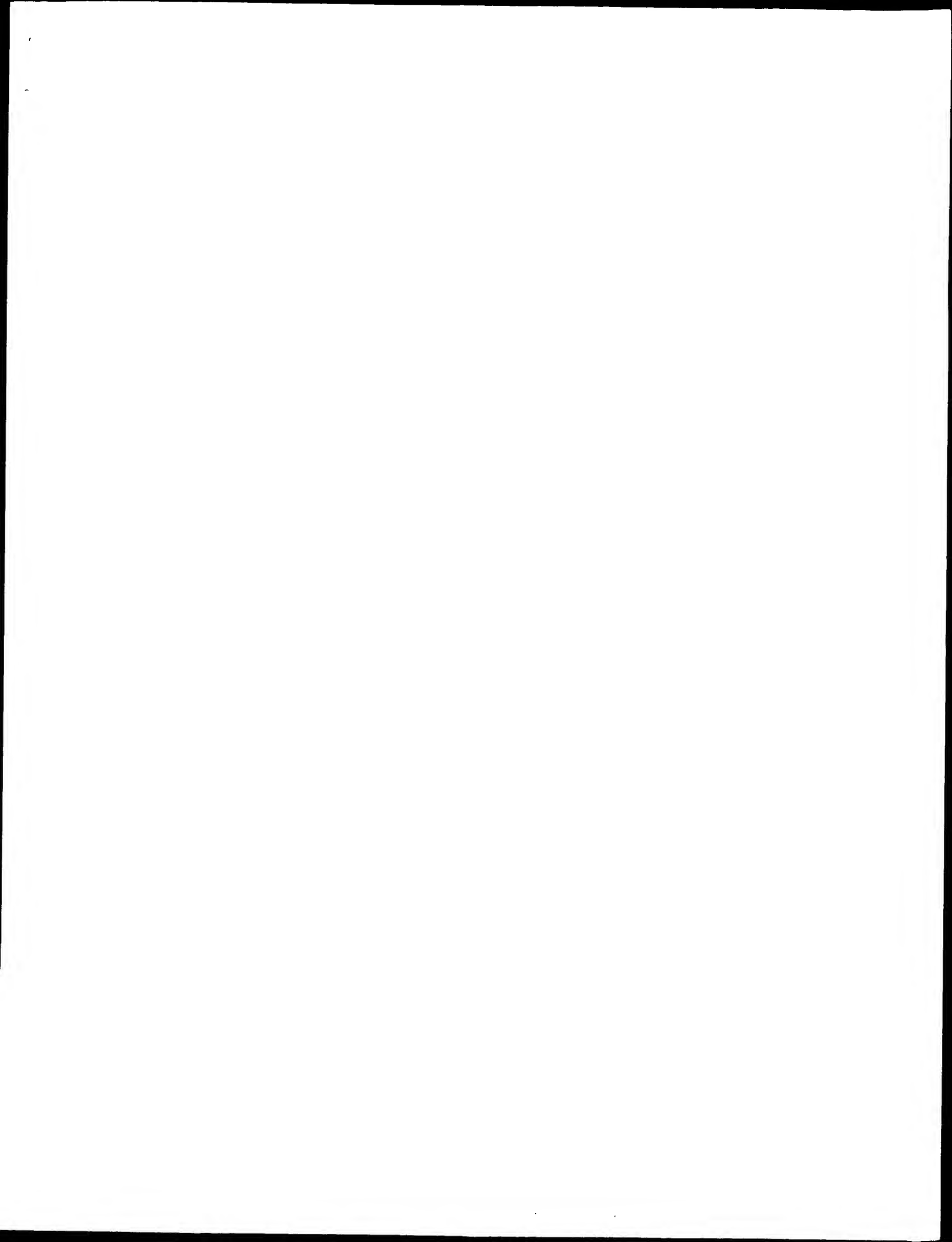
QY	6061	gttggcaaggttctgtagtggagatcttggaacttgacctgtggaagtaatggaagaaaa	6120
QY	6061	gttggcaaggttctgtagtggagatcttggaacttgacctgtggaagtaatggaagaaaa	6120
Db	6358	gttggcaaggttctgtagtggagatcttggaacttgacctgtggaagtaatggaagaaaa	6417
QY	6121	tatgctgtgaactatagtggaagcaacaacgcaagctctctcaagccatgagcttggatc	6180
Db	6418	tatgctgtgaactatagtggaagcaacaacgcaagctctctcaagccatgagcttggatc	6477
QY	6181	ggcggagccctcctgtgtgtcttctgtagtgaacccacacacgcatgatacccaagcccg	6240
Db	6478	ggcggagccctcctgtgtgtgtcttctgtagtgaacccacacacgcatgatacccaagcccg	6537
QY	6241	cggttcttgtaggaatctgtgacctaaagctgtgtctcaaggaagggagatcagtagtctaca	6300
Db	6538	cggttcttgtaggaatctgtgacctaaagctgtgtctcaaggaagggagatcagtagtctaca	6597
QY	6301	tctcatagatggaagaatgtgaagctctcttgcaataggaatggcaatcgtgcaatgga	6360
Db	6598	tctcatagatggaagaatgtgaagctctcttgcaataggaatggcaatcgtgcaatgga	6657
QY	6361	aggttcagatgtgcttgtagcagtgctcagcaatcctaaanaataggtttggaatggtataga	6420
Db	6658	aggttcagatgtgcttgtagcagtgctcagcaatcctaaanaataggtttggaatggtataga	6717
QY	6421	atagtttgtagaataagcagggtccaaacccggaacctgaaagcctgtccagatctcttga	6480
Db	6718	atagtttgtagaataagcagggtccaaacccggaacctgaaagcctgtccagatctcttga	6777
QY	6481	cttgatattctccggaagtggtcttaaaagaagaacccggaagaatgtctaaataacagctt	6540
Db	6778	cttgatattctccggaagtggtcttaaaagaagaacccggaagaatgtctaaataacagctt	6837
QY	6541	ccatcttcattatctctctgtagcaggaatctcaagcatctctccacagaagcaaaagcga	6600
Db	6838	ccatcttcattatctctctgtagcaggaatctcaagcatctctccacagaagcaaaagcga	6897
QY	6601	cttccaatagaaagactactctgtgttctcagaacaacttgaccaagtatttgtgaactt	6660
Db	6898	cttccaatagaaagactactctgtgttctcagaacaacttgaccaagtatttgtgaactt	6957
QY	6661	gccaaaggaccaaagctgatatcaccacttaaaagacgtctctatcacaaaaaccagaca	6720
Db	6958	gccaaaggaccaaagctgatatcaccacttaaaagacgtctctatcacaaaaaccagaca	7017
QY	6721	gtatgtgacgttgcaggtcttcacatcttcttctcaagatgtagaaagtgaagaagcgtat	6780
Db	7018	gtatgtgacgttgcaggtcttcacatcttcttctcaagatgtagaaagtgaagaagcgtat	7077
QY	6781	gtataagaatccctgttcatacgg 6804	
Db	7078	gtataagaatccctgttcatacgg 7101	
RESULT 15			
LOCUS	AB055982	6786 bp	Linear PRI 18-AUG-2001
DEFINITION	Homo sapiens mRNA for ABCA1, complete cds.		
ACCESSION	AB055982		
VERSION	AB055982.1	GI:15212106	
KEYWORDS			
SOURCE	Homo sapiens cDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;		
AUTHORS	Mammalia: Eutheria: Primates: Catarrhini: Homnidae; Homo.		
TITLE	1 (bases 1 to 6786)		
REFERENCE	Tanaka,A.R., Abe-Dohmae,S., Arakawa,R., Sadanami,K., Kidera,A.,		
AUTHORS	Kloka,N., Anachi,T., Yokoyama,S. and Ueda,K.		
JOURNAL	A new topological model of functional human ABCA1-Signal peptide		
REFERENCE	cleavage and glycosylation of a large extracellular domain		
AUTHORS	Unpublished		
TITLE	2 (bases 1 to 6786)		
	Ueda,K., Kloka,N. and Tanaka,A.R.		
	Direct Submission		

Db 1201 AAGACCTTCAGAGAACTGGCTGTGTTCCATGATCTGGAAGGATGTGGAGAACTCAGC 1260
QY 1261 cccaaagctcggacctcattgagaaacagccaaagaaatgacctgtccgagtgctgtg 1320
Db 1261 CCCAAGATCTGGACCTTTCATGAGGAACAGCCAAAGAAATGACCTTGTCCGAGTGTG 1320
QY 1321 gacagaaggagcaatgaccacttttgggaacagcaatgtgatggtcttagatggagacc 1380
Db 1321 GACAGAGAGGACAAATGACCACTTTTGGAAACAGCACTTGTGATGGCTTACATTGGACAGC 1380
QY 1381 caagacatcgtgaccttttttggccaaagcccaagagatgtccagtcaglaatgttct 1440
Db 1381 CAAAGACATGCTGGCTGTTTTTGGCAAGCACCCAGAGAGTCCAGTCCAGTATGTTCT 1440
QY 1441 gtgtacacctgagagaaagcttccaagagactaaacagagcaatccggagcaatcttc 1500
Db 1441 GTGTACACCTGGAGAGAACCTTTCACAGACTAACACAGGCAATCCGGACCTATCTCC 1500
QY 1501 ttcatgagatgtgtcaacctgaaacagctagaaaccatagcaacagaaatctgtgtc 1560
Db 1501 TTCATGAGATGTGTCAACCTTGAACAAAGCTAGAACCCATAGCAACAGAACTGTGGCTCATC 1560
QY 1561 aacaaatccatggagctgtgtgatagagaaagttctgggtggtatgtgttcaatgga 1620
Db 1561 AACAAATCCATGAGAGTGTGTGATGAGAGAAAGTTCTGGGCTGTGATGTGTCTCACTGGA 1620
QY 1621 attactcagagagcaatltgagctgtcccaatcagtaagtaagaatccgaatgtgacatt 1680
Db 1621 ATTACTCCAGGACAGATTGAGCTGCCCATTCATGTCAAGTACAAATATCCGAATGACATT 1680
QY 1681 gacaaatgtgagagagcaataaatacaagatgtggaactgggacctgtgtccagact 1740
Db 1681 GACAAATGTGAGAGAGCAAAATAAATCAAGATGGTACTGGGACCCGTGCTTCAGACT 1740
QY 1741 gaccccttggagagatcgtgtgagctcgtgggggcttcgcctacttgcagatgtgtg 1800
Db 1741 GACCCCTTGGAGAGATGCGGTACCTGTGGGGGCTTGGCTACTTCCAGAGATGTGGTG 1800
QY 1801 gagcagagcaatcaatgaaggtgtgacggtgacaggaagaaatctgtgtcatalatgaa 1860
Db 1801 GAGCAGGCAATCATAGAGGTGTGTGACGGGGACCCGAGAGAAACTGTGTCTATATGCA 1860
QY 1861 cagatgacctacacctgttgaatgatacatcttctcgggggtgatagaacctgcaatg 1920
Db 1861 CAGATGACCTTACCTGTTAGCTTATGATACATCTTCTGCGAGTGAATGACCGGCTCAATG 1920
QY 1921 cccctcttcaatgacgtgtgacctgataatcaatgagtgctgtgacatcaagagacgtg 1980
Db 1921 CCCCTCTTCATGAGAGCTGTGGCTGATTTACTCAGTGGCTGTGATCATCAAGGCAATCTG 1980
QY 1981 tatgagaagagagcaaggtgtgaagaagacatgagatcaltgaggtcctlgagacaagata 2040
Db 1981 TATGAGAAGGAGGACGCGCTGAAGAGACCATGCGGATCATGCGCTTGAGAACAGCATC 2040
QY 2041 ctctgtgttagctgttgaatgaatgaatcttctctctctctgtgtgagagctgtgcctgta 2100
Db 2041 CTCTGTGTTAGCTGTGATTAATGATGACCTCATCTCTCTCTTGTGAGACGCGCTGCTGTA 2100
QY 2101 gtgtgcatcctgaaagttagaagacgtgtgcctacagatgatacccaagctgtgtgtg 2160
Db 2101 GTGTGATCCCGAAGTAAAGAACTGTGCTTACAGTATCCCAAGCGTGTGTGTGTGTC 2160
QY 2161 ttctcgtcgt 2220
Db 2161 TTCTCTGTCCGTTGT 2220
QY 2221 tccgaagcaaacctgtgagcaagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2280
Db 2221 TCCGAGACCAACCTGTGAGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2280
QY 2281 taactcctgt 2340
Db 2281 TACGTCTGT 2340

QY 2341 ctgctgtctcctgt 2400
Db 2341 CTGCTGTCTCCTGT 2400
QY 2401 ggcatttgagctcagtgagagacaacctgttgaagctcgtgtgtgtgtgtgtgtgtgtgt 2460
Db 2401 GGCAATTGAGAGTGCAGATGGGACCAACCTGTTTGAAGATCTGTGGAGGAATGCTTCAAT 2460
QY 2461 ctccaccacttcagatccatgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2520
Db 2461 CTCACCACTTGT 2520
QY 2521 ttacattgaggt 2580
Db 2521 TTAATGTAGGCTGT 2580
QY 2581 accaagctcactgt 2640
Db 2581 ACCAAGTCTACTGT 2640
QY 2641 aagaagatgtcgaagaatcgtgaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2700
Db 2641 AAGAGAAATATCAGAAATCTCATGAGAGGAACCCACCACTTGAAGCTGTGGCGTGTGC 2700
QY 2701 attagaacctgt 2760
Db 2701 ATTGAGAACTGT 2760
QY 2761 ctgaatttttatgagggcagatcaacctcctcctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2820
Db 2761 CTGAATTTTATGAGGGCCAGATCACCTCTCTGTGGCCACAAATGAGCGGGAGGAAGAG 2820
QY 2821 accaacaatgtcaactcgtgacgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2880
Db 2821 ACCAACAATGTCAATCTGTGACCGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2880
QY 2881 ggaagaaagacatcgcctcgtgagatgagacacatccggcagaacctgtgtgtgtgtgtgt 2940
Db 2881 GGAAGAAACATTTGCTGT 2940
QY 2941 cataaagctgt 3000
Db 2941 CATTAACGT 3000
QY 3001 aaaggtgtcctcgtgaagaagcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3060
Db 3001 AAAGGCTCTGTGAAGACAGTGAAGGCGGAGATGAGCAAGATGCTGTGTGTGTGTGTGT 3060
QY 3061 ttgcatcaagcaagctgtgaagaagcaagaacagcagctgtcaaggtgtgtgtgtgtgtgt 3120
Db 3061 TTGCGCATCAAGCAAGCTGAAAGCAAAACCAAGCAGCTGTCAAGGTGTGTGTGTGTGTGT 3120
QY 3121 ctatctgt 3180
Db 3121 CTATCTGT 3180
QY 3181 gctgt 3240
Db 3181 GCTGT 3240
QY 3241 ggcgcagcatattctctctacacacacacatgagatgtgaagcagagctgtgtgtgtgtgt 3300
Db 3241 GGCGCAGCATATTCTCTCTACACACACATGATGGAAGCGAGCTGTGTGTGTGTGTGTGT 3300
QY 3301 attgcatcatctccatgtgaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3360
Db 3301 ATTGCAATATCTCCATGTGAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3360
QY 3361 cagctgt 3420
Db 3361 CAGCTGT 3420

QY 3421 tcttgcagaaacagtagtagcactgtgtacataccttgaaagaagagacagtggtttctcag 3480
|||||
Db 3421 tcttgcagaaacagtagtagcactgtgtacataccttgaaagaagagacagtggtttctcag 3480
QY 3481 agcagtttctgtctgtcgtccttgagcagcagcaatagagttacacagctgcacatctgctc 3540
|||||
Db 3481 agcagtttctgtctgtcgtccttgagcagcagcaatagagttacacagctgcacatctgctc 3540
QY 3541 tctgtatctccaacatcatcaggaagcagtgctgtgaagcccgctgtgtgaagacata 3600
|||||
Db 3541 tctgtatctccaacatcatcaggaagcagtgctgtgaagcccgctgtgtgaagacata 3600
QY 3601 gggcagtgagtgacctaagtgctgcacataagagctgtcaagggagagccttctgtgaa 3660
|||||
Db 3601 gggcagtgagtgacctaagtgctgcacataagagctgtcaagggagagccttctgtgaa 3660
QY 3661 cctcttcagatgagatgagcagcgtctcagacgttgagcattcttaattatgacatca 3720
|||||
Db 3661 cctcttcagatgagatgagcagcgtctcagacgttgagcattcttaattatgacatca 3720
QY 3721 ggaagaccccttgagaaataatcttcccaaggctggcagagaagctggagtgagtgag 3780
|||||
Db 3721 ggaagaccccttgagaaataatcttcccaaggctggcagagaagctggagtgagtgag 3780
QY 3781 accctagatgtagtacctgtgcagcagaacgaagcgggccttcggggagacaagcagc 3840
|||||
Db 3781 accctagatgtagtacctgtgtgcagcagaacgaagcgggccttcggggagacaagcagc 3840
QY 3841 tctctgcgcgttcaactgaagaatgctgtctgaatcccaatgattctgacatgaccca 3900
|||||
Db 3841 tctctgcgcgttcaactgaagaatgctgtctgaatcccaatgattctgacatgaccca 3900
QY 3901 gaatccagaagacagactgtctcagtgagatgagctggcaagggctctaccaggtgaa 3960
|||||
Db 3901 gaatccagaagacagactgtctcagtgagatgagctggcaagggctctaccaggtgaa 3960
QY 3961 ggtctgaaacttacaagaagaagtttggccttggtagaagaagactctaattgcc 4020
|||||
Db 3961 ggtctgaaacttacaagaagaagtttggccttggtagaagaagactctaattgcc 4020
QY 4021 agacgagatcggaagaagatttctgtcagatgtctgtcagcagctgtgtgtctgcacat 4080
|||||
Db 4021 agacgagatcggaagaagatttctgtcagatgtctgtcagcagctgtgtgtctgcacat 4080
QY 4081 ggccttgtagtcaagcctgtacgtgcacaccccttgagcaagtaaccagcctgtgaattcag 4140
|||||
Db 4081 ggccttgtagtcaagcctgtacgtgcacaccccttgagcaagtaaccagcctgtgaattcag 4140
QY 4141 cccctgagatgagaaagacagatcatctgtcagcaatgagctgtccctgaagagacagga 4200
|||||
Db 4141 cccctgagatgagaaagacagatcatctgtcagcaatgagctgtccctgaagagacagga 4200
QY 4201 accctggaacttctaaagcgccttcacccaagaacctgtgtctcggagacccgtgtatgaa 4260
|||||
Db 4201 accctggaacttctaaagcgccttcacccaagaacctgtgtctcggagacccgtgtatgaa 4260
QY 4261 ggaagacccaatccacagacagccttcagcagcagggagagaagatgagacacactgccca 4320
|||||
Db 4261 ggaagacccaatccacagacagccttcagcagcagggagagaagatgagacacactgccca 4320
QY 4321 gttccccaagacatcatgagccttctccagatgaggaactgtgacaatgtgaagacccttca 4380
|||||
Db 4321 gttccccaagacatcatgagccttctccagatgaggaactgtgacaatgtgaagacccttca 4380
QY 4381 cctgtacatgcaagtgagcagcagcaaaaatcaagaagaatgtctgtcctgtgtcccccaggg 4440
|||||
Db 4381 cctgtacatgcaagtgagcagcagcaaaaatcaagaagaatgtctgtcctgtgtcccccaggg 4440
QY 4441 gcaaggggggctgtcctctccacaagaagaacaacacactgcacatactcctcaagacactg 4500
|||||
Db 4441 gcaaggggggctgtcctctccacaagaagaacaacacactgcacatactcctcaagacactg 4500
QY 4501 acaggaagaacatcttcgattatctgtgagaagcgtatgtgcagatcatagccaagaagc 4560
|||||

Db 4501 ACAGGAACAAACATTTGGATTATCTGGTGAAGACGTATGTGACGATCATAGCCAAAC 4560
|||||
QY 4561 ttaagaacaagatctgggtgaaatgagtttagttatgagggcttctcccggtgtgcagt 4620
|||||
Db 4561 ttaagaacaagatctgggtgaaatgagtttagttatgagggcttctcccggtgtgcagt 4620
QY 4621 aatctcaagacacttccctccagatccaagaatgtaatatgcatccaacaatgaaga 4680
|||||
Db 4621 aatctcaagacacttccctccagatccaagaatgtaatatgcatccaacaatgaaga 4680
QY 4681 caactaaagcttgagccaaggaagatctgcagatcagatcttcccaagccttggagaatt 4740
|||||
Db 4681 caactaaagcttgagccaaggaagatctgcagatcagatcttcccaagccttggagaatt 4740
QY 4741 atgacaagacttgagacaaccaagaataatgtaaggtgtgtgttcaataacagggctgcat 4800
|||||
Db 4741 atgacaagacttgagacaaccaagaataatgtaaggtgtgtgttcaataacagggctgcat 4800
QY 4801 gcaatcagctcttctctgaatgtcaacaatgcatcttcccgagccaaacttgcaaaag 4860
|||||
Db 4801 gcaatcagctcttctctgaatgtcaacaatgcatcttcccgagccaaacttgcaaaag 4860
QY 4861 ggaagaaacccctagccattatgaaatctgcttcaatcaatccctgaaatctcaacag 4920
|||||
Db 4861 ggaagaaacccctagccattatgaaatctgcttcaatcaatccctgaaatctcaacag 4920
QY 4921 cagcagcctcagaagtggtctgtgtgagccaatcaatgaaggtgtcctgtgtcaatctgt 4980
|||||
Db 4921 cagcagcctcagaagtggtctgtgtgagccaatcaatgaaggtgtcctgtgtcaatctgt 4980
QY 4981 gtcacatcttgcaatgtcctctgtcccaagcagccttgcgtatcttccatccagagaagc 5040
|||||
Db 4981 gtcacatcttgcaatgtcctctgtcccaagcagccttgcgtatcttccatccagagaagc 5040
QY 5041 gtcagcaagaacaacacactgcagttcatcagtgagtgagagcctgtcatctatctgtctc 5100
|||||
Db 5041 gtcagcaagaacaacacacactgcagttcatcagtgagtgagagcctgtcatctatctgtctc 5100
QY 5101 tctaatcttgctggagatgtgtgaatlaagctgttccctgcacacactgtcatctatc 5160
|||||
Db 5101 tctaatcttgctggagatgtgtgaatlaagctgttccctgcacacactgtcatctatc 5160
QY 5161 ttcacatgcttccagcagaagctcatgtgttccctcacaacatctgtcctgtcagcctt 5220
|||||
Db 5161 ttcacatgcttccagcagaagctcatgtgttccctcacaacatctgtcctgtcagcctt 5220
QY 5221 ctactctgtctgtagtggtgtgtcaatcaacacttccatgtaacagccttctgtgtctc 5280
|||||
Db 5221 ctactctgtctgtagtggtgtgtcaatcaacacttccatgtaacagccttctgtgtctc 5280
QY 5281 aagatccccagcagcactatgtgtgtcaccacagtgtaacacttccatgtaacat 5340
|||||
Db 5281 aagatccccagcagcactatgtgtgtcaccacagtgtaacacttccatgtaacat 5340
QY 5341 ggcagcgtgagcacttgtgtcagagctgttcaaccgacaataagctgaataataatcaat 5400
|||||
Db 5341 ggcagcgtgagcacttgtgtcagagctgttcaaccgacaataagctgaataataatcaat 5400
QY 5401 gatacttgagagcgtgtgtctgatacttccacatcttctgctggagaagagctcatc 5460
|||||
Db 5401 gatacttgagagcgtgtgtctgatacttccacatcttctgctggagaagagctcatc 5460
QY 5461 gacatggtgaaaaaacaagcagatgagctgtgccttgaaaggttggggagaaatcgctt 5520
|||||
Db 5461 gacatggtgaaaaaacaagcagatgagctgtgccttgaaaggttggggagaaatcgctt 5520
QY 5521 ggtgcacatctatctgtgagcctgtgtggagagaaacacttgcacatgagcgttgaaag 5580
|||||
Db 5521 ggtgcacatctatctgtgagcctgtgtggagagaaacacttgcacatgagcgttgaaag 5580
QY 5581 gtggtcttccctcatctatgttctgatacagtaagatcttccatcagcagcagact 5640
|||||



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2002, 10:13:52 ; Search time 20132.5 Seconds
(without alignments)
10853.833 Million cell updates/sec

```

Title: US-09-595-526B-1
Perfect score: 10442
Sequence: 1 ggcgcggaccgcgcagagccg.....aaaaaaaaaaaaaaaaaa 10442

```

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

```
Searched:      1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312
```

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :
GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_com: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_inu: *
20: em_com: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_inv: *
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
---------------	-------	----------------	--------	----	----	-------------

1	10438	100.0	10442	6	AX060713	AX060713	Sequence
2	10438	100.0	10442	6	AX060892	AX060892	Sequence
3	10438	100.0	10442	6	AF285167	AF285167	Homo sapi
4	10429	99.9	10474	6	AX060721	AX060721	Sequence
5	10429	99.9	10474	6	AX060721	AX060721	Sequence
6	10429	99.9	10474	6	AX060898	AX060898	Sequence
7	10429	99.9	10474	6	AX060900	AX060900	Sequence
8	9777.8	93.6	9854	6	AX127831	AX127831	Sequence
9	9777.8	93.6	9854	6	AX127830	AX127830	Sequence
10	9672.8	92.6	9741	6	AX139817	AX139817	Sequence
11	9672.8	92.6	9741	6	AX351038	AX351038	Sequence
12	9672.8	92.6	9741	6	AX059973	AX059973	Sequence
13	9444.6	90.4	9497	6	AF165261	AF165261	Homo sapi
14	9444.6	90.4	9497	6	AX059978	AX059978	Sequence
15	9430.6	90.3	9495	6	AX059976	AX059976	Sequence
16	9325.8	89.3	9593	6	AX092594	AX092594	Sequence
17	7825.8	74.9	7860	6	AX135712	AX135712	Sequence
18	7800.6	74.7	7862	6	AX253452	AX253452	Sequence
19	7198.8	68.9	7260	6	AX253450	AX253450	Sequence
20	7198.8	65.7	6880	6	HS0A12376	HS0A12376	Homo sapi
21	6862.4	65.7	6880	9	AB055982	AB055982	Homo sapi
22	6771.6	64.8	6786	9	AB055982	AB055982	Homo sapi
23	5983.8	57.3	7878	10	MMAB01	MMAB01	Mus musculu
24	4952.8	47.4	5097	6	BD005026	BD005026	Genes rel
25	4952.8	47.4	5097	9	AK027864	AK027864	Homo sapi
26	4352.6	41.7	7074	5	AF362377	AF362377	Gallus ga
27	3362	32.2	3366	6	AX060718	AX060718	Sequence
28	3362	32.2	3366	6	AX060897	AX060897	Sequence
29	3315.2	31.7	201144	9	AF287262	AF287262	Homo sapi
30	3314.6	31.7	182012	9	AF135984	AF135984	Homo sapi
31	3314.6	31.7	149034	9	AF275948	AF275948	Homo sapi
32	3282.8	31.4	5352	6	AX127778	AX127778	Sequence
33	3282.8	31.4	5352	6	AX139765	AX139765	Sequence
34	3277.6	31.4	183999	6	AX092589	AX092589	Sequence
35	2875.6	27.5	2894	6	AX127797	AX127797	Sequence
36	2875.6	27.5	2894	6	AX139784	AX139784	Sequence
37	2581.6	24.7	2617	6	AF001945	AF001945	Homo sapi
38	1934.6	18.5	7298	9	BTU90126	BTU90126	Bos taurus
39	1933	18.5	7709	4	HS0A000148	HS0A000148	Homo sapi
40	1929.8	18.5	7323	10	MMAF000149	MMAF000149	Mus muscu
41	1928.8	18.5	7268	6	HS086657	HS086657	Human
42	1921.8	18.4	7276	6	AX060717	AX060717	Sequence
43	1908.2	18.3	2011	6	AX060896	AX060896	Sequence
44	1908.2	18.3	2011	6	AF328787	AF328787	Homo sapi
45	1742.2	16.7	6704	9	AF328787	AF328787	Homo sapi

ALIGNMENTS

RESULT	1				
AX060713	AX060713	10442 bp	DNA	linear	PAT 22-JAN-2001
LOCUS	Sequence	1 from Patent WO0078972.			
DEFINITION	AX060713				
ACCESSION	AX060713.1	GI:12406103			
VERSION					
KEYWORDS	.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 10442)				
AUTHORS	Law, R. M., Wade, D., and Garvin, M.				
TITLE	Regulation of binding cassette transporter protein abcl				
JOURNAL	Patent: WO 0078972-A 1 28-DEC-2000;				
	CV THERAPEUTICS, INC. (US)				
FEATURES	Location/Qualifiers				
Source	1..10442				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
BASE COUNT	2898 a	2408 g	2835 t	4 others	
ORIGIN	2297 c				

Query Match 100.0%: Score 10438; DB 6; Length 10442;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 10442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggcggagaccgagagccgagccgacctctctccgggctgagcgagcgagcg 60
Db 1 ggcggagaccgagagccgagccgacctctctccgggctgagcgagcgagcg 60
QY 61 gggagctcgagccgagccgagccgagccgagccgagccgagccgagccgag 120
Db 61 gggagctcgagccgagccgagccgagccgagccgagccgagccgagccgag 120
QY 121 gttctgttttctccctctccgagagctgtgcaagggtgagagagagagag 180
Db 121 gttctgttttctccctctccgagagctgtgcaagggtgagagagagagag 180
QY 181 acaaaagtgagaaacagttatgagccagccagcgccctgctgtgagctgagcgc 240
Db 181 acaaaagtgagaaacagttatgagccagccagcgccctgctgtgagctgagcgc 240
QY 241 tgcctccagagctcccgagccagccagcgctgctgtgagctgagagagagag 300
Db 241 tgcctccagagctcccgagccagccagcgctgctgtgagctgagagagagag 300
QY 301 ggcctcagctgagctgtgctgtgagagagccctacattcagagagagagag 360
Db 301 ggcctcagctgagctgtgctgtgagagagccctacattcagagagagagag 360
QY 361 agctgtactgagagagctgtgctgtgagagagccctacattcagagagagag 420
Db 361 agctgtactgagagagctgtgctgtgagagagccctacattcagagagagag 420
QY 421 tgaagctaccagccctatgagagagagagagagagagagagagagagag 480
Db 421 tgaagctaccagccctatgagagagagagagagagagagagagagagag 480
QY 481 cagagacactctctgtgtgagagagagagagagagagagagagagagag 540
Db 481 cagagacactctctgtgtgagagagagagagagagagagagagagagag 540
QY 541 acccgactcgtggagagctcccgagctgtgtgagagagagagagagagag 600
Db 541 acccgactcgtggagagctcccgagctgtgtgagagagagagagagagag 600
QY 601 ggcctgttctcagagctgtgagagagagagagagagagagagagagagag 660
Db 601 ggcctgttctcagagctgtgagagagagagagagagagagagagagagag 660
QY 661 acatgagcaagctgtgagagagagagagagagagagagagagagagag 720
Db 661 acatgagcaagctgtgagagagagagagagagagagagagagagagag 720
QY 721 ttcagagcttctgtgtgagagagagagagagagagagagagagagag 780
Db 721 ttcagagcttctgtgtgagagagagagagagagagagagagagagag 780
QY 781 tcccaaaatctactgtgagagagagagagagagagagagagagagag 840
Db 781 tcccaaaatctactgtgagagagagagagagagagagagagagagag 840
QY 841 tgcagagctacagcttactgagagagagagagagagagagagagagagag 900
Db 841 tgcagagctacagcttactgagagagagagagagagagagagagagagag 900
QY 901 ttcagagctgtgagagagagagagagagagagagagagagagagagag 960
Db 901 ttcagagctgtgagagagagagagagagagagagagagagagagagag 960
QY 961 cag 1020
Db 961 cag 1020

QY 1021 acctacatctccctcccgagcaagagctgtgctgagagccagaaacattgtgata 1080
Db 1021 acctacatctccctcccgagcaagagctgtgctgagagccagaaacattgtgata 1080
QY 1081 gtttggagctcgtggcggagagctgttcaagatgaagagctgtgagatcgagag 1140
Db 1081 gtttggagctcgtggcggagagctgttcaagatgaagagctgtgagatcgagag 1140
QY 1141 aggtgaagctgtgagagagagagagagagagagagagagagagagagag 1200
Db 1141 aggtgaagctgtgagagagagagagagagagagagagagagagagagag 1200
QY 1201 tgcctgtatctgtgagagagagagagagagagagagagagagagagag 1260
Db 1201 tgcctgtatctgtgagagagagagagagagagagagagagagagagag 1260
QY 1261 ggtatgag 1320
Db 1261 ggtatgag 1320
QY 1321 aaactctctatgagagagagagagagagagagagagagagagagagag 1380
Db 1321 aaactctctatgagagagagagagagagagagagagagagagagagag 1380
QY 1381 ctatgctctctcccgagagagagagagagagagagagagagagagagag 1440
Db 1381 ctatgctctctcccgagagagagagagagagagagagagagagagagag 1440
QY 1441 tglataacactgagagagagagagagagagagagagagagagagagagag 1500
Db 1441 tglataacactgagagagagagagagagagagagagagagagagagagag 1500
QY 1501 aggaagctgtgtgtcatgagagagagagagagagagagagagagagagag 1560
Db 1501 aggaagctgtgtgtcatgagagagagagagagagagagagagagagagag 1560
QY 1561 ggaacttcaag 1620
Db 1561 ggaacttcaag 1620
QY 1621 acaatgag 1680
Db 1621 acaatgag 1680
QY 1681 tggcgttttggcagagagagagagagagagagagagagagagagagag 1740
Db 1681 tggcgttttggcagagagagagagagagagagagagagagagagagag 1740
QY 1741 ggaag 1800
Db 1741 ggaag 1800
QY 1801 gttgaacactgagagagagagagagagagagagagagagagagagagag 1860
Db 1801 gttgaacactgagagagagagagagagagagagagagagagagagagag 1860
QY 1861 tggagctgtgag 1920
Db 1861 tggagctgtgag 1920
QY 1921 gcaagatgagctgtgagagagagagagagagagagagagagagagagag 1980
Db 1921 gcaagatgagctgtgagagagagagagagagagagagagagagagagag 1980
QY 1981 ag 2040
Db 1981 ag 2040
QY 2041 ag 2100
Db 2041 ag 2100
QY 2101 tcatcaggtgtgtgagagagagagagagagagagagagagagagagag 2160


```
|||||
Db 2101 TCATCAAGGGTGCAGAGGACCGAGAAACCTGCTCATATGCAAGATGACCT 2160
Oy 2161 atcccggttacgttgatgacatcttcgaggtgtagacgggtcaatgccccctca 2220
Db 2161 ATCCCTGTTACGTTGATGACATCTTTTCGCGGTGATGACCGGTCAATGCCCCCTTCA 2220
Oy 2221 tgaagctggcctggatcttaactcaatggtctgtagatcaatgaaggacatgtagaagg 2280
Db 2221 TGACGGTGGCGCTGATTTACTCAGTGGCTGTGATCATCAAGGCGCATCGTGTATGAGAAG 2280
Oy 2281 aggcacggctgaaagagaccatgagatcaatgagcctggacacacgactactctgttta 2340
Db 2281 AGGCACGGCTGAAAGAGACCATGCGGATCATGGCTTGACACAGCATACTCTGTGTTTA 2340
Oy 2341 gctggttcaatagtaagccatctctctctctgttagcgctgacctgtagtgcaccc 2400
Db 2341 GCTGCTTCATTAATACCTCATTTCCCTCTTGTGTAGCGCTGGCCGTGAGTGTATCC 2400
Oy 2401 tgaagtgaagaaacctgtgacctacatgataccagcggtgtgttctctctgcg 2460
Db 2401 TGAAGTTAGGAAACCTGTGCTCCCTACAGTATCCAGCGTGTGTGTCTTCCGTGCG 2460
Oy 2461 tttttgtgtgtgaaacaatccctgacgtgcttctctgtagtagcaactctctcagaagca 2520
Db 2461 TGTGTGCTGTGTGACAACTCTGCACTGCTTCTGTATGACACTCTTCTCAGACCA 2520
Oy 2521 acctggaagacgcctgtgaggacatcatctactcaagctgtaacctgcctcaagctcgt 2580
Db 2521 ACCTGGAAGACGCTGTGGGGCATCATCTTACGCTGTATCCGCTGTACGCTCTGT 2580
Oy 2581 gtgtggaatgagagactaagtggtgttcaactcaagcttctgtagcctgcgtctc 2640
Db 2581 GTGTGGAATGAGAGACTAAGTGTGGCTTCACTCAAGATCTTCTGCTTACCTGTCTCTC 2640
Oy 2641 ctgtgcttctgtggtctgtgctgtaacttgccttcttgaagagcaggacatgtgag 2700
Db 2641 CTGTGCTTCTGTGGTGTGGCTGTGACTTGTGCTCTTTTGTGAGAGCAGGCAATGAG 2700
Oy 2701 tgcagtgagacaacctgtttagagatccctgttgaagaaatgagcttcaatctcaacct 2760
Db 2701 TGAGTGGGACACCTGTTTGAAGTCTGTGAGGAAGATGGCTTCAATCTCACCACTT 2760
Oy 2761 cgaatccatgatatgttctgacacctctctctatgaggtgtagacatgtagatgag 2820
Db 2761 CGATCTCATGATGCTGTTTGACACTTCTCTATGGGGTGAAGACTGTGATCATTTGAG 2820
Oy 2821 ctgtcttccagagcagtaagaaatcccaagccctgtgatttctctgcaaccaagctc 2880
Db 2821 CTGCTTCCAGGCGCATAGGAATCCAGGCGCTGTATTTTCTTGCACCAACTCTCT 2880
Oy 2881 actggttctgagaaagatgtagaagagcaacctgtgttccaacagaagaatg 2940
Db 2881 ACTGTTTGGCGAGAAAGTATGAGAGACCACTGTGTTCCAAACCAAAAGAAATGT 2940
Oy 2941 cagaatctgcatgagagagaaacccaactgaaagctgagcggtgctcatcagaacc 3000
Db 2941 CAGAAATCTGCATGAGAGAGAACCCACACTTGAAGCTGGCGGTGCATTCAGAAC 3000
Oy 3001 tggtaaaagtctacagagatgagatgaaagtgtgctgcgtgagcctggaatatttt 3060
Db 3001 TGGTAAAGTCTACCGAATGGAATGGAAGGTGCTGTGATGCTGGCACTGAATTTT 3060
Oy 3061 atgaagcagatcacctcctctctgagcaaatgagagggagaaagacacacatgt 3120
Db 3061 ATGAGGGCAATCACTCTCTCTCTGGCCCAATGAGAGGGGGAAGAGACACACATGT 3120
Oy 3121 caatctgacgggtgtgttcccccgaaacttgagacgcctacatccctgagaaagaca 3180
Db 3121 CAATCTGACGGGTTGTGTCCCGGAACTTGCGACCGCTCATCTCTGGGAAAGACA 3180
Oy 3181 ttgcgtctgagatgagacccatccgcaagaacctgggggtctgtccccagcataaagtc 3240
|||||

Db 3181 TTGCTCTGAGATGAGACCATCCGAGAACCTGGGGTCTGTCCACGATTAAGCTGC 3240
Oy 3241 tgttgaatgctgactgtcgagaacacatctggttctatgccccgttgaagagctc 3300
Db 3241 TGTGTACATGCTGACATGTGCAAGAACATCTGTGTTATGCCCCGCTTGAAGGGCTCT 3300
Oy 3301 ctgaagaacgttgaagggagatgtagagacatgacctgtagtgtgttctgcatcaa 3360
Db 3301 CTGAGAAAGCATGTGAAGCGGAGATGAGACAGATGGCCCTGGATGTTGTTGGCATCA 3360
Oy 3361 gcaagctgaagaaacaaagccagctgctcagtgagatgcaagaaagctatctgtg 3420
Db 3361 GCAAGCTGAAGAAACAAACAGCCAGCTGTAGTGAATGAGAGAAAGCTATCTGTGG 3420
Oy 3421 ccttggccttctgagggatctaaggtgtcatctctgaagaccacacgtgtgtg 3480
Db 3421 CCTTGGCCTTGTGCGGGATCTTAAGTGTGATTTCTGGATGAACCCACAGCTGTGTGG 3480
Oy 3481 acccttactccgcaagggaataatggaagctgtgctgaatataccgaagaagccgacaa 3540
Db 3481 ACCCTTACTCCCGCAGGGAATATGGAGCTGTCTGTAAATACCGACAGCGCCACCA 3540
Oy 3541 ttaatctctacacaacacatggaatggaagcgagctcgggggacagatgcatca 3600
Db 3541 TTATTTCTCTACACACACACATGATGAAGCGAGCTCTGTGGGGACAGATTGCAATCA 3600
Oy 3601 ttcccaatggaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3660
Db 3601 TCTCCATGGGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3660
Oy 3661 caggctactacctgaccttgtgtcaagaagaatggaatccctccctcaagctcgtcagaa 3720
Db 3661 CAGGCTACTACCTGACCTTGTGTCAAGAAAGATGTGAATCTCCCTCACTTCTCCAA 3720
Oy 3721 acaagtagtaacactgtgtgtaacttgaagaaagagagagagttctcgaagacgttcg 3780
Db 3721 ACAATGACTACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3780
Oy 3781 atgtctgcttggcagcagacatgagaatgtagacagctgacatcgatgtctgtatct 3840
Db 3781 ATGCTGCGCTGGGAGCGACCATGAGAGTACACGCTGACCATTCGATGCTGTATCT 3840
Oy 3841 ccaactccatcaaggaagcatgtgtctgaagcccggtgtgtgaagacataagacatgagc 3900
Db 3841 CCAACTCATCAGGAACCATGTGTGAAGCCCGGCTGTGGGAACATAGGGCATGTGAGC 3900
Oy 3901 tgaactatgtgtgtcgaatgaaagctgaagagagacgttgtggaactcttcatg 3960
Db 3901 TGACCTATGTGTCTGCATATGAAGCTCTAAGAGAGGAGGCTTTGTGGAACCTTTCA 3960
Oy 3961 agatttgtacggctctcagacctgggcatctcagatagatgacatcaagaagacc 4020
Db 3961 AGATTGTATGACCGGCTCTCAGACCTGTGGCATTTCTGTATGTGCAATCTAGAGACACC 4020
Oy 4021 tggaaagaataatctctaaaggtgagaaagagatgaggtgtgtgtgtgtgtgtgtgtgt 4080
Db 4021 TGGAAGAATATTTCTCTAAGGTGGCCGAAAGACTGGGTGTGTGTGTGTGTGTGTGTGT 4080
Oy 4081 gtaacttgcagcaagaacgaacagcgagccttcggggaacagcagagctgtctgc 4140
Db 4081 GTACTTCCAGCAAGACGAAGACGAGCGGCTTGGGGACAGAGAGCTGTCTTGTG 4140
Oy 4141 cgttcaatgaaatgtagtgcgtgtgtatccaaatgattctgtacatagccccagaatccagag 4200
Db 4141 CGTTCACTGAAGATGATGCTGTGATCTCAATATGATTTCTGTGATAGACCAAGATTCAGAG 4200
Oy 4201 agacagacttgcagtgagatgagatgcaaaaggttccactcagagtgaaagctgtgaac 4260
Db 4201 AGACAGACTTGTGATGTGATGTGATGTGCAAAAGGTCTCTACAGGTGAAGCTGTGAAC 4260
Oy 4261 ttacaagaacagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4320
Db 4261 TTACACACACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4320
```

QY	4321	ggaagagatllttttgtcgaattctgtccagctgtgttctgtcattgcctcttgt	4380
Db	4321	GGAAAGATATTTTGTCTCAGATTGTCCTGGCCAGCTGTGTTGTCTCATTTGCCCTTGTGT	4380
QY	4381	tcagctgtatctgtccaccctttggcaagtaccccaaccctggaccttgagcccttgatgt	4440
Db	4381	TCAGCTGATCTGTGCACCCCTTTGGCAAGTACCCAGCCTGGAACTTCAGCCCTGGAATGT	4440
QY	4441	acaaagaaacgtatacaatttgcacgaatgatgtcctctgaagacagggaaaccttgac	4500
Db	4441	ACAAAGAAAGTACACATTTTGTACGCAATATGTCTCTGAGGACACGGGAACCTTGGAAAC	4500
QY	4501	tcctaaagccctccaaagaacctgtcttgaggcccgctgtgtatgaagaagaaaccaa	4560
Db	4501	TCCTAAAGCCCTTCACCAAAACCCCTTGCTTGGGACCCGCTGTATGGAAGGAACCCAA	4560
QY	4561	tcccaagacagccctgtccagagcagggaggaagaaglygaaccactgtcccaagttcccca	4620
Db	4561	TCCCAAGACAGCCCTGTCCAGGCAAGGGAGAGAGTGGACACTGTGCCAGTTCCCCAGA	4620
QY	4621	ccataatgacctctccagaatgggaactggacaatgcgaaccccttaacctgtatgcc	4680
Db	4621	CCATCATGGACCTCTTCCAGATGGGAACGTGGCAATGCGAACCCTTCACTGTGATGCC	4680
QY	4681	agltgtagcagcacaanaatcaagaagatgtctgcctgtgtccccaaggcagggggagc	4740
Db	4681	AGTGTAGCAGCGCAAAATCAAGAAGATGCTGCTGTGTGTCTCCCAAGGGGAGGGGGGC	4740
QY	4741	tgcctctccacaagaanaaacactgtcagatatacctctaagaccttgacaggaaga	4800
Db	4741	TGCTCTCTCCACAAAGAAACAAACACTCGACATATCTTCCAGACCTCAGACAGGAAGA	4800
QY	4801	aaatttcgatatctatgttgaagaagcgratitgacatactctagaacaaagcttaagaaca	4860
Db	4801	AAATTTCCGATTATCTGTTGAAGACGTAITGTGANGTCTATACCAAAAGCTTTAAAGACA	4860
QY	4861	agatctgggtgaatgaagttaagtatagtgagcgttttccctgggtgtctcaagtaatactaag	4920
Db	4861	AGATCTGGGTGAATGAGTTTGAAGTATGGCGGCTTTCCCTGGGTGTGATATCTCAAG	4920
QY	4921	caattcccccgaagccaagaagtaatgatgccaataaacaatgaagaanaacctaaagc	4980
Db	4921	CACCTTCTCCAGTCCAAAGAAAGTTAATGATGTCCATCAAAATAATGAAAGAACCTTAAGC	4980
QY	4981	tggccaaggaacagttctgtcagatcgatcttctcaacacagctttggaagatlla tgaacagac	5040
Db	4981	TGGCCAAAGAACAGTTCTGTSCAGATCGATTTCTCAACAGCTTGGGAAGATTATGACAGAC	5040
QY	5041	tggacaacagaataaagttaagaagtgttggttcaataaacaagaaggtctgca tgcatacagct	5100
Db	5041	TGGACACCAAGAAATTAATGTCAAGAGTGTGGTTCAATTAACAAAGGGCTGGATGTCAATCGCT	5100
QY	5101	cttctctgaatgtcatcaaaacaatgcacattctccggccaacctgtcaaaaggaagaagac	5160
Db	5101	CTTCTCTGAATGTCAATCAACATGCGCATTTCTCGGGCCAACTGTCAAAAGGAGACAAAC	5160
QY	5161	ctgaaccttttggaattactacgtctttaaatacattcccttgaatccaagaagcagactct	5220
Db	5161	CTTGAACATTATAGGAATTAATCGCTTTTCAATCAATCCCTCAAACTCAACCAAGAGAGCTCT	5220
QY	5221	cagaggttgagctctgatagacacatacagtgagatgtctctgtgttcaactgtgtcatcttg	5280
Db	5221	CAGAGGTGGCTCTGATAGACACATCAAGTGGATGTCTTGTGTTCATCTGTGTATCTTTTG	5280
QY	5281	caatgtccctctgtccagccagcttctgtcatctctgatccaggaagcggtaagcaag	5340
Db	5281	CAATGTCTTCTGTGCCAGCACAGCTTTGTCTGTATCTTGATCAAGAGCGGGTACGCAAG	5340
QY	5341	caaaaacccggaagttcaacagtggaaggaagccgtgcatatactactgtctcctaatttg	5400
Db	5341	CAAAACCCGTGACCTTCACTGATGGAGTGAACCGCTGTATCTACTGTGGCTCTCTTAATTTTG	5400

QY	5401	tggggatbtggaactatgctgtgcttgccgaacatgctatcatcttcactgct	5460
Db	5401	tctgggatattggaacattatgcgttgccctgcacacatggacattatcaattcatctgct	5460
QY	5461	tccagagaagctccatgctgctctccacaaactgcgctgctcaagccctcaacttgc	5520
Db	5461	tccagagaagctccatgctgctctccacaaactgcgctgctcaagccctcaacttgc	5520
QY	5461	tccagagaagctccatgctgctctccacaaactgcgctgctcaagccctcaacttgc	5520
Db	5461	tccagagaagctccatgctgctctccacaaactgcgctgctcaagccctcaacttgc	5520
QY	5521	tgtatggtgtgtcactcaacactctcatgtaaccagctctcttgttcaagatccca	5580
Db	5521	tgtatggtgtgtcactcaacactctcatgtaaccagctctcttgttcaagatccca	5580
QY	5581	gcacagccatbtgtgtctcaacagcgctgaaccccttcattgtcattatgtgcacgtg	5640
Db	5581	gcacagccatbtgtgtctcaacagcgctgaaccccttcattgtcattatgtgcacgtg	5640
QY	5641	ccaccttgtctgtgagctgtctcaacagcaataagctgtaataatcaatgtaatacctga	5700
Db	5641	ccaccttgtctgtgagctgtctcaacagcaataagctgtaataatcaatgtaatacctga	5700
QY	5701	agtcggtgtctgtgcttcccaactttgtcctgggaagaggtctcatcgacatgtga	5760
Db	5701	agtcggtgtctgtgcttcccaactttgtcctgggaagaggtctcatcgacatgtga	5760
QY	5761	aaaacaggaacatgtgctgctgctgcaagcgttgggaagatcgcttgtgtacacat	5820
Db	5761	aaaacaggaacatgtgctgctgcaagcgttgggaagatcgcttgtgtacacat	5820
QY	5821	tatcttgggacttggctggagcgaaccccttcgcaatggcgttgggaagaggtgtgtct	5880
Db	5821	tatcttgggacttggctggagcgaaccccttcgcaatggcgttgggaagaggtgtgtct	5880
QY	5881	tcccatcactgcttctgtatccagaaagatcttctcaagccagagccttaataatcaa	5940
Db	5881	tcccatcactgcttctgtatccagaaagatcttctcaagccagagccttaataatcaa	5940
QY	5941	agctatctccctctgaatgaatgaatgaatgaatgtgagcgcggaagacagagaacttctg	6000
Db	5941	agctatctccctctgaatgaatgaatgaatgaatgtgagcgcggaagacagagaacttctg	6000
QY	6001	atcggtggagggccaagaatgaacactctgaagaaatgaagagcttgcagaagataataatga	6060
Db	6001	atcggtggagggccaagaatgaacactctgaagaaatgaagagcttgcagaagataataatga	6060
QY	6061	agcggaacactgctgtctgaagagattgcgttgggcacttccctctgtgtgaagcttggc	6120
Db	6061	agcggaacactgctgtctgaagagattgcgttgggcaacttccctctgtgtgaagcttggc	6120
QY	6121	tccctggaggttaatggggcgctggaaatcatcaacttgaagatgttaacagagatatcca	6180
Db	6121	tccctggaggttaatggggcgctggaaatcatcaacttgaagatgttaacagagatatcca	6180
QY	6181	ctgttaccagaagaagatgcttctcttcaaaaaaatagatatcttcaacaacccatgaag	6240
Db	6181	ctgttaccagaagaagatgcttctcttcaaaaaaatagatatcttcaacaacccatgaag	6240
QY	6241	taacttgaagaataatgggtctactgcccctcaatttgaatgccaatacagagctgttgaatggga	6300
Db	6241	taacttgaagaataatgggtctactgcccctcaatttgaatgccaatacagagctgttgaatggga	6300
QY	6301	gagaaacagtgtgagcttcttgcctcttgaagggaggtcccaagaaagaagatttggcaag	6360
Db	6301	gagaaacagtgtgagcttcttgcctcttgaagggaggtcccaagaaagaagatttggcaag	6360
QY	6361	tgtgtgtgagtggtgcgattcgggaacttgggctcgtgtgaagtatgtgagaagaaatatgtctgtga	6420
Db	6361	tgtgtgtgagtggtgcgattcgggaacttgggctcgtgtgaagtatgtgagaagaaatatgtctgtga	6420
QY	6421	actatgtggaagcaacaacagcaagctctcaagccaatgtcttitaatggggcttc	6480
Db	6421	actatgtggaagcaacaacagcaagctctcaagccaatgtcttitaatggggcttc	6480
QY	6481	ctgtgtgcttctgtatgaaccaccacaagcatatgatacccaagcccgcgcttctgt	6540

Db	6481	CTGGGGGTTTCGGATGTAACCCACCAAGGATGATCCAAAGCCCGGTTCTTGT		6540
Qy	6541	ggaatttgccccaagtgctgtcaaggaggagatcaatgagtctacatccatagta		6600
Db	6541	GGATTGTGGCCCTAACTGTTGTGCAGSAGGGAGATAGTAGTCTTCAATCTCAAGTA		6600
Qy	6601	tggagaagatgtgaagctctcttgcaatgagatggcaatcagtgtaatggaagttcga		6660
Db	6601	TGGAAAGAAATGTGAAGCTCTTTCACATAGAGTGCATATATGTCTCAATGAAGATTTAGGT		6660
Qy	6661	gacctggcagtgcccaagatcccaaaaagaattgagatggttatcacatagttgtac		6720
Db	6661	GCCTTGGCACTGTCCAGCATCTAAAAAATAGTTTGGAGATGTTTATACAAATAGTTGTAC		6720
Qy	6721	gaatagcaaggtcccaaccggagcttgaagcctgtccagaattcttggacgtgcattc		6780
Db	6721	GAATAGCAGGGTCCAAACCCGGACCTGAAACCCGTCCAGAGATTTCTTGGACTTGCATTTTC		6780
Qy	6781	cttgaagtggtctcaaaaagagaacacccggagaatgctcaatcacagctccatctcat		6840
Db	6781	CTGGAAGTGTCTTAAAGAGAAACACCGGAAATCTCTCAATACAGCTTCATCTCTCAT		6840
Qy	6841	tatctctctgcccagagatatcgaatccctctccagaagcaaaagcgactccaatag		6900
Db	6841	TATCTCTCTGGCCAGGATATTTACAGATCTCTCTCCAGACGAAAGGACATCCACATAC		6900
Qy	6901	aagactctcgtttctcagaacaacgttcagcaagatcttgtaaccttggccaagacc		6960
Db	6901	AAGACTCTCGTTCCTCAACAAACCTTGACCAGATATTGTGTGACTTGGCAAGACC		6960
Qy	6961	aaagtgatgatgacacattaaagaacctctcatcacaaaaaccagaagtagtgaag		7020
Db	6961	AAAGTAGATGAGACACTTAAAAAGCTCTCATTTACAAAAACGACAGCTAGTGAGC		7020
Qy	7021	ltgcagttctcaactctttctcagagatgagagaagaatgaagaagaagctatgtgaagaa		7080
Db	7021	TTGCAGTCTCACATCTTTTCTACAGAGTAGAAGATGAAGAAAGCAATATATGAAGAA		7080
Qy	7081	tccctgtcaatacggggtgctgtgaagtlaaagaggaactagacttcccttgcacatgtg		7140
Db	7081	TCCCTGTCAATACGGGGTGGGCTGAAGTAAGAAGACTATGACTTCTTCCACCATGTG		7140
Qy	7141	aagtgctgttgagaagaagagccgaagtgtgagtgtggaagaagtaactgatactgtac		7200
Db	7141	AAGTGTGTGAGAAAGAGCCAAATGTGATGTGGAGAAAGTAACTGATCTGTGAC		7200
Qy	7201	tgaatacttcaatgaatgaatgaatcgaatgaaatgaacaaatctcatcacagggtga		7260
Db	7201	TGATACTTATTCAAATGCAATGCAATTCATGCAATGAAAAAATAATTCATTACAGGGCA		7260
Qy	7261	gtgcctctgttagcctatgctctgtatagtcctcctaagtgaagacttgatagttctt		7320
Db	7261	GTGCCTGTGTAGCCATATGTCTTGTATGGCTCTCAAGTGAAGAACTTGAATTTAGTTTTT		7320
Qy	7321	acctataactatgtaaaactctatataggaaaccaatggaactatgggtttgaactaca		7380
Db	7321	ACCTAATACCTATGTAAACTATTAATGAAACCAATGAAACATATGGGTTTGAATCTACA		7380
Qy	7381	cttttttttttttttgttctcgtgtatctcatatggggttgcaacaataattctacaag		7440
Db	7381	CTTTTCTTTTCTTTTGTCTCGTGTCTTCATTTGGGGTGTGCACAAATTAATCTATCAAG		7440
Qy	7441	taaatatgvcagagatatttgatcaaaaatcaaaaaggtlaatgcacatccctatctacaa		7500
Db	7441	TAAATCATGGCCCGCATTTATGATCAAAATCAAAAGGTATATGACATCTCTATTCTACPA		7500
Qy	7501	gcaatgccatgcccagagactgtttcccggtgaacatccatctgctgcaatgaagt		7560
Db	7501	GCCATGCCATGCCCGAGACTGGTTTTCCCGGTACACATCCATTTGCTGGCAATGAAGT		7560
Qy	7561	gccagagttattagtgccaagatttltcaagaaglttgaagcacatggtgtgtaagtc		7620

Db	7561	GCACAGATTAATAGTGCAGAGTTTTCAGAAAAGTTTGAAGACCATGAGTGTGACATGC	7620
Qy	7621	actcttgagaacgtctgctcgtcagagctcatalcaacatlgatlatcagltgacgaatg	7680
Db	7621	ACTTTTGTGAAGCGTCTGCTGCACAGCTATCAACATTGAATATCAGTTGCACAAATG	7680
Qy	7681	gtgcacatgctgagctaacatcctgctcttgatctccctcgataaagctgtctctgtgagcat	7740
Db	7681	GTGCATACCGGCGTAAACATCCGCTTTGATATTCCTCTGAAATACCTTTCTGTGGTGCACCT	7740
Qy	7741	aacctagacacaaaatgttggtgtctccctcagagcaaggaaactgtgtccatctgtacatt	7800
Db	7741	AACATGCAACAAATAATGTGGTGTCTCTTAGCAGCGGAACCTTGTTCCATTGTTATATT	7800
Qy	7801	gtccatagctctcgagccatggtgtctacaggtgacatcccttatgagactcttaatacatt	7860
Db	7801	GTCCATATCCTTTCGAGCCATGGGTCTACAGGCGCATCTTATGAGACCTTAAATATACCTT	7860
Qy	7861	agatccctgtaagagagcaagaatcaaacgccaactctctgggctctcaagctgcgtgaag	7920
Db	7861	AGATCTCTGTGAAGGGGCAAAAGATCAACAGCCCAACTCTGGGGCTGAGACCTGCGAAG	7920
Qy	7921	ccaagagcatggagtaataagagatctgtgcgtccaacccctagaggaaacctgtgcccattgt	7980
Db	7921	CCAGGGCATGGGATTAAAGAGATTGTGCGTCAAACTAAGGAAGCCGTGGCCCATTTG	7980
Qy	7981	ccctgactgtctgtctaacaatgtaacactgcatctcaagatglttatctgtacaacaagtgtat	8040
Db	7981	CCGTGACTGTCTGCTAACTATGATGGTACATCGCATCAAGATGTTTATCTGACCAAGTGTAT	8040
Qy	8041	tattctcgctcttttgatlaatacctagaataatgaagaatggaggtgtgattttgacaaa	8100
Db	8041	TATTTCTGGCTTTTGAAATTATCTAGAAAATGAAGAATGAGATGTGTATTTTACAAAA	8100
Qy	8101	agctttgtaacttttaatgltatlttgaaatttaagtttctacagtgactctgaaatcct	8160
Db	8101	ATGCTTTGTACTTTTAAAGTTATTTGGAATTTAAGTTCTATCAGTGACTCTGAATCT	8160
Qy	8161	tagaatgagccctcttgtagaaacctgtgtgataagagatagagccatctggcccaactatt	8220
Db	8161	TAGAAATGGGCTCTTGTGTGAACCCCTGTGCTATAGAGAGATTAAGGCCACATGGCCCATATT	8220
Qy	8221	tttatcttcttaatgaaattgacatcagatcagtagactagtcctcagaagaacatlgat	8280
Db	8221	TTTTATTTTCTAATGTAAGTTTGCAATACAGTCAATGACTAGTGGCTTAGAAGCAATGTGAT	8280
Qy	8281	ggtcagagatcctatcacatlatattgagttcttcacagatcaattaggaataccttaatt	8340
Db	8281	GGTCAGAGATCTCATACATTATTTAGTTCTTTACAGATCATTTAGGATACCTTTAAT	8340
Qy	8341	ctcacttccatcaatcaaatatcttttgagtgatagctgtatagctgtgaagaagatgtaagta	8400
Db	8341	CTCAGTTTCATCATCAATATTTTATTTAGAGTATAGCTGATCGAAGAGATGTACTCTA	8400
Qy	8401	cgtataagactagaagatattaagtcctagatcaactctctgtgccaatgltataagctc	8460
Db	8401	CGTATAGACTGTAGAGATTAATTAAGTCTCACTGACTTCTGTGCCATGTTATTCAGCTC	8460
Qy	8461	actggtttcaaatatagttgtctctgtgtgtgtaagagcccaactgttaacaatatltggcc	8520
Db	8461	ACTGGTTTACAATATAGTGTCTCTGTGTGTGTAGAGGCCACCTGTAACTATTATGGCC	8520
Qy	8521	agcctttctttttttttttttaaattgcaacaatgcaaaagccaagaagaatataaaggtcac	8580
Db	8521	AGCCTTTTCTTTTCTTTTATTTGCAACATGCAGAAAGCCAAAGAAATATTAAGGCTAC	8580
Qy	8581	aagtttaacaatgtaattcttccacacagggaaaacaaagctgtcttgaanaactctgtcaaaa	8640
Db	8581	AAGTTTAAACAATGAATTTCTCAAGAGGAAAACCTACTCTGAAATCTTCTGAAAAA	8640
Qy	8641	caacaacttggttaatgagcatctgtaaccttcaacaatattgctcttgacagatatgtgata	8700
Db	8641	CACACATTGTGTTTATGSCATTATGTAACCTTCAAAATATTTGGCTTTCGAGATATTGTATA	8700

QY 8701 cccattaaatctgacagctcacaattttcattctcctcaactaactagccaagaanaata 8760
 |||||
 Db 8701 cccattaaatctgacagctcacaatttttctcattcttcaactagccaagaanaata 8760
 |||||
 QY 8761 taataaacaataactcctacataggaacattttcaaggtttcctcaaccagcttatt 8820
 |||||
 Db 8761 taataaacaataactcctacataggaacattttcagaggttttcaaccagcttatt 8820
 |||||
 QY 8821 ttctatagtaaacatttgtaaaaatactgtttcaactaactactactcgttaactgtct 8880
 |||||
 Db 8821 ttctatagtaaacatttgtaaaaatactgtttcactaactaactactactcgttaactgtct 8880
 |||||
 QY 8881 tgaagagaaagaaataatagagagaaactatgtttggggaagttcaagtgatcttcaat 8940
 |||||
 Db 8881 tgaagagaaagaaataatagagagaaactatgtttggggaagttcaagtgatcttcaat 8940
 |||||
 QY 8941 atattactaactctctcactcttttccaataattgaaatataacgcgtaaagtgtaaga 9000
 |||||
 Db 8941 atattactaactctctcactcttttccaataattgaaatataacgcgtaaagtgtaaga 9000
 |||||
 QY 9001 ctccagattccaataactccttctcattttttaaatttaagagataatataaccaca 9060
 |||||
 Db 9001 ctccagattccaataactccttctcattttttaaatttaagagataatataaccaca 9060
 |||||
 QY 9061 ctgctgaaagaaagaaataatgtatgttttaagaagttaagtaactgatttaaatat 9120
 |||||
 Db 9061 ctgctgaaagaaagaaataatgtatgttttaagaagttaagtaactgatttaaatat 9120
 |||||
 QY 9121 aagtaagagagacatacttccaataactagatagatgacacgctgtgcaacttcaagatc 9180
 |||||
 Db 9121 aagtaagagagacatacttccaataactagatagatgacacgctgtgcaacttcaagatc 9180
 |||||
 QY 9181 ttcaaaaaatacagaattatagaaataattcctccactaataatttttcaaaaatacaga 9240
 |||||
 Db 9181 ttcaaaaaatacagaattatagaaataattcctccactaataatttttcaaaaatacaga 9240
 |||||
 QY 9241 ttatgtttccctcatttactaaatgcatcttcaattcttcaatataagtaactctga 9300
 |||||
 Db 9241 ttatgtttccctcatttactaaatgcatcttcaattcttcaatataagtaactctga 9300
 |||||
 QY 9301 gcaactccttactcgttccctcgtatctcaagggccatattttaaanaatacaaaagcac 9360
 |||||
 Db 9301 gcaactccttactcgttccctcgtatctcaagggccatattttaaanaatacaaaagcac 9360
 |||||
 QY 9361 tctgaactattttgagaagaacaagacatttaacagatgtaagaccccttctga 9420
 |||||
 Db 9361 tctgaactattttgagaagaacaagacatttaacagatgtaagaccccttctga 9420
 |||||
 QY 9421 gctagaacaactcctatagttataactccttaactactggttaactttaaataagta 9480
 |||||
 Db 9421 gctagaacaactcctatagttataactccttaactactggttaactttaaataagta 9480
 |||||
 QY 9481 atttttcaatttctcgttgtaaaactaatgtgtgtaagaatttttcaactctact 9540
 |||||
 Db 9481 atttttcaatttctcgttgtaaaactaatgtgtgtaagaatttttcaactctact 9540
 |||||
 QY 9541 caatcaagcaaaaatttctgtatattccctgtggaagtacactatgtgaatttcaagaatt 9600
 |||||
 Db 9541 caatcaagcaaaaatttctgtatattccctgtggaagtacactatgtgaatttcaagaatt 9600
 |||||
 QY 9601 ctcaaaaactgttctcaaaaatttctgttcttgcatttgggacacactaagaanaacta 9660
 |||||
 Db 9601 ctcaaaaactgttctcaaaaatttctgttcttgcatttgggacacactaagaanaacta 9660
 |||||
 QY 9661 ttaaaactgttgaataagaaatacagaagaanaataaagaacctctatataaagc 9720
 |||||
 Db 9661 ttaaaactgttgaataagaaatacagaagaanaataaagaacctctatataaagc 9720
 |||||
 QY 9721 caagacaaactcattgtttaaaaaaacaactcaactcactactgtattctatctgt 9780
 |||||
 Db 9721 caagacaaactcattgtttaaaaaaacaactcaactcactactgtattctatctgt 9780
 |||||

QY 9781 actgaagcaaatgcttctgtgactattaaatgttgcacatcattcactctatagta 9840
 |||||
 Db 9781 actgaagcaaatgcttctgtgactattaaatgttgcacatcattcactctatagta 9840
 |||||
 QY 9841 atcattgacaaagacatttgcgtgttcttctctgtggnlnatataagtaaat 9900
 |||||
 Db 9841 atcattgacaaagacatttgcgtgttcttctctgtggnlnatataagtaaat 9900
 |||||
 QY 9901 atttccaagagacatgttgcataactgaaccccttgatattgagacataatt 9960
 |||||
 Db 9901 atttccaagagacatgttgcataactgaaccccttgatattgagacataatt 9960
 |||||
 QY 9961 ggaaccttgatttctactagaaataatgtataactcgnagaatatgtcttaattct 10020
 |||||
 Db 9961 ggaaccttgatttctactagaaataatgtataactcgnagaatatgtcttaattct 10020
 |||||
 QY 10021 tcaaaaatgtgacaccccttaaaaagtctcattccaataagattagctgttctc 10080
 |||||
 Db 10021 tcaaaaatgtgacaccccttaaaaagtctcattccaataagattagctgttctc 10080
 |||||
 QY 10081 ctcttataccctaaagatgaagctgttctgtgctccttgatcaactggaacctc 10140
 |||||
 Db 10081 ctcttataccctaaagatgaagctgttctgtgctccttgatcaactggaacctc 10140
 |||||
 QY 10141 caagcacttaacgctgtctgtaattggaatcttcttgacatggaatctggaattgc 10200
 |||||
 Db 10141 caagcacttaacgctgtctgtaattggaatcttcttgacatggaatctggaattgc 10200
 |||||
 QY 10201 aaactagaacaaagttcacacagatcttcaatgaatcaattcattcaaaagaa 10260
 |||||
 Db 10201 aaactagaacaaagttcacacagatcttcaatgaatcaattcattcaaaagaa 10260
 |||||
 QY 10261 aaagaaaaaaatttggatctcaataacttataagaatataaataatcttca 10320
 |||||
 Db 10261 aaagaaaaaaatttggatctcaataacttataagaatataaataatcttca 10320
 |||||
 QY 10321 tctgtataataatgagtcacaaataaagctgtgacagcttctgttaaaaaa 10380
 |||||
 Db 10321 tctgtataataatgagtcacaaataaagctgtgacagcttctgttaaaaa 10380
 |||||
 QY 10381 aaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa 10440
 |||||
 Db 10381 aaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa 10440
 |||||
 QY 10441 aa 10442
 |||||
 Db 10441 aa 10442
 |||||

RESULT 2
 AX060892 10442 bp DNA linear PAT 22-JAN-2001
 LOCUS AX060892
 DEFINITION Sequence 1 from Patent WO0078971.
 ACCESSION AX060892
 VERSION AX060892.1 GI:12406270
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 10442)
 AUTHORS Lwin,R.M., Wade,D., Oram,J.F. and Garvin,M.
 TITLE Atp binding cassette transporter protein abcl polypeptides
 JOURNAL Patent: WO 0078971-A 1 28-DEC-2000;
 CV THERAPEUTICS, INC. (US)
 FEATURES
 source location/Qualifiers
 1. 10442
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 2898 a 2297 c 2408 g 2835 t 4 others
 ORIGIN

[illegible]

Db	1021	ACTCTACATCTCCCTTCCCGACCAAGAGCTGGCTGAAGCCACAAAACATTGCTGCATTA	1080
Qy	1081	gtctctgagacctcgcgcgcagagagctgtcttcagcatbaagaagctgagatgacatgycgcagag	1140
Db	1081	GTCTTGGAGACTCTGGCCCAAGGAGCTGTTTCAGCATGAGAAAGCTGGAGTCATCCGACAG	1140
Qy	1141	aggtgatgtcttcgcaccaatgtgaacagctccagctccctccaccacaaattaccagctg	1200
Db	1141	AGGTGAATGTTTCTGACCAATATGGAACAGCTCCAGCTCTCCACCCAAATCTACCAAGCTG	1200
Qy	1201	tgctctgattatgtctgcgcgcacatcccgagagagagggcttgaagaatcaagtcctcaact	1260
Db	1201	TGCTCTGATTATGTTCTGCGGGACATCCCGAGGAGGGGGGCTCAAGATCAAGTCTCTCAACT	1260
Qy	1261	ggtatgagagacaactacatacaagccctctttggaagcaatgycacctggaagaatgctg	1320
Db	1261	GGTATGAGGACAACACTACAAAAGCCCTTTTGGAGGCAATGGCACTGAGAGAAGATGCTG	1320
Qy	1321	aaacctctatgaacactctacaaacctctactgcaatgatttgaatgaagaatctggagt	1380
Db	1321	AAACCTTCTATGACAACTCTACAACTCCTTACTGCAATATTTGATGAGAATTTGGAGT	1380
Qy	1381	ctagtcctctctccgcgcatatctggaagaagctcgaagcgcgtgcgtgttggagaatcc	1440
Db	1381	CTAGTCCCTTCTCCCGATATCTCGGAAAGAGCTGTGAACCCCTCCTGTTGGGAAGATCC	1440
Qy	1441	tgatataacctggaacctcgcgcgcacagaagcgaatgataatgctggaagtgaacaagacctcc	1500
Db	1441	TGTATACACCTGAGACATCCAGCCACAAAGCAAGCTATGCTGATGAGTGAAACAAGACTTCC	1500
Qy	1501	aggaactgcgtgttccatgcatctggaagagcatgtgggaagaaactcaagcccaagatct	1560
Db	1501	AGGAACCTGGCTGTTCATGATCTGGAAGGCATGAGGAGGAATCAAGCCCCAAGATCT	1560
Qy	1561	ggaacctcattgagagaacacgcacagaagaatggacctgtgtccggaatgctgttggacgcaggg	1620
Db	1561	GGACCTTATGAGAAACAGGCAAGAAATGGACTCTTCCGATGCTGTGGACAGCGAGG	1620
Qy	1621	acaatgaccaccttttgggaacaagaatgtgatgtctctagatgtgaacgaagcccaagacatcg	1680
Db	1621	ACAAATGACCACTTTTGGGMAACAGCAAGTGGATGGCTTAATTTGGACAGCCCAAGACATCG	1680
Qy	1681	tgagcttcttggccaagacaccgaagagatgtccagtccagtaatgtgttcgtgtgaacct	1740
Db	1681	TGCGCTTTTGGCCAAACACCCAGAGAGATGTCAGTCCAGTCAATGTTCTGTGACACT	1740
Qy	1741	ggaagagaagctttaaagagagactaacaggacaaatccgcagcctatctgcgtctcatggagt	1800
Db	1741	GGAGGAAGACTTTTCAACAGAGCTTAACAGGCAATCCGGACATATCTGGCTTCAATGGAGT	1800
Qy	1801	gtgtcaacctgaacagcttaagaaccctatgcaacagaagaatctgtgctatcaacaagaatcca	1860
Db	1801	GGTTCACACTGAAACGCTAGAACCCCTATGACAAAGAAATCTGGCTCATCAACAAAGTCCA	1860
Qy	1861	tggaagctctgtgatgagaggaagttctggagctgtgatgttcttcaactggaattactccag	1920
Db	1861	TGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTTGATATGTGTTCACTGSAATTACTCCAG	1920
Qy	1921	ggaagctgaagctgcccacatcatgtcaagtacacagaatccgaatbgacatttgaacaatgtg	1980
Db	1921	GCAAGCTTAGCTGGCCCATCATGTCAATGACAAAGATCCGAATGCGAATGACATTCGAATGTGG	1980
Qy	1981	agagagaacaataatacaagaatggtgtactcgggacccctggtctcgtgaagtggcccccttg	2040
Db	1981	AGAGGCAAAATTAATTAAGAGATGGGTACTGGGACCCCTGTCTCTCGAGCTGACCCCTTTTG	2040
Qy	2041	agagaactgagtagctctggagggagctctgcctcaacttgcaggaatgtgtgtaggcagagcaa	2100
Db	2041	AGGACATGCGGTACTGCTGGGGGGGCTTCGGCTACTTGCAAGGATGTGGTGAGCAGGGCAA	2100
Qy	2101	tcatcaggtgtcgaaggagcccgagaagaactgtgtctatctatgcaacagaatgacct	2160

Db 2101 TCATCAGGCTCTACGCGGACCGAGAAAGAACTGGTGTCTATATGCAACAGATGCCCT 2160
QY 2161 atccctgttactgtatgacatctcttcggtgtatgagccggtcaagcccccttca 2220
Db 2161 ATCCCTGTAGCTTGATGACATCTTCTGGGGGTGATGACCGGTCAATGCCCTTTCA 2220
QY 2221 tgaagcttgcttgatattactcaagtgtgtatcatcaaggacatcgtgtatgaaag 2280
Db 2221 TGAGGCTGGCTGGATTACTCACTGGCTGTGTATCATCAAGGGCATCTGTATGAAAGG 2280
QY 2281 aggaacgctgaaagagacacatgcyatcaatggccctggaacaacacatctgttta 2340
Db 2281 AGGACGGCTGAAGAGACCATGGGATCATGGGCTGGACACACATATCTGTGTTTA 2340
QY 2341 gctgttcaatagtacacctaatctctctctgtgagcgctgagctgtagtgtatcc 2400
Db 2341 GCTGGTTCAATTAGTAGGCTCATCTCTCTGTGTGAGCGGTGGCTGTAGTGTATCC 2400
QY 2401 tgaagttagaagaacctgtctccctacagtgatccagcgtgtgtgttctgtccgtcg 2460
Db 2401 TGAAGTTAGGAACCTGCTCCCTACAGTATCCAGCGTGGTGTGTCTCTGTCCG 2460
QY 2461 tgttctgtgtgtgaaatccctgagtgcttccgtatagcacatctctccagagca 2520
Db 2461 TGTTTGTGTGTGACAAATCTGAGTGTCTGTATGACAACTCTTCCAGAGCA 2520
QY 2521 acctgagcagcctgtgtgggagcatcatctactcaagcgtgtacccctcagtcgt 2580
Db 2521 ACCTGAGCAGCCTGTGGGGGATCATCTACTTCAAGCTGTATACCTGCTTACGTCGT 2580
QY 2581 gtgtgtgcatgagcagactatgagcttcaacatcaagaacctcagctgtgtctc 2640
Db 2581 GTGTGGCATGGAGGACTAGTGGGCTTCACTCACTCAAGTCTTGGTACCTGTCTC 2640
QY 2641 ctgtgcttctgt 2700
Db 2641 CTGTGGCTTGTGGT 2700
QY 2701 tgcagtgagcaaacctgt 2760
Db 2701 TGCAGTGAGCAACCTGT 2760
QY 2761 cgaatccatgagctgt 2820
Db 2761 CGATTCATGATGCTGT 2820
QY 2821 ctgtcttccagcagatgagcaatcccaagccctgtgtgtgtgtgtgtgtgtgtgtgt 2880
Db 2821 CTGTCTTCCAGGCCAGTACGGAATTCACAGGCCCTGTGTGTGTGTGTGTGTGTGT 2880
QY 2881 actgt 2940
Db 2881 ACTGT 2940
QY 2941 cagaatctgcatgag 3000
Db 2941 CAGAAATCTGCATGAG 3000
QY 3001 tggtaaaagtctacagagatggatgaaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3060
Db 3001 TGGTAAAGTCTTACCGAGATGGATGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3060
QY 3061 atgag 3120
Db 3061 ATGAGAGGCGAGATCACT 3120
QY 3121 caatcctgacagcgt 3180
Db 3121 CAATCCTGACGGGTTGT 3180
QY 3181 ttccgtctgagatgagacatccgagagagagagagagagagagagagagagagagag 3240
Db 3181 TTCCGCTTGAGATGAGACCATCCGGCAGAACTGGGGGTCTGTCCCCAGCATTAACGTGC 3240

QY 3241 ttttgaacatgctgacgt 3300
Db 3241 TTTTGAACATGCTGACGT 3300
QY 3301 ctgaaagacagcgt 3360
Db 3301 CTGAAGACAGCGTGAAGGGCGAGATGAGACAGATGGCCCTGTGTGTGTGTGTGTGTGT 3360
QY 3361 gcaagcgtgaaagcaaaacaaagccagctgtcaagtgtgaaatgcagagaaagatcgtgtg 3420
Db 3361 GCAAGCTGAAACCAAAACCAAGCCAGCTGTCAAGTGTGAATGCAAGAAAGCATCTGTGG 3420
QY 3421 ccttgagccttctgt 3480
Db 3421 CCTTGGCCCTTGTGTGGGGATCTAAAGTTGTCTATCTGTGTGTGTGTGTGTGTGTGTGT 3480
QY 3481 acccttactccgcagagagaaatgtggagctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3540
Db 3481 ACCCTTACTCCGCAAGGGAAATGTGGAGCTGTCTGTGAATTAACGACAAAGCGCACCA 3540
QY 3541 ttaattctctac 3600
Db 3541 TTAATTCCTCTAC 3600
QY 3601 tctcccatggaagcgt 3660
Db 3601 TCTCCCATGGGAAGCTGT 3660
QY 3661 caggtctactaacctgtgacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3720
Db 3661 CAGGCTACTAAGCTGACCTGT 3720
QY 3721 acagtagtagcagctgt 3780
Db 3721 ACAGTAGTAGCAGCTGT 3780
QY 3781 atgt 3840
Db 3781 ATGT 3840
QY 3841 ccaactctacagagagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3900
Db 3841 CCAACTCTATCAGGAAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3900
QY 3901 tgaacctatgt 3960
Db 3901 TGAACCTATGT 3960
QY 3961 agatgtatgacagcgt 4020
Db 3961 AGATGTATGACCGGCTGT 4020
QY 4021 tggaaagaaatctctcaagt 4080
Db 4021 TGGAAAGAAATATCTCTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4080
QY 4081 gtaaccttgccaag 4140
Db 4081 GTAACCTTGCCAG 4140
QY 4141 cgttcaactgaagatgagctgt 4200
Db 4141 CGTTCACTGAAGATGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4200
QY 4201 agacagactgtctcaagt 4260
Db 4201 AGACAGACTTCTCAAGT 4260
QY 4261 ttacaacagcaacagctgt 4320
Db 4261 TTACAGCAGCAACAGTTGT 4320

Db 6481 CTGTGTTTCTGGATGAACCAACGACATGATCCAAAGCCCGGCTTCTGT 6540
Qy 6541 ggaatttggccctaaagtgttcaagaaggagagatcagtaagtgttacctcaatla 6600
Db 6541 ggaatttggccctaaagtgttcaagaaggagagatcagtaagtgttacctcaatla 6600
Qy 6601 tgaagaatgtgaagctcttctcagtagagatgcaatcctggtcaatgaagttcagct 6660
Db 6601 tgaagaatgtgaagctcttctcagtagagatgcaatcctggtcaatgaagttcagct 6660
Qy 6661 gcccttgcagatgtccagcaatcctcaaaataagtttggagatggttatcaatagttac 6720
Db 6661 gcccttgcagatgtccagcaatcctcaaaataagtttggagatggttatcaatagttac 6720
Qy 6721 gaataagaggtccaaacccgagaccctgaagcctgtccagatcttcttggacttgcattc 6780
Db 6721 gaataagaggtccaaacccgagaccctgaagcctgtccagatcttcttggacttgcattc 6780
Qy 6781 ctggaagatgtctaaagaagaaacacggaacatgctatacaatcagcttccatctcat 6840
Db 6781 ctggaagatgtctaaagaagaaacacggaacatgctatacaatcagcttccatctcat 6840
Qy 6841 tatcttctcagcagagatatacagatctctccagagcaaaaagcagctcacaatag 6900
Db 6841 tatcttctcagcagagatatacagatctctccagagcaaaaagcagctcacaatag 6900
Qy 6901 aagaactactgttctcagacaacacttgcacaaatattgtgaacttgcagaagacc 6960
Db 6901 aagaactactgttctcagacaacacttgcacaaatattgtgaacttgcagaagacc 6960
Qy 6961 aagaatgaatgaac 7020
Db 6961 aagaatgaatgaac 7020
Qy 7021 ttgcagtttccacatcttctcagagatgagaagttgaagaagacacacacacacacac 7080
Db 7021 ttgcagtttccacatcttctcagagatgagaagttgaagaagacacacacacacacac 7080
Qy 7081 tctgttctcagagatgagatgagatgagatgagatgagatgagatgagatgagatgag 7140
Db 7081 tctgttctcagagatgagatgagatgagatgagatgagatgagatgagatgagatgag 7140
Qy 7141 aagttgttggagaaagagacagagatgagatgagatgagatgagatgagatgagatgag 7200
Db 7141 aagttgttggagaaagagacagagatgagatgagatgagatgagatgagatgagatgag 7200
Qy 7201 tgaatacttcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgca 7260
Db 7201 tgaatacttcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgca 7260
Qy 7261 gttgcttctgtagcctatcttctgtagcctatcttctgtagcctatcttctgtagcctat 7320
Db 7261 gttgcttctgtagcctatcttctgtagcctatcttctgtagcctatcttctgtagcctat 7320
Qy 7321 acctatactatgaaac 7380
Db 7321 acctatactatgaaac 7380
Qy 7381 ctt 7440
Db 7381 ctt 7440
Qy 7441 taatcatgagcagatattgatcaaatcaaatcaaatcaaatcaaatcaaatcaaatcaaatca 7500
Db 7441 taatcatgagcagatattgatcaaatcaaatcaaatcaaatcaaatcaaatcaaatcaaatca 7500
Qy 7501 gccatgcatgagcagagatggttcccgatgagacacacacacacacacacacacacacacac 7560
Db 7501 gccatgcatgagcagagatggttcccgatgagacacacacacacacacacacacacacacac 7560
Qy 7561 gccagagttatagtgcaagtttttcaagaagtttgaagaacacacacacacacacacacacac 7620
Db 7561 gccagagttatagtgcaagtttttcaagaagtttgaagaacacacacacacacacacacacac 7620

Qy 7621 acttttgaagaagctgtctgtcagagatcctacacatgcaatgaatgaatgaatgaatgaatga 7680
Db 7621 acttttgaagaagctgtctgtcagagatcctacacatgcaatgaatgaatgaatgaatgaatga 7680
Qy 7681 gttcagatgagtgagatcagatcagatcagatcagatcagatcagatcagatcagatcagat 7740
Db 7681 gttcagatgagtgagatcagatcagatcagatcagatcagatcagatcagatcagatcagat 7740
Qy 7741 aacatgcaac 7800
Db 7741 aacatgcaac 7800
Qy 7801 gttcagatgagtgagatcagatcagatcagatcagatcagatcagatcagatcagatcagat 7860
Db 7801 gttcagatgagtgagatcagatcagatcagatcagatcagatcagatcagatcagatcagat 7860
Qy 7861 agatcctgtagagagac 7920
Db 7861 agatcctgtagagagac 7920
Qy 7921 ccaagagatgagtgagatcagatcagatcagatcagatcagatcagatcagatcagatcagat 7980
Db 7921 ccaagagatgagtgagatcagatcagatcagatcagatcagatcagatcagatcagatcagat 7980
Qy 7981 cctgagatgagtgagatcagatcagatcagatcagatcagatcagatcagatcagatcagat 8040
Db 7981 cctgagatgagtgagatcagatcagatcagatcagatcagatcagatcagatcagatcagat 8040
Qy 8041 ttttctgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcag 8100
Db 8041 ttttctgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcag 8100
Qy 8101 atgttctgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcag 8160
Db 8101 atgttctgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcag 8160
Qy 8161 tagaatgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcag 8220
Db 8161 tagaatgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcag 8220
Qy 8221 ttttctgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcag 8280
Db 8221 ttttctgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcag 8280
Qy 8281 gttcagatgagtgagatcagatcagatcagatcagatcagatcagatcagatcagatcagat 8340
Db 8281 gttcagatgagtgagatcagatcagatcagatcagatcagatcagatcagatcagatcagat 8340
Qy 8341 ctcaatgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagat 8400
Db 8341 ctcaatgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagat 8400
Qy 8401 gttcagatgagtgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcag 8460
Db 8401 gttcagatgagtgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcag 8460
Qy 8461 actggttcaac 8520
Db 8461 actggttcaac 8520
Qy 8521 agccttctgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcag 8580
Db 8521 agccttctgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcag 8580
Qy 8581 aagtttcaac 8640
Db 8581 aagtttcaac 8640
Qy 8641 cacaactgttctgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcag 8700
Db 8641 cacaactgttctgagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcagatcag 8700

QY 8701 cccatlaaactgacagctcacaatttttcaatcctcaactgacagcaagaata 8760
 |||||
 Db 8701 ccccatlaaactgacagctcacaatttttcaatcctcaactgacagcaagaata 8760
 QY 8761 taaaaaacaacaaacttccatataatgagcaattttcagagtttctaaacacagcttatt 8820
 |||||
 Db 8761 taaaaaacaacaaacttccatataatgagcaattttcagagtttctaaacacagcttatt 8820
 QY 8821 tttctagctagaacatttgaataaactgttccactaaacttactgtttaaactgtct 8880
 |||||
 Db 8821 tttctagctagaacatttgaataaactgttccactaaacttactgtttaaactgtct 8880
 QY 8881 tgaagaaaaagaataatgagagaactatgtttggggaagtccaagtacattcaat 8940
 |||||
 Db 8881 tgaagaaaaagaataatgagagaactatgtttggggaagtccaagtacattcaat 8940
 QY 8941 atcattactaacttctccacttttccaaaattgaaatataagcgaaggtgtaaga 9000
 |||||
 Db 8941 atcattactaacttctccacttttccaaaattgaaatataagcgaaggtgtaaga 9000
 QY 9001 ctccagatttcaaatatccttctataatttttaaatattacagaataatataaacc 9060
 |||||
 Db 9001 ctccagatttcaaatatccttctataatttttaaatattacagaataatataaacc 9060
 QY 9061 ctgctgaaaaaagaataatgattgttttaagaagttaagtaattatgtatttaaat 9120
 |||||
 Db 9061 ctgctgaaaaaagaataatgattgttttaagaagttaagtaattatgtatttaaat 9120
 QY 9121 aagtaagaagacataatccaaataactagatagatgacatgctgtgcaatttaccag 9180
 |||||
 Db 9121 aagtaagaagacataatccaaataactagatagatgacatgacatgctgtgcaatttaccag 9180
 QY 9181 tccaataatcagaattatagaaataattccctcacttaataattttcaaaaacaaag 9240
 |||||
 Db 9181 tccaataatcagaattatagaaataattccctcacttaataattttcaaaaacaaag 9240
 QY 9241 ttatggttccacttacttactaaactcgttactaaacttctcactaagtaagtaacta 9300
 |||||
 Db 9241 ttatggttccacttacttactaaactcgttactaaacttctcactaagtaagtaacta 9300
 QY 9301 gcaactccttactcgggtccctcgtatgttcaagccatattttaaaaaatcagaagcc 9360
 |||||
 Db 9301 gcaactccttactcgggtccctcgtatgttcaagccatattttaaaaaatcagaagcc 9360
 QY 9361 tgttaactatttgaagaaaaacagacatttactaagaatgagaagccctctctgaa 9420
 |||||
 Db 9361 tgttaactatttgaagaaaaacagacatttactaagaatgagaagccctctctgaa 9420
 QY 9421 gctagaacaacatactatgctatataccttcaactaactgttactcctttaaataag 9480
 |||||
 Db 9421 gctagaacaacatactatgctatataccttcaactaactgttactcctttaaataag 9480
 QY 9481 atttttcaacttccctcgtgttaaacctaatgtgtgtagaatttttccaacacttact 9540
 |||||
 Db 9481 atttttcaacttccctcgtgtgttaaacctaatgtgtgtagaatttttccaacacttact 9540
 QY 9541 caatcaagcaaaatttctgtatattccctcgtgtgaaatgtactaactgtgagtttcaaga 9600
 |||||
 Db 9541 caatcaagcaaaatttctgtatattccctcgtgtgaaatgtactaactgtgagtttcaaga 9600
 QY 9601 ctcaaaatagtgctcaaaaatttctgtccttctgacatttgggagacactcagaagaact 9660
 |||||
 Db 9601 ctcaaaatagtgctcaaaaatttctgtccttctgacatttgggagacactcagaagaact 9660
 QY 9661 ttaacaactgtgaatataatgaataacagaagaataataagccctctatcacataatgc 9720
 |||||
 Db 9661 ttaacaactgtgaatataatgaataacagaagaataataagccctctatcacataatgc 9720
 QY 9721 ccagacaacttcaattgtttaaanaaaccaaacactcacaactgtatttcaatattcgt 9780
 |||||
 Db 9721 ccagacaacttcaattgtttaaanaaaccaaacactcacaactgtatttcaatattcgt 9780
 QY 9781 actgaagaacaaatgcttcttgactataatgttgcacacatcattcattcaactgtatag 9840

Db 9781 ACTGAAGCAAAATGCTTTGTGACTATTAATGTGACACATCATTCATTCAGTATAGTA 9840
 |||||
 QY 9841 atcaatgactaaagcaacttgcgtgttcttcttctgtgntgntatataatcagaataat 9900
 |||||
 Db 9841 atcaatgactaaagcaacttgcgtgttcttcttctgtgntgntatataatcagaataat 9900
 QY 9901 attttccaagaagcattgtgtcattgtaactgaaccccttggatattgagacataatt 9960
 |||||
 Db 9901 attttccaagaagcattgtgtcattgtaactgaaccccttggatattgagacataatt 9960
 QY 9961 ggaacctgttacttactaactgaataatgtaactcgtgagaataatgtccttacttct 10020
 |||||
 Db 9961 ggaacctgttacttactaactgaataatgtaactcgtgagaataatgtccttacttct 10020
 QY 10021 tcaaaatgtgtacccctccttaaaangttctatttccaaaggttttagctgttctac 10080
 |||||
 Db 10021 tcaaaatgtgtacccctccttaaaangttctatttccaaaggttttagctgttctac 10080
 QY 10081 ctctctataccctagaatgaagctgttctgtccttctgttccatcatttgcctcattc 10140
 |||||
 Db 10081 ctctctataccctagaatgaagctgttctgtccttctgttccatcatttgcctcattc 10140
 QY 10141 caagcaacttaccgctgtcgtatggatctatttgcactggaatatcggagaattgc 10200
 |||||
 Db 10141 caagcaacttaccgctgtcgtatggatctatttgcactggaatatcggagaattgc 10200
 QY 10201 aaacagagaaaaagtttcaacacagatcttcaagtttaacttcaatcaaaagaaa 10260
 |||||
 Db 10201 aaacagagaaaaagtttcaacacagatcttcaagtttaacttcaatcaaaagaaa 10260
 QY 10261 aaagaaaaaaatlttgtatgttcaactatataatgaagtaataaatgcatatttca 10320
 |||||
 Db 10261 aaagaaaaaaatlttgtatgttcaactatataatgaagtaataaatgcatatttca 10320
 QY 10321 tgttgaataataggttcaaaaatgaagctgtgacgttctgtttaaanaaaaaaa 10380
 |||||
 Db 10321 tgttgaataataggttcaaaaatgaagctgtgacgttctgtttaaanaaaaaaa 10380
 QY 10381 aaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaa 10440
 |||||
 Db 10381 aaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaaanaaaaaa 10440
 QY 10441 aa 10442
 |||||
 Db 10441 aa 10442

RESULT 3
 AF285167 10442 bp mRNA linear PRI 09-AUG-2000
 LOCUS
 DEFINITION Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA,
 complete cds.
 ACCESSION AF285167
 VERSION AF285167.1 GI:9755158
 KEYWORDS
 SOURCE
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 10442)
 Schwartz, K., Lawn, R.M. and Wade, D.P.
 ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
 regulated by LXR
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 10442)
 Lawn, R.M., Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,
 Porter, J.G., Seilhamer, J.J., Vaughan, A.M. and Oram, J.F.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
 3172 Porter Drive, Palo Alto, CA 94304, USA
 FEATURES
 source 1..10442

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/map="9q31"
/cell_type="fibroblast"
/tissue_type="skin"
1..10442
/gene="ABCA1"
291..7076
/codon_start=-1
/product="ATP-binding cassette transporter 1"
/protein_id="AA098175.1"
/db_xref="GI:9755159"
/translation="MACROPHAGE-INDUCIBLE TRANSPORTER 1"
SYRPTDHECHPNNKAMPAGTLPWQGITCANPCCRYPGPGAPVONENKSIY
ARLESDARLLYSQDKMDKMRKVLRTLOIKKSSNKILQDLYVNEFSGFLYH
NLSPEKSTVDKMLRADVILAKVFOGLHLSLNGSKSEEMIQLOQVSELGLP
KEKIAAEVFLNSNMIIKPLIRLTNSGPPSKELAEATTLISGLTLOAELPSMR
SWSDMEVFLTNVSSSSSTOIOASRIVCCHPEGGGLKTSIMNYEDNNKALE
GNGTEDEAETPYDNSTPYCNLMKLNLESPLSITIKALKPLLVGLIYPTPAT
ROYMAEVNKTPOELAFPHDLRGMEELEKLTWFENSOEDVLYMLDSNDHNE
OQIDGDTADQIVAFIAKHPEVDSNGSVYTWENAEENNOAIRTISRMEDVNE
KLEPIATEVWLINSMELLDERKFWAGIVGTIGTSTELPHHYKIRMDIDVERT
NKIKDGYMDPGPRADPEEDMRYVWGFGALQVDEOATIRVLTGHEKKGYMOQMY
PCYVDIPLRVASRSMPLMTLAWISVAVILIKGIVYKELAEKEMIMKINDSLIM
SRANLAAGCGITTEPIYLYCYAMDQYGTFLTKTASLSPVAFGCEYFALFE
BOGICVQMDNLESEFVEEDGENLTISIMLFDPLVYVMTWYIEAVPQOYIPRW
YFECTKSYWGESEDESKHPSNOKRMEICMEEPPLKLGVSIONLVKRYRGMVY
AVDGLALNPFEGOILTSFLHNGAGKTTMSILTGPEPTSTAVILKQDJRESKSTR
OMGVCPOHNVLFDMLIVENHFWYARLKGISEKVKEMEMOALDYGDSKIKSTP
SOLSGMOKRLSVALAFVSGKVVTLDEPTAGVDPYSRGTEWELLRYROGRTIIST
HMDQVADVGLRIATISHGKICQVSSSTFLKNOGTGYTLTVLRKDVSSLSRNS
STVSYLAKEDSYOSSSPAGUSDSHESPLIIVASLSNLRKHVSARLVEDGHL
TYVLEPEAKBEAEVELHEIDRLSDIGISSYGISETLEELIKVAESGVADTS
DGLTPARRRRRAFGDKQSLRPEEDDAQNDSDIPESRETDLSGMGKGYQVK
GMLTQOQFVALLMRRLIARSRKGFPAQIVLPAVEGCIALVSLVPPKQPSLE
LOPMYNEQYFVNDAPEDTGTLELALTKDQEGKCEGVEDIDPMCOAGEPEW
TAPVORTMDLFGNMNTQONSPACCCSDIKKIMPCVPAGASITPPOKORNTA
DILQDITGNISDLYVTYVOITAKSLKNTWNEPVGKSPVCSLQVSTOALPSOEVN
DAIKMKKIKIADSSADRLNSIGRMTGLDIRNNVAKWPNKGMHAISSFLNIN
NALIRANIQKGNESHGITAHPNLITKQOLESVALMTSVDVLSIVIPMSFV
PASVEVLEQKVSNAKHLQISGVKPIVIMSNWDMCNVYVPAVLVILIFICQO
KSYVSTINPVIALLLDLYGWSITPLMPASFVGRKIPSTAVVLTIGVINGSAV
TVELEFTDNKLNINILKSVFLIPHEFCRGLIMVKNQOAAALDEBNGRREVS
PLSMDLVGNLFAMAVEGVFLLTVLOYRFRPRAVNAKSLPNDDEVDYRERO
RLDGGGNDILEIKELKTYRRKRKPAVRCVGPDPGECFGLGVNGAGKSTTKM
LTGDTTVRGDAFLNKNSITSNHIEVQNNQCYQOPATITELINGRHVEFFALLGV
PEKBYGKYGMAIKRLGLVYKGEKTAQNSGGRKRIKSTMAALIGGPVVEFDEPTG
MDPKARRLMLCALSVKESRVSVLTSHEMECALCTRNAIVNGNFRCLGVOHLK
NREGDGYTVIRIAGSNPDLKPVODPFGFLAEFKERNNIYQOLPSSLSLARI
FSLISQSKRLHIEDYVSQTTLDQVFNFAKQSDSDHDKLHLKNGQVVDVAVLT
SFLQDEKKESEYV"

```

BASE COUNT 2898 a 2297 c 2408 g 2835 t 4 others
ORIGIN

Query Match 100.0%; Score 10438; DB 9; Length 10442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ggcgggagccgcaagagccgacccctctcccgagctgagcgaaggaagcgg 60
   |||||||
Db 1 ggcgggagccgcaagagccgacccctctcccgagctgagcgaaggaagcgg 60
   |||||||
QY 61 ggaagctccgcaaccaagaagcgttctcaaggcgttgctgccccttgcttcc 120
   |||||||
Db 61 ggaagctccgcaaccaagaagcgttctcaaggcgttgctgccccttgcttcc 120
   |||||||
QY 121 gttcgttttctccctctcccgaaagcgttgcgaagggttaggaagaagaagcgaac 180
   |||||||
Db 121 gttcgttttctccctctcccgaaagcgttgcgaagggttaggaagaagaagcgaac 180
   |||||||

```

```

QY 181 acaaaagtggaaaacagtaataaccagcgcaaggcgctccctgctgtgagctctggccgc 240
   |||||||
Db 181 ACAAAAGTGGAAAACAGTTAATACCA6CCAGG6GCTCCCTGCTGTGAGCTCTG6CCGC 240
   |||||||
QY 241 tgcctccagggctcccgagcaacaacgcttggcgctgctgagcgaaggaacagcgtgt 300
   |||||||
Db 241 TGCCCTCCAGGGCTCCCGAGCCACAGCCTGGGCTGCTG6CTGAGGGAACATGGCTTGT 300
   |||||||
QY 301 ggcctccagcgaagctgtgctgtggaagaacctcaacttcgaagaagaacaacatgtc 360
   |||||||
Db 301 GGCTCCAGCTGAGGCTGCTGCTGTGGAAGAACCTCACTTTCAGAGAACAAACATGCTC 360
   |||||||
QY 361 agctgttactggaagtgagcctgagcctctatctctccctgctccatctgtctggc 420
   |||||||
Db 361 AGCTGTACTGGAAGTGCGCTG6CCTATTATCTCTGATCTGATCTGTGCTG6C 420
   |||||||
QY 421 tgaagctcccaacctatgaacaacatgaatgcacatttcctaaataaagccatgcccctg 480
   |||||||
Db 421 TGAAGCTACCCACCCCTATGAACAACATGAATGCATTTTCCAAATTAAGCCATGCCCTCG 480
   |||||||
QY 481 caggaacactcctctggttcaagggaatatctgtaatgccaacaaccccgcttccgt 540
   |||||||
Db 481 CAGGAACACTCTCTTG6GTTCAAGG6ATTTATCTGTAATGCCAAACACCCTGTTCCGTT 540
   |||||||
QY 541 acccgactcctgggagagctcccgagctgtgttgaaacttaacaacatccatctgctc 600
   |||||||
Db 541 ACCCGACTCCTGGGAGGCTCCCGAGGTTGTTGGAACATTTAACAAATCCATTG6GCTC 600
   |||||||
QY 601 gctgttctcagaatgcttggagagctctcttcttaacagccagaagaacccagcatgaag 660
   |||||||
Db 601 GCTGTCTCAGATGCTGCGAGGCTTCTTWTATACAGCCAAAGAACCCAGCATGAAG 660
   |||||||
QY 661 acatgagcaaatgctcgaagaacatlaacagaagataaagaatccagctcaacttgaagc 720
   |||||||
Db 661 ACATGAGCAAAAGTTGGAACAATTAACAGCAATCAAAATCCAGCTCAAACTTGAAGC 720
   |||||||
QY 721 ttcaaatctctctgtgtggaacatgaacacctctctggttccctatatacaaacctcttc 780
   |||||||
Db 721 TTCAAAATTTCTGTGTGGAACAATGAACCTTCTG6GTTCTTATACCAACCTCTCTC 780
   |||||||
QY 781 tcccaaatctactgtggaacaagatgctgagggcctgagatctctcaaaagatattt 840
   |||||||
Db 781 TCCCAAAAGCTACTGTGGAACAAGATGCTGAGG6CTGATGTTATCTCCACAGGATATTT 840
   |||||||
QY 841 tgcagagctacagttacatttgacaagctctgtgaaatgaaatcaaaaatcagaagagatga 900
   |||||||
Db 841 TGCAGAGCTACAGTTACATTGACAAAGTCTGTGCAATGATCAAAATCAGAAGAGATGA 900
   |||||||
QY 901 tccaactgtgtaacaagaagtttcttgagctcttggtccttaacaaagaaagaaactgtgtg 960
   |||||||
Db 901 TTCACCTGTGTACCAAAAGATTTCTGAGCTTTTGTG6CTTACCAAAAGAAACTGTGCTG 960
   |||||||
QY 961 cagcagagcgaagtaacttcgttccacaatgacatcccttgaaagccaatccttgaacaactaa 1020
   |||||||
Db 961 CAGCAGAGCGAGTACTTGTCTCCAAACATGACATCTTGAAGCCAAATCTGAGAACCTAA 1020
   |||||||
QY 1021 actctaacctccctccctcccgagcaagagctgctgtgaagccacaacaaactgtgtcata 1080
   |||||||
Db 1021 ACTCTAACCTCCCTCCCTCCGAGCAAGAGCTGCTGTGAAGCCAAACAAATCTGCTCATTA 1080
   |||||||
QY 1081 gcttggagactctggcccaagagctgttcaagcaatgaagaacttgagtgacgacgaag 1140
   |||||||
Db 1081 GCTTGGGACTCTGGCCAGAGCTGTTCAGCATGAGAAACTTGAGATGACATGCGACAG 1140
   |||||||
QY 1141 aggtgagatgttctcgaaccaatgtgaacagctccagctctccacccaactctacagagctg 1200
   |||||||
Db 1141 AGGTGAGATGTTCTGACCAAGTGTGAACAGCTCCCTCCACCAAAATCTACAGAGCTG 1200
   |||||||
QY 1201 tgtctgfatgtgtcggcgacatcccgaggaaggaggggctggaagatcaagttctccaact 1260
   |||||||
Db 1201 TGTCTGATGTGTCTGCGG6CATCCGAGGAGG6G6GCTGAGAGATCAAGTCTCTCAACT 1260
   |||||||

```


QY 5641 caacccttgctgagctgttcaccgacaataaactgaataataataatgatacttga 5700
|||||
Db 5641 CCACCTTGTGCTGGAGCTGTACCGACATAGCTGATATATATCATATGATATCTTGA 5700
QY 5701 agtccgtgtcttgatctctccacaatttgccttggaagaggtctatcgacatgtga 5760
|||||
Db 5701 AGTCGCTGTTGTGATCTTCCACATATTTTGGCTGGAGAGGGCTCATCGACATGTGA 5760
QY 5761 aaacacagacatgtctgtatgcctggaaaggttgggaggaatgcttggatcat 5820
|||||
Db 5761 AAAACGAGCAATGCTGTATGCCCTGGAAAGTTGGGAGATGCTTTGTGTACCAT 5820
QY 5821 tatctggagactgtgtggagcaaacctcttcgcaatggcgtggaaaggtgtgtct 5880
|||||
Db 5821 TATCTTGGGACTTGTGGGACCAAACTCTTGCCATGGCCGTGGAAGGGTGGTGTCT 5880
QY 5881 tccctactcgttctgataccaglaagatcttctatcagcccgacactgttaattgca 5940
|||||
Db 5881 TCCTCATCTGTTGATGATCCAGTACAGATCTCTATCAGGCCCGACCTGTAAATGCA 5940
QY 5941 agctatctctctgaaatgataatgaaatgtgagggagggaaagacagaaattcttg 6000
|||||
Db 5941 AGCTATCTCTCTGAAATGATGAAGATGATGAGCGGGAAGACAGAAATTTCTTG 6000
QY 6001 atgttgagagccagaaatgacatcttagaaatcaagaggttgaacgaatataagaaga 6060
|||||
Db 6001 ATGCTGAGAGCCCAATGATCATCTTGAATCAAGAGATTTGAAGAAATATATAGAGA 6060
QY 6061 aagcgaagccctgtcttgacaagatttgcgtggcaatccctcctgtgtgacttgggc 6120
|||||
Db 6061 AGCGAAGCCCTGCTGTGACAGATTTGGCGGCATTCCTCTGCTGTGATGCTTTGGGC 6120
QY 6121 tctctgagatgaatggggtcgaataatcaacttcaagttgaagttgaagagatgaca 6180
|||||
Db 6121 TCTTGGAATTAATGGGGCTGGAAATCATCACTTTCAAGATGTTAAAGAGGATACCA 6180
QY 6181 ctgttaccagaagagatgtcttctcttaacaaataglatctatcaaaacatcatgaag 6240
|||||
Db 6181 CTGTTACCAAGAGATGCTTCTTACCAAAATAGTATCTTATCAAAACATCATGAAG 6240
QY 6241 taacatgaacatgtgctactcctcctcaagttgataatgcatcaagagctgttgatgga 6300
|||||
Db 6241 TACATAGAACATGGGCTACTGCTCATAGTTGATGCCATCACAGCTGTGTACTGGGA 6300
QY 6301 gaaacacatgtgaggtcttgcctcttggaagaggttccacagaagaagaggtggcaag 6360
|||||
Db 6301 GAGAACGCTGAGAGTCTTGTGCTTTGAGAGAGTCCAGAGAAAGAGTTGGCAAG 6360
QY 6361 ttggtgagtgagcatcgaacactggcctcgtgaaglatgagagaaaaatagtctgta 6420
|||||
Db 6361 TTGGTGAATGGGATTCGGAACACTGGGCTCGTGAAGTATGAGAAATATGCTGGTA 6420
QY 6421 actatagtgaggaacaacaagcaagctctctacagcatgtcttgatcgcgggctc 6480
|||||
Db 6421 ACTATAGTGAAGCAACAAACGCAAGCTCTACAGCCATGCTTGTGATGGGGGCTC 6480
QY 6481 ctgtgtgttcttgatgaacacacacacagcatgataatccaaagcccggtcttctg 6540
|||||
Db 6481 CTGGGGTGTCTGATGAACCAACACAGGATGATGCCAAAGCCCGGCTTCTGT 6540
QY 6541 ggaattgtccctlaagtgtctgaagagagagatcaagtagtctatactcatagta 6600
|||||
Db 6541 GGAATTTGCTTGAAGTGTGTCAAGAGAGGAGATCAGTAGTGTATCATATGTA 6600
QY 6601 tggagaagatgaaagctcttgcatagatgagcaatcagtcataggaagttcaagt 6660
|||||
Db 6601 TGGAGATGTGAAGCTCTTGTGCACTAGATGCAATCATAGTCAAGGAGGTTCAGT 6660
QY 6661 ggccttgacgtgtcagcatctaaataatagtttggagatggttatacatatgtgtac 6720
|||||
Db 6661 GCCTTGGCAGTGTACACATCTAAATAATAGTTTGGAGATGTTATACATAGTTTAC 6720
QY 6721 gaataagcaggttcaaccggagactgaagcctgacagatcttcttgagactgtcat 6780
|||||

Db 6721 GAATAGCAGGGTCCACCCGACCTGAAGCCTGCCAGATTTCTTGTGACTGTGATTC 6780
QY 6781 ctggaagtgtcttaagaagaacaacacgggaacatgtctataatccagcttccatctac 6840
|||||
Db 6781 CTGAAAGTCTTAAAGAGAAACCGGAACAGTGTACATATACCACTTCCATCTTCAT 6840
QY 6841 tatctctctgagagatctcagcatcctctccagagcaaaagagactccacatag 6900
|||||
Db 6841 TATCTTCTGTGCGCAGATATTACGATTCCTCCAGAGCAAAAACGACTCCACATAG 6900
QY 6901 aagactactgttctcagaacaaacttgacaaatattgtgaacttggcaagagac 6960
|||||
Db 6901 AAGACTACTGTTCTTCAGCAACACTTGCACCAAGTATTTGTGAATTTGCCAAGGACC 6960
QY 6961 aaagtatgtagacacttaagaacctctatctacaaacacagacagtagtgag 7020
|||||
Db 6961 AAAGTATGATGACCTTAAGAACCTCTCATTTACACAAAACCAACAGTATGTGACG 7020
QY 7021 ttgcaqtlcacaatcttctacaggaatgaaagatgaaagaaagctatgtatgaaga 7080
|||||
Db 7021 TTGCAATCTCATCTTTCTTACAGATGAGAAAGTGAAGAAAGCTATGTATGAAGAA 7080
QY 7081 tccgttcaacaggggtgtgtgaagaatgaagaaactagacttctcttgacacatgtg 7140
|||||
Db 7081 TCCTGTATACGGGGTGTGTAAGATGAAGAGAACTTTCCTTGCACCATGTG 7140
QY 7141 aaggttgtagaagaagaagcagaagtgtatgtgtggaagaagttaactgtatcttac 7200
|||||
Db 7141 AAGTGTGTGGAAGAAAGCCAGAGTGTATGTGGAGAGATGAACCTGATCTGTAC 7200
QY 7201 tgatactatcaatgaaatgcaatcaatgaaatgaaacaaatccatcatcagggca 7260
|||||
Db 7201 TGATCTATTTCAATGCAATGCAATTCGCAATGCAATGAAGAAATTCATATACAGGGCA 7260
QY 7261 gtgccttgtagactatgtctgtatgtgtcctcaagtgaagaacttgaattgtttt 7320
|||||
Db 7261 GTGCTTTGTACCTATTTCTTGTATGTGCTCTCAAGTGAAGACTGTGATTTACTTTT 7320
QY 7321 acctaacatgtgaactatataatgaaccccaatgacatatgtgtgaactcaca 7380
|||||
Db 7321 ACCTTATCTATGTAAACTCATATATGAAACCAATGACATATGCGTTGAACTGCA 7380
QY 7381 ctttcttcttcttctgtcctgtatctcctcaatgtgggttgcacaatataatcaag 7440
|||||
Db 7381 CTTTTTTTTTTTTTGTGCTGTATTTGCATTTGGGGTGAACAATATATCATCAAG 7440
QY 7441 taatcatgcaagcatatgtatcaaaatcaaaagttaatgtcacatccatctactcaa 7500
|||||
Db 7441 TAATCATGCCCGCATATTTGATCAAAATCAAAAGTATGACATCTCATTTCACTAA 7500
QY 7501 gccatgccatgcccaggaagactgttcccggtgacacatccatctgtcgtgaatgt 7560
|||||
Db 7501 GCCATGCCATGCCCAGAGACTGTGTTCCCGGTGACACATCATGTGCTGGCAATAGTGT 7560
QY 7561 gccagatgatagtgccaagtttctcagaagtttgaagcaatggatgtgtcatgtc 7620
|||||
Db 7561 GCCAGGTATATAGGCCAAAGTTTTCAGAAAGTTTGAAGCCCATGTGTGTCTGCTC 7620
QY 7621 accttgtgaaagctgtcctgtcagagttctataaatltgaatatcaagttgaagagtg 7680
|||||
Db 7621 ACTTTTGTAAAGCTGCTGTGTCAGAGCTATTAACCATTTGAATVCAAGTTGACGAATG 7680
QY 7681 gtgcacgtcgtgtgacacacatccctgtatccctctgataagctgtctgtgtgagag 7740
|||||
Db 7681 GTGCCATGCGTGGCTAACATCTCTGTGATTCCTGTGATAGCTGTGTGGTGGCAGT 7740
QY 7741 aaacatgcaacaaatgtgtgtgtctcgaagcagggaaactgtgtccatgtgtatct 7800
|||||
Db 7741 AACATCAACAAATAATGTGGTGTCTGTAGGCAACGGAAACTTGTGTATGTATAT 7800
QY 7801 gtccatgtcttgagacatgaggttcaagaggtcatccctatgtgaagctttaaataact 7860
|||||

Db 7801 GTCTATGCTTGAAGCCATGGGCTCTACAGGCTATCCTTATGAGACTCTTAAATATACTT 7860
QY 7861 agatccctgtaagaagcaagaalcaacagccaaactgctgggctgcaagctgctgaag 7920
Db 7861 AGATCTGTAAGAGGCAAGAAATCAACAGCCAACTGCTGGGGCTGCAGCTGCTGAAG 7920
QY 7921 ccagggatagggatlaaagaagatgctgctcaaacctagaaggagccctgtgccattgt 7980
Db 7921 CCAGGGATAGGGATTAAGAGATTTGCTTCAACCTAGAGGAAGCCTGTGCCCATTTGT 7980
QY 7981 cctgactgctgtaacatgtaactgtaactgcaatcccaagaagtattatctgacacaagtgtat 8040
Db 7981 CCTGACTGCTGCTGAACATGTAATGTAACCTGCAATCTTATCTGACACAAGTGTAT 8040
QY 8041 taattcctgcttctgtaactaactagaanaaagaagaatgagctgtgattcttgacaanaa 8100
Db 8041 TATTTCTGGCTTTTGTGAATTAATCTGAAAAATGAAAAAGATGGAGTTGTATTGTGAAAAA 8100
QY 8101 atgttctacttcttaagtctatcttgaaatttgaattctcaatgtaactgtaactgct 8160
Db 8101 ATGTTTACTTCTTAAATGTAATGTAATTTGAATTTTAACTTCTATGATGACTTCTGAATTCCT 8160
QY 8161 tagaagagcctcttgtaagaacccctgtaagaagaatgagcaatgagccactat 8220
Db 8161 TAGAATGGCCTCTTTGTGAGAACCTGTGTATGAGAGATGAGCACTGGCCACTTAT 8220
QY 8221 ttatttctctatgtaagttgataatgataatgataatgataatgataatgataatgataat 8280
Db 8221 TTTATTTTCTTATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 8280
QY 8281 ggtcagagatcctgataatataatgagttctctcaagataatlaagataacttaact 8340
Db 8281 GGTGAGAGATCTCATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8340
QY 8341 ctcaactcacaatcaaatatlltttgagtgatgctgtaagctgaaagtgatgtaact 8400
Db 8341 CTCACTTCACTCAATCAATTAATTTTGTGAGTAATGTAATGTAATGTAATGTAATGTAAT 8400
QY 8401 cgtataagactagaagataatlaagctcagtaactctcgtgcaatgtaactcagctc 8460
Db 8401 CGTATAAGACTAGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8460
QY 8461 actggtttcaaatatagtgctgctgctgctgctgctgctgctgctgctgctgctgct 8520
Db 8461 ACTGGTTTCAAAATTAATGAGTGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8520
QY 8521 agccttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 8580
Db 8521 AGCCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 8580
QY 8581 aagtttaacaatgaatctctcaacaggaanaaagaagctgaactgtaactgctgaanaa 8640
Db 8581 AAGTTTAAACAAATGAATTTCTTCAACAGGGAACACCTGATTTGAATTTGCTGTGAAAA 8640
QY 8641 cacaacttgcttgaagcttgaactgaactcaaatgaatgcttgaactgctgaactgctga 8700
Db 8641 CACAACCTTGTGTTTATGGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8700
QY 8701 ccccatlaaatctgacagctcacaatcttctcctcctcaatcactgaagcaagaanaa 8760
Db 8701 CCCCATTAATCTGACAGCTCAAAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 8760
QY 8761 taanaaacaacaatctcctcactatgagcaatcttcaagaatcttcaaccagcttcat 8820
Db 8761 TAAAAACAACAATCTCTCATATGAGCAATTTTCTTCAAGATTTTCTTCAACCCAGTCTTAT 8820
QY 8821 ttctagtcagtaaacattgtaaaaaatgcttctcactcaactactgtaactgcttcaact 8880
Db 8821 TTTCTAGTGAAGAAATTTGTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8880
QY 8881 taagaanaaagaanaaataatgagaagaactatgcttggaagaatgtaactgcttcaact 8940
Db 8881 TGAGAGAAAGAAATATGAGAGAACTATGTTGGGGAAGTTCAAGTGAATTTCTTCAAT 8940
QY 8941 atcattactaactctctcacaactcttccaaaattgtaataatgaactgaagaagtgaaga 9000
Db 8941 ATCATTACTAATCTTCTTCCACTTTTCCAAATTTGAAATTAATTAACCTTAAGGCTGAAGA 9000
QY 9001 ctccagattcacaatlaactcttctcatalatttcaaatlaagaanaatlaataaccca 9060
Db 9001 CTTCAGATTTCAAAATTAATCTTCTTATATTTTAAATTTACAGAAATTAATTAACCCA 9060
QY 9061 ctgctgaanaaagaanaaataatgcttctgaagaatgaagaatgaagaatgaagaat 9120
Db 9061 CTGCTGAAAAAAGAAAAATGATTTGTTTGAAGTTTGAAGCAATTAATTAATTAATTAAT 9120
QY 9121 aagtaatgaagcatalcttccaaatcactagatgataatgagcactgtaactgaactatc 9180
Db 9121 AAGTAATGAAGCATATTTCCAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9180
QY 9181 ttcaaaaatacaagaattatagaataatcttctcacttaataatcttcaaatcaaga 9240
Db 9181 TTTCAAAAATCAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9240
QY 9241 ttaatgcttctcatalcttcaaaaatcgtatctcaatctcatalatagtaaatctatga 9300
Db 9241 TTATGTTTCCATCTTACTTAATAATGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9300
QY 9301 gaaactccttactgctgctcctctgattcgaagcacaattttaaaaaatcaagaagcac 9360
Db 9301 GCAACTCTCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9360
QY 9361 tctgaactatcttgaagaacacagacatttaatacagattgaagaagcctctctga 9420
Db 9361 TGTGAATTAATTTGAAGAAACAGCACTTTTAATTAATTAATTAATTAATTAATTAATTAAT 9420
QY 9421 gctagaacaactatagatatacactctcaatlaactgltacttcaaatlaaata 9480
Db 9421 GCTAGAAACAAATCTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9480
QY 9481 atttttcaattctctgctgaacccaattggtgtaagaatttttcaaaccttact 9540
Db 9481 ATTTTTCAATTTCTGCTGTAACCTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9540
QY 9541 caatcaagaanaaattctctatctccctgtaactgtaactgtaactgtaactgtaact 9600
Db 9541 CAATCAACCAAAATTTCTGTAATTTCTGTAATTTCTGTAATTTCTGTAATTTCTGTAATTT 9600
QY 9601 ctcaaaaatgcttcaaaaattctctcttcttgaacttcttggagacccctcagaanaact 9660
Db 9601 CTCAAAAATACGTGTTCAAAAATTTCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9660
QY 9661 ttaacaaactgtaatatgaagaatacagaagaanaaataaagccctctatacatala 9720
Db 9661 TTAACAACTGTGATTAATGAGAAATTAACAGAAATTAATTAATTAATTAATTAATTAATTAAT 9720
QY 9721 ccagacaaatcattgtttaaanaaacaacaaectcaactactgtaattctcattactgt 9780
Db 9721 CCAGCACAAATTCATTTGTTAAAAAACCAACCAACCTCACTAGTAATTAATTAATTAATTAAT 9780
QY 9781 actgaagaacaaatgcttctgtaacttaaatggtgcaactcattcacttaactatagta 9840
Db 9781 ACTGAAGCAAAATCTTGTGACATTAATTAATTTGCAACATCAATTCATCTGTAATTAATTAAT 9840
QY 9841 atcattgaactaagaacatctgctgctgcttcttcttcttcttcttcttcttcttcttct 9900
Db 9841 ATCATTTGACTTAAGCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9900
QY 9901 atttccaaagaagcactgctgctgctgctgctgctgctgctgctgctgctgctgctgct 9960
Db 9901 ATTTCCAAAAGAGCCATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9960
QY 9961 ggaaccttggtatatactatagaanaatgtaataactgaagaaatgctgcttcaacttct 10020
Db 9961 GGACCTTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10020

Db 1294 GTATGAGACACACTACAAAGCCCTTTGGAGCAATGACATGGAAGATGCTGA 1353
QY 1322 AACCTTATGAAACACTCACAACCTTACTGCAATGATTTGAAAGATTTGAGTC 1381
Db 1354 AACCTTATGAAACACTCACAACCTTACTGCAATGATTTGAAAGATTTGAGTC 1413
QY 1382 TAGCCCTTCCCGAATCTGGAAGCTGGAAGCGCTGCTGTTGGGAAGATCCT 1441
Db 1414 TAGTCTCTTTCCCGAATCTGGAAGCTGGAAGCGCTGCTGTTGGGAAGATCCT 1473
QY 1442 GTATACACCTGACACTCACAAGCAGTCATGCTGAGGTGACAGACCTTCCA 1501
Db 1474 GTATACACCTGACACTCACAAGCAGTCATGCTGAGGTGACAGACCTTCCA 1533
QY 1502 GGAAGCTGCTGCTGCTGATGATGGAAGGCTGGAAGGAACTCAGCCCAAGATCTG 1561
Db 1534 GGAAGCTGCTGCTGCTGATGATGGAAGGCTGGAAGGAACTCAGCCCAAGATCTG 1593
QY 1562 GAACCTATGAGAGAACCAAGAAATGACCTGTCGGATGCTGTTGACAGAGAGA 1621
Db 1594 GAACCTATGAGAGAACCAAGAAATGACCTGTCGGATGCTGTTGACAGAGAGA 1653
QY 1622 CAATGACACTTTTGGGAAACAGAGTGGATGAGATTGAGACAGCCCAAGATCTG 1681
Db 1654 CAATGACACTTTTGGGAAACAGAGTGGATGAGATTGAGACAGCCCAAGATCTG 1713
QY 1682 GAGCTTTTGGGAAACAGAGTGGATGAGATTGAGACAGCCCAAGATCTG 1741
Db 1714 GAGCTTTTGGGAAACAGAGTGGATGAGATTGAGACAGCCCAAGATCTG 1773
QY 1742 GAGAGAAGCTTCAACGAGACTAACCAAGATGACAGATCCTGCTCACTGAGT 1801
Db 1774 GAGAGAAGCTTCAACGAGACTAACCAAGATGACAGATCCTGCTCACTGAGT 1833
QY 1802 TGTCACCTGAAACAGCTGAAACCTTACAGCAAGCTGCTCATACAGAGCTCAT 1861
Db 1834 TGTCACCTGAAACAGCTGAAACCTTACAGCAAGCTGCTCATACAGAGCTCAT 1893
QY 1862 GAGCTGCTGAGAGAGAGAGTCTGAGCTGATGCTGCTCACTGAGATCTCAAG 1921
Db 1894 GAGCTGCTGAGAGAGAGTCTGAGCTGATGCTGCTCACTGAGATCTCAAG 1953
QY 1922 CAGCATGAGCTGAGCAATGCAAGTCAAGATCCAAATGAGCAATGAGATGGA 1981
Db 1954 CAGCATGAGCTGAGCAATGCAAGTCAAGATCCAAATGAGCAATGAGATGGA 2013
QY 1982 GAGGACAATAAATGAGGATGAGTCAAGTCAAGATCCAAATGAGCAATGAGATGGA 2041
Db 2014 GAGGACAATAAATGAGGATGAGTCAAGTCAAGTCCCTGAGCTGAGCTCTTGA 2073
QY 2042 GAGCATGAGCTGAGCAATGCAAGTCAAGTCAAGATCCAAATGAGCAATGAGATGGA 2101
Db 2074 GAGCATGAGCTGAGCAATGCAAGTCAAGTCAAGTCCCTGAGCTGAGCTCTTGA 2133
QY 2102 CAGCATGAGCTGAGCAATGCAAGTCAAGTCAAGATCCAAATGAGCAATGAGATGGA 2161
Db 2134 CAGCATGAGCTGAGCAATGCAAGTCAAGTCAAGTCCCTGAGCTGAGCTCTTGA 2193
QY 2162 TCCCTGATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2221
Db 2194 TCCCTGATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2253
QY 2222 GAGCTGAGCTGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2281
Db 2254 GAGCTGAGCTGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2313
QY 2282 GAGCTGAGCTGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2341
Db 2314 GAGCTGAGCTGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2373
QY 2342 CTGATCTGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2401
Db 2374 CTGATCTGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2433
QY 2402 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2461
Db 2434 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2493
QY 2462 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2521
Db 2494 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2553
QY 2522 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2581
Db 2554 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2613
QY 2582 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2641
Db 2614 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2673
QY 2642 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2701
Db 2674 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2733
QY 2702 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2761
Db 2734 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2793
QY 2762 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2821
Db 2794 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2853
QY 2822 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2881
Db 2854 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2913
QY 2882 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2941
Db 2914 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 2973
QY 2942 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3001
Db 2974 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3033
QY 3002 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3061
Db 3034 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3093
QY 3062 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3121
Db 3094 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3153
QY 3122 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3181
Db 3154 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3213
QY 3182 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3241
Db 3214 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3273
QY 3242 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3301
Db 3274 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3333
QY 3302 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3361
Db 3334 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3393
QY 3362 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3421
Db 3394 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3453
QY 3422 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3481
Db 3454 GAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAATGAGTCAAT 3513

QY	3482	cccllacccgcgagggaataatggaagctctgtctgaataaccgaagccgcacat	3541
Db	3514	cccttactcccccaggggaattggaacctgtgtgtgaataaccgaaggccgcacat	3573
QY	3542	tattctctcaacacacatgatgaaagcgaagcttcctggggagacagattgcacat	3601
Db	3574	tattctctcagcacaccacatggatgaagccgagactcctggggagacagattgcacat	3633
QY	3602	ctcccatggaagctgtgtgtgtgtgtcctccctgttcttgaagaaccagctggagc	3661
Db	3634	ctcccatggaagcctgtgtgtgtgtgtcctccctgttcttgaagaaccagctggagc	3693
QY	3662	aggctactactgaacttggttaagaagaatbtggaatccctccctgaattcctcaaaa	3721
Db	3694	aggctactactgaacttggttaagaagaatbtggaatccctccctgaattcctcaaaa	3753
QY	3722	cagtagtagactgtgtcaaccctgaanaaggaagcagtgltcttccagagcagttctga	3781
Db	3754	cagtagtagactgtgtcaaccctgaanaaggaagcagtgltcttccagagcagttctga	3813
QY	3782	tgctgagcttgggaagaccatgagaatggaacgctgaaccctgaatgctgtgatactc	3841
Db	3814	tgctgagcttgggaagaccatgagaatggaacgctgaaccctgaatgctgtgatactc	3873
QY	3842	caacctcatgaagaacatgtgtctbtaaaccccgctgtgtggaagacataagatgaact	3901
Db	3874	caacctcatgaagaacatgtgtctbtaaaccccgctgtgtggaagacataagatgaact	3933
QY	3902	gaectatgtgtgtccataatgaagctgtctaaaggaaggagccttgttgaaactcttcatga	3961
Db	3934	gaectatgtgtgtccataatgaagctgtctaaaggaaggagccttgttgaaactcttcatga	3993
QY	3962	gattgatgaacgagctctcaagacctgtggaattctcagtaatgtcatctcaagagacacct	4021
Db	3994	gattgatgaacgagctctcaagacctgtggaattctcagtaatgtcatctcaagagacacct	4053
QY	4022	ggaagaaatatctccatgaagttgtgcgaagaagttgggtgtgatgtctgaagacctcaagtgtg	4081
Db	4054	ggaagaaatatctccatgaagttgtgcgaagaagttgggtgtgatgtctgaagacctcaagtgtg	4113
QY	4082	taccttgcgcagcaagaagcaagcagcgaggcctctcggggcaagcagaagctgtcttcgccc	4141
Db	4114	taccttgcgcagcaagaagcaagcagcgaggcctctcggggcaagcagaagctgtcttcgccc	4173
QY	4142	gttcaactgaagaatgaatgtgtgtatcccaaatgtatctgcacatagaccagaatccagaga	4201
Db	4174	gttcaactgaagaatgaatgtgtgtatcccaaatgtatctgcacatagaccagaatccagaga	4233
QY	4202	gaagagactgtctgaatgtgtggaatgacgaaggtctctacccagcgtggaagactggaact	4261
Db	4234	gaagagactgtctgaatgtgtggaatgacgaaggtctctacccagcgtggaagactggaact	4293
QY	4262	tacacagaacacagtttgttgcccccttctgtggaagagactgtacaaatgtccagaacgagatcg	4321
Db	4294	tacacagaacacagtttgttgcccccttctgtggaagagactgtacaaatgtccagaacgagatcg	4353
QY	4322	gaagagatttttgcctaagttgttcttgccagatgtggttgcctcaatttgccccctgtgtt	4381
Db	4354	gaagagatttttgcctaagttgttcttgccagatgtggttgcctcaatttgccccctgtgtt	4413
QY	4382	cagcctgtatctgtgcaccccttgtgcaagtaaccacacccctggaacttccagccctgtatga	4441
Db	4414	cagcctgtatctgtgtcctcagatgtgttgccacgtgtgtgtgtgtgtgtgtgtgtgtgt	4473
QY	4442	caaggaacagtacacatttgttcagcaatgtatgtctctctgaggaacaggggaaccccttggaact	4501
Db	4474	caaggaacagtacacatttgttcagcaatgtatgtctctctgaggaacaggggaaccccttggaact	4533
QY	4502	cttaagcgcctcaacaaagacccctgtgcttcggagccgcgtgatatgaaagaaaccccat	4561
Db	4534	cttaagcgcctctacacaaagacccctgtgcttcggagccgcgtgtatgtatgaaagaaaccccat	4599

QY	4562	cccgagacagccctcgtccaggcaggaggaagagtgagcacctgcgcccgattccccaagc	4621
Db	4594	cccgagacagccctcgtccaggcaggaggaamaagtgagcacctgcgcccgattccccaagc	4653
QY	4622	catcatgacctctccagaatbggaactggagcaatggacaaccttcaactgatgcga	4681
Db	4654	catcatgacctcttccagaatbggaactggagcaatggacaamaaccttcaactgatgcga	4713
QY	4682	gtgtagcagcgacaanaatcaagaagatgctgcctgtgtgtccccaaggcgaggggct	4741
Db	4714	gtgtagcagcgacamaaatacaagaagatgctgcctgtgtgtccccaaggcgaggggct	4773
QY	4742	gacctctccaaaagaanaaaaacactgcagatatccctcaaggacctggacaggaanaa	4801
Db	4774	gacctctccaaaagaaaanaaaaacactgcagatatcttccagagacctggacaggaanaa	4833
QY	4802	catlccgattatctgtgtgaagacgtatgtlgaagatcatagccaagaactaaagaaca	4861
Db	4834	catlccgattatctgtgtgaagacgtatgtgcagatcatagccaamaaccttaagaacaa	4893
QY	4862	gattcgggtgaagattagttagatgtgacggtcttcccggtgtgcataactcaagc	4921
Db	4894	gattcgggtgaagattagttagatgtgacggtcttcccggtgtgcataactcaagc	4953
QY	4922	actlccctccggatcaagaatltaatgtgcatacaacaatgaaagaacactaaagct	4981
Db	4954	actlccctccgactcaagaatltaatgtgcatacaacaamaatgaagaacactaaagct	5013
QY	4982	ggccaagacagtlctgcagatcgattctcaacagcttgggaagattatgaagagct	5041
Db	5014	ggccaagacagcttctgcagatcgattctcaacagcttgggaagattatgaagagact	5073
QY	5042	ggacacaggaataatgtcaagtggtgtgttcaatacaaggctgtgcatlcaagctc	5101
Db	5074	ggacacacgaaatattgtcgaagtggtgtgttcaatacaaggcctgtgcatlcaagctc	5133
QY	5102	tttctctgaatgtlcaacaatgtccattctcgggccaaccttgcaaaagggaaggacct	5161
Db	5134	tttctctgaatgtcattcaacaatgtccattctcgggccaaccttgcaaaagggaaggacct	5193
QY	5162	tagcattatgtgaattactgtcttcaatcaatcccccgaattccacaagaacagcagcttc	5221
Db	5194	tagcattatgtgaattactgtcttcaatcaatcccccgaattccacaagaacagcagcttc	5253
QY	5222	agaagtgagctctgatabgacacatacagtgagatgagctgtcatctactgtgctctaattgt	5281
Db	5254	agaagtgagctctgatabgacacatacagtgagatgagctgtcatctactgtgctctaattgt	5313
QY	5282	aattgtccttggtcccgagcaactgtgtcgtattctcgtatccagagcgaggttaagcaaac	5341
Db	5314	aattgtccttggtcccgagcaactgtgtcgtattctcgtatccagagcgaggttaagcaaac	5373
QY	5342	aaaacacctgcagtlcatcagatggagtgaaagcctgtcatctactgtgctctaattgt	5401
Db	5374	aaaacacctgcaggttcatcagatggagtgaaagcctgtcatctactgtgctctaattgt	5433
QY	5402	ctggagatatgtgcaattacgtgtgtccctgcgaacacgtgtcatatatacatcttaactgtt	5461
Db	5434	ctggagatatgtgcaattacgtgtgtccctgcgaacacgtgtcatatatacatcttaactgtt	5493
QY	5462	ccagagaagctcatgtgtctccacaacatctgcgcgtgtgctagccctctactgttct	5521
Db	5494	ccagagaagctcttatgtgtcctccacaacatctgcgcgtgtgctagccctctactgttct	5553
QY	5522	gtatgggtgtgtlcaatcacaccttcaatgttaccagcctccttgtgttcaagaatcccaag	5581
Db	5554	gtatgggtgtgtlcaatcacaccttcaatgttaccagcctccttgtgttcaagaatcccaag	5613
QY	5582	caaaagctatgtgtgtccacacagcgttgaaccttcaatgtgatatgaatgagcgtgtgc	5641
Db	5614	caaaagctatgtgtgtcctcaccacagcgttgaaccttcaatgtgatatgaatgagcagcgtgc	5673
QY	5642	caaccttgtgtcgtgagcgtgttccacgcgaataaagcttgaataatacatatgatactcgaa	5701

```
Db 5674 CACCTTGTGCTGAGCTGTTACCGACAAFAAGCTGAATATATCATATATCTCCGAA 5733
Qy 5702 gtccgtgttcttgatcttcccacaatttttgccttggaagagggctcaatcagatgltgaa 5761
Db 5734 GTCCGTTTCTTGTGATCTCCACATTTTTCCTGGGACGAGGCTCATCGACATGTGTGAA 5793
Qy 5762 aaaccagaatcgtcgtatgccccggaagaagtttggaagaatccgtttgtgcacatc 5821
Db 5794 AAACGAGGCAATGCTATGCTATGCTCCGAAAGTTTGGGGAATGCTTTGTGTCCCAT 5853
Qy 5822 atcttggacttggtaggaacacctctgcacatggccgttggaaggggtgtgtctt 5881
Db 5854 ATCTTGGAGCTTGGTGGAGCAAAACCTTTCGCGATGGCGGTGGAAAGGGTGTGTCTT 5913
Qy 5882 ccttattactgttcttgatccagatagatcttccatcagagccagacctgtataatgcaaa 5941
Db 5914 CCTCATTTAGTGTGTGATCCAGTACAGATTTCTTCATCAGCCCGACCTGTAAATGCAAA 5973
Qy 5942 gctatcctcctgaatgatgaagaatgtagagcggaagaagaagatcttga 6001
Db 5974 GCATCTCCTCTGATGATATGAATGATGATGAGGCGGGAAGACAGATTTCTTGA 6033
Qy 6002 tggtagagagccagaatgacatcttgaagaalcaagaggttgaagaaatataagaagaa 6061
Db 6034 TGCTGGAGGCCAGAAATGACATCTTAGAAATCAAGAGATTGACAGATATATAGAAAGAA 6093
Qy 6062 ggggaagccctgtgttgagagagattgctgtgagcatctcctcgtgtgagttgttggct 6121
Db 6094 GCGGAAGCCCTGCTGTGTGACGGATTTGGCGGATTTCTCCGTGGAGATGCTTTGGGCT 6153
Qy 6122 ccttggagtttaatgaggcttggaataatcaatcattcaagatgttaacagagatcacac 6181
Db 6154 CTTGGAGATTAAATGGGCTGGAATAATCATCAACTTTCAAGATGTTAAGAGATATCCAC 6213
Qy 6182 tgttaccagagagatgcttcttcttaacaaaataglatcttatacaacatcagaagt 6241
Db 6214 TGTTACCAAGGAGATGCTTTCTTAAACAAAATACTATCTTAAACATCCATGAAAT 6273
Qy 6242 acatcagaacatggtcactgcctcactgattgatgcacacaaagcttgaactggag 6301
Db 6274 ACATCAGAACATGCGCTACTGCCCTAGTTTATGTCATCACAAGACCTTTTACCTGGAG 6333
Qy 6302 agaacacgttggagttcttgccttcttgaagagagtcacagaaagaaagtttggcaagt 6361
Db 6334 AGAACACGCTGAGTCTTTGCCCTTTGAGAGAGATCCAGAGAAAGAAAGTTGGCAAGT 6393
Qy 6362 tggtagtggagagatcggaaactggcctgtgaaatgtaagaaatataatgctgttaa 6421
Db 6394 TGCTGAGTGGCGATTCGGAACCTGGCCTCGTGAAGATGGAAGAAATATGCTGGTAA 6453
Qy 6422 ctataatgagagcaacaacagcaagctctacagccatggtcttgatggcgccctcc 6481
Db 6454 CTATAGTAGAGGCAACAAACGCAAGCTCTTACAGCATGGCTTTGATCGGGGCGCTCC 6513
Qy 6482 tgtgtgttcttggatgaaacccaacaggaatgataccaaagccggcggttctgtg 6541
Db 6514 TGTGGTGTTCGTGATGAACCCACACAGCATGATCCCAAGCCGCGGCTTCTTGTG 6573
Qy 6542 gaattgtgcccataagtgtgtcaaggaagagagatcagtaagtcctacatcacaagt 6601
Db 6574 GAATGTGCGCTTAAGTGTGTCAAGAGGAGGAGATCAGTAAGTCTTACATCTCATAGAT 6633
Qy 6602 ggaagaatgtgaagctcttgcactaggaatggcaatcagtcaatggaagtgtcagtg 6661
Db 6634 GGAAGAATGTGAAGCTTTTGCACTAGATGSCATCATGTCATGGAAGTTCAGTGG 6693
Qy 6662 ccttggcaggttccagatcttaaaaaatagtttggagaatggttatacaatgctgtacg 6721
Db 6694 CTTTGGCAGTGTCCAGCATCTAAAAAATAGTTTGGAGATGGTTATTAACAAATAGTTGATG 6753
Qy 6722 aatagcaggttcaaccggacctaagccgttccagattcttggactgtgacattcc 6781
|||||
Db 6754 AATFAGCAGGCTCAACCCGGACCTGATGAGATTTCTTGGACTTGCATTTCC 6813
Qy 6782 tggaaagtgttctaaagaagaacacccggaacatgctacaaatcagacttccatcalt 6841
Db 6814 TGAAGTGTCTTAAAGAGAAACACCGGACATGCTACATATACAGCTTCATCTTCAAT 6873
Qy 6842 atcttctctggcagatataatcagatcctctccagagcaaaaagagatccacataga 6901
Db 6874 ATCTTCTCTGGCCAGAAATATTCAGATCTCTCCAGAGCAAAAAAGGACCTCCACATAGA 6933
Qy 6902 aagactactgttctcagaacaacactgacaaagtatttgaacttggcagagcca 6961
Db 6934 ACATGACTCTGTTTCTGAGAACACTTGGACCAATATTGTGAACTTTGCCAAGGACCA 6993
Qy 6962 aagtgatgacacacttaaaagaccttcatlacaaaaaacagacagtagtgcagt 7021
Db 6994 AAGTATGATGACCACTTAAAAAGACCTCTCATTTACACAAAAACAGACAGTAGTAGAGT 7053
Qy 7022 tgcagtttcaatcttcttctacaggaatgagaagtgaaagaaagctatgtatgaagt 7081
Db 7054 TGCACTTCTCACTCTTTCTTACAGAGATGAGAAAGTGAAGAAAGCTATGTATACAAAT 7113
Qy 7082 cctgttcaacgggtggtcgtgaagaagaggaactagacttcttggacatgtga 7141
Db 7114 CCGTTTCAATAGCGGGTGGCTGAAGTAAAGAGAACTAGACTTTCTTGGACCATGTGA 7173
Qy 7142 agtgtgtggaagaaagagccagaagtgtgtaggaagaatgaactgtgactgtact 7201
Db 7174 AGTGTGTGGAGAAAGAGCCAGAAAGTGAAGTGGGAAGAAAGTAACTGATCTGACT 7233
Qy 7202 gatactatcaatgcaatgcaatcgaatgcaatgaagaagaatctcattagagggcag 7261
Db 7234 GATAGTATTCATGATGCAATGCAATTCATGCAATTAACAAATTCATTTACAGGGGAG 7293
Qy 7262 tgcctttagcctatgcttctgtatggcctcctcaagtgaagaacttgaatttttla 7321
Db 7294 TGCCTTTGTAGCCTATGCTGTATGGCTCTCAAGTGAAGACTTGAATTTAGTTTTTA 7353
Qy 7322 ccttaccatgtgaactctctatataagaaaccaaagacataggttgaactcaac 7381
Db 7354 CCTATACCTATGTAAGAACTGATTTATGGAACCAATGAGATAGGGTTGAACCTCACAC 7413
Qy 7382 ttttttttttttttgcctgttctcctgtatctcatttgggttggcaacaataatcaaat 7441
Db 7414 TTTTTTTTTTTTTTTGTTCCTGCTATCTTCATTTGGGGTTCGAACATATTTATCAAGT 7473
Qy 7442 aatcagggccagagatctatgatcaaaaacaaaagtaatgacatccatcactaaag 7501
Db 7474 AATCATGGCCAGCGATTTATGATCAAAATCAAAAGTAAATGACATCCATTCACATAAG 7533
Qy 7502 ccatgcatgcccagagagactgtgttccgggtgaacaaatccatgtcgggaatgagt 7561
Db 7534 CCATGCCATGCCAGGAGACTGTTTCCGGTGAACATATCATTTGGGCAATGAGATGTG 7593
Qy 7562 ccaagatctatagtgccaagtltttcagaagaagtttgaagacacatggtgtcatgtca 7621
Db 7594 CCAGAGTTTATAGGCCAAGCTTTTTCAGAAAGTTTGAAGCAACATGAGTGTGATCTCA 7653
Qy 7622 ctlttfgaagaagctgtcctcgaaggtcatacaacattgaatatcaagtgaagaagt 7681
Db 7654 CTTTGTGAAAGGCTGCTCTGAGATGATCAAGATGGAATGTAAGTTGACAGAAATG 7713
Qy 7682 tgcacatgctgtcctlaacatcctgttcttgcctcctcgtataaactgttctggtggcagta 7741
Db 7714 TGCCATGCGTGGCTAAACATCTCTGTTGATTCCTCTGATTAACCTGTCTGCGGGCAGTA 7773
Qy 7742 acatgcaaaaaaattgtgggtgtcctcagacgggaacttggttccatgtgtatattg 7801
Db 7774 ACATGCAAAAAAATGTGGGTGTCTCTAGGCACGGGAAACTTGGTTCATTTGATATTG 7833
Qy 7802 tccatagcttcagagcaatggtctacaggtacaccttcttggagacttaaatataacta 7861
Db 7834 TCCATGCTTCAGACCATGGGTCTTACAGGGGTATCTTATGAGACTTAAATATATCTTA 7893
```


QY 7862 gatccctgtaagaggcaagaatcaacagccaaactgctgaggctgcaagctgctgaagc 7921
|||||
Db 7894 gatccctgtaagaggcaagaatcaacagccaaactgctgaggctgcaagctgctgaagc 7953
QY 7922 caggagcaaggagtaagaagatctgctgcttaaacctaggagagctgtgcccattctc 7981
|||||
Db 7954 caggagcaaggagtaagaagatctgctgcttaaacctaggagagctgtgcccattctc 8013
QY 7982 cgaactgctgtaacacatgtaacactgcaactcaagatgtaactgtaacacagatgatt 8041
|||||
Db 8014 ctgacactgctgtaacacatgtaacactgcaactcaagatgtaactgtaacacagatgatt 8073
QY 8042 attctgagcttctgaatcaatcctagaanaatgaagaatgagatgtaattctgcaaaaa 8101
|||||
Db 8074 attctgagcttctgaatcaatcctagaanaatgaagaatgagatgtaattctgcaaaaa 8133
QY 8102 tcttgtaacttttaatgtaatttggaatttaagttcctacagtgactctgtaactcct 8161
|||||
Db 8134 tcttgtaacttttaatgtaatttggaatttaagttcctacagtgactctgtaactcct 8193
QY 8162 agaatgacctcttgtaagaccctgtaagagagatgagcaactgcccactattt 8221
|||||
Db 8194 agaatgacctcttgtaagaccctgtaagagagatgagcaactgcccactattt 8253
QY 8222 ttaattcttaatgtaagttgcaatcagtcagtaagtgctcctagaagaatgtaag 8281
Db 8254 ttaattcttaatgtaagttgcaatcagtcagtaagtgctcctagaagaatgtaag 8313
QY 8282 gtaagagatcctacagatattatgtaagttcttcaagatcttaagatcttaact 8341
Db 8314 gtaagagatcctacagatattatgtaagttcttcaagatcttaagatcttaact 8373
QY 8342 tcaacttcaatcaatcaatatttcttgatgtaagtgctgtaagagatgtaagtaag 8401
Db 8374 tcaacttcaatcaatcaatatttcttgatgtaagtgctgtaagagatgtaagtaag 8433
QY 8402 gtaagagatcctacagatattatgtaagttcttcaagatcttaagatcttaact 8461
Db 8434 gtaagagatcctacagatattatgtaagttcttcaagatcttaagatcttaact 8493
QY 8462 ctgagttacaataatgtaagttgctgtaagtgctgtaagagagagagagagagagag 8521
Db 8494 ctgagttacaataatgtaagttgctgtaagtgctgtaagagagagagagagagagag 8553
QY 8522 gaccttt 8581
Db 8554 gaccttt 8613
QY 8582 agtttaacaagaatcttcaacagagagagagagagagagagagagagagagagagagag 8641
Db 8614 agtttaacaagaatcttcaacagagagagagagagagagagagagagagagagagagag 8673
QY 8642 acaactgctgtaagatgtaagttgtaagttgtaagttgtaagttgtaagttgtaagttg 8701
Db 8674 acaactgctgtaagatgtaagttgtaagttgtaagttgtaagttgtaagttgtaagttg 8733
QY 8702 ccaacttaactgagagctcctcaaatcttcaatcttcaatcttcaatcttcaatcttcaat 8761
Db 8734 ccaacttaactgagagctcctcaaatcttcaatcttcaatcttcaatcttcaatcttcaat 8793
QY 8762 aaaaaaacaatactcgaatgagagagagagagagagagagagagagagagagagagag 8821
Db 8794 aaaaaaacaatactcgaatgagagagagagagagagagagagagagagagagagagag 8853
QY 8822 tttcagacatgaacatttgaataactgtaactgtaactgtaactgtaactgtaactgtaact 8881
Db 8854 tttcagacatgaacatttgaataactgtaactgtaactgtaactgtaactgtaactgtaact 8913
QY 8882 gagagaaagagaaatactgag 8941
Db 8914 gagagaaagagaaatactgag 8973

QY 8942 tcaattactacttcttccactttttccaaaaattgaaatatttaacgctgaagagagagag 9001
Db 8974 tcaattactacttcttccactttttccaaaaattgaaatatttaacgctgaagagagagag 9033
QY 9002 ttcagatttcaaatcttctcatalatttttaaatcttcaaatcttcaaatcttcaaatcttca 9061
Db 9034 ttcagatttcaaatcttctcatalatttttaaatcttcaaatcttcaaatcttcaaatcttca 9093
QY 9062 tgcgtaaaaaagaaaaatgagttcttgaagatgaagatcaatattgatttcaaatata 9121
Db 9094 tgcgtaaaaaagaaaaatgagttcttgaagatgaagatcaatattgatttcaaatata 9153
QY 9122 agtaatgaagcatttccaaatcagatgataatgagatgagatgagatgagatgagatgag 9181
Db 9154 agtaatgaagcatttccaaatcagatgataatgagatgagatgagatgagatgagatgag 9213
QY 9182 tcaaaaaatcaagaatttataagaatatttcccaatcttcaaatatttcaaatctcaagt 9241
Db 9214 tcaaaaaatcaagaatttataagaatatttcccaatcttcaaatatttcaaatctcaagt 9273
QY 9242 tatggttcccaatcttcaatcaaatctgtaattctcaatctcaatctcaatctcaatctca 9301
Db 9274 tatggttcccaatcttcaatcaaatctgtaattctcaatctcaatctcaatctcaatctca 9333
QY 9302 caactccttacttgcgttccctgatttcaagagcatalatttcaaaaaatcaaaagagact 9361
Db 9334 caactccttacttgcgttccctgatttcaagagcatalatttcaaaaaatcaaaagagact 9393
QY 9362 gtaagacttcttgaagaagaacagagacttcaatcaagatgtaagaagagagagagagag 9421
Db 9394 gtaagacttcttgaagaagaacagagacttcaatcaagatgtaagaagagagagagagag 9453
QY 9422 ctgaagaacaatcctagatgataatcttcaatctcaatctcaatctcaatctcaatctca 9481
Db 9454 ctgaagaacaatcctagatgataatcttcaatctcaatctcaatctcaatctcaatctca 9513
QY 9482 ttttctacatttccctgtaag 9541
Db 9514 ttttctacatttccctgtaag 9573
QY 9542 aatcaagaanaattctgtaataatccctgtaagagagagagagagagagagagagagagag 9601
Db 9574 aatcaagaanaattctgtaataatccctgtaagagagagagagagagagagagagagagag 9633
QY 9602 tcaaatagcgttcaaaaatttctgcttggatcttggagagagagagagagagagagagag 9661
Db 9634 tcaaatagcgttcaaaaatttctgcttggatcttggagagagagagagagagagagagag 9693
QY 9662 taacaacgtgtaatactgaagaataacagagagagagagagagagagagagagagagag 9721
Db 9694 taacaacgtgtaatactgaagaataacagagagagagagagagagagagagagagagag 9753
QY 9722 cagcaaatcttctgtaaaaaaacaacacacacacacacacacacacacacacacacac 9781
Db 9754 cagcaaatcttctgtaaaaaaacaacacacacacacacacacacacacacacacacac 9813
QY 9782 ctgaagaacaatgcttctgtaataatcttgaacacacacacacacacacacacacacac 9841
Db 9814 ctgaagaacaatgcttctgtaataatcttgaacacacacacacacacacacacacacac 9873
QY 9842 tcaattgactaaagcatttgcgtgttcttctctgtaagagagagagagagagagagagagag 9901
Db 9874 tcaattgactaaagcatttgcgtgttcttctctgtaagagagagagagagagagagagagag 9933
QY 9902 ttttccaaagaagcatttgcgtgttcttctctgtaagagagagagagagagagagagagagag 9961
Db 9934 ttttccaaagaagcatttgcgtgttcttctctgtaagagagagagagagagagagagagagag 9993
QY 9962 gaccttggtatctactactaagaataatgtaatactgtaagagagagagagagagagagag 10021
Db 9994 gaccttggtatctactactaagaataatgtaatactgtaagagagagagagagagagagag 10053
QY 10022 caaatgagagatcccccttaaaangtttctatcttcaataagagattagctgctatccc 10081

Db 10054 CAAATGTCATCCCCCTTAAANGTCTATTTCATAGATTTAGCTTGTATCCC 10113
QY 10082 tcttataccctaagaatgaagctgttttctgtctcttctgtlcaatcttgccctcatcc 10141
Db 10114 TTTCTATACCTTAAGATGAAGTGTGTTTGTGCTTTGTCATCATGCGCCCTCATTC 10173
QY 10142 aagcatttagctgtctgtatgtgatalctattttgacctggaatatctgaattgca 10201
Db 10174 AAGCACTTATGCTGTGTGTAATGAGATCTATTGTCATGGAATATCTGAGAAATGCA 10233
QY 10202 aaactagacaaagtttccacaagaatcttaagtttaactcttcaatcttcaataaagaaaa 10261
Db 10234 AAACCTAGACAAAGTTTCAACAAGATTTCTAAGTTAATCATTTTCAATTAAGAAAA 10293
QY 10262 aagaaaaaaaatttctgtatgtcaataacttatatagaaglatnaaalycataattctat 10321
Db 10294 AAGAAAAAAATTTTGTATGTCATTAATTAATGATTAATTAATTAATTAATTAATTTCTAT 10353
QY 10322 gtgtataataatgagtcacaataaagctgtgacagctgttgaataaataaataaataa 10381
Db 10354 GTTGTATATTAATGATGTCACAAATTAAGCTGTGACAGTTCTTTAAATAAATAAATAA 10413
QY 10382 aaaaaaaataaataaataaataaataaataaataaataaataaataaataaataa 10441
Db 10414 AA 10473
QY 10442 a 10442
Db 10474 A 10474

RESULT 5
AX060721 10474 bp DNA linear PAT 22-JAN-2001
LOCUS AX060721
DEFINITION Sequence 9 from Patent WO0078972.
ACCESSION AX060721
VERSION AX060721.1 GI:12406109
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Law, R.M., Wade, D. and Garvin, M.
TITLE Regulation with binding cassette transporter protein abcl
JOURNAL Patent: WO 0078972-A 9 28-DEC-2000;
CY THERAPEUTICS, INC. (US)
FEATURES
source 1. 10474
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2907 a 2304 c 2415 g 2844 t 4 others
ORIGIN

Query Match 99.9%; Score 10429; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10436; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 214 CAAATGTAATAACGTTAATGACCAAGCCAGGCGTCCCTGCTGATGCTGGCCGCT 273
QY 242 gcttccagagctcccgagacacagctgagctgtgctgtgagagacatgtgttg 301
Db 274 GCTTCCAGGGCTCCCGAGCCACAGCTGGGCGTGTGCTGAGAGGAACATGCTTGTG 333
QY 302 gctcagctgagtgctgtctgtgtgaagaacacttcaatgaagaagaacaatgtca 361
Db 334 GCTCAGCTGAGGTGCTGCTGTGAGGAAGCACTTCAATTAAGAAGAACAAATGTC 393
QY 362 gcttctactgaagtgagctgagctgctatattcttccatcttccatcttcttctgct 421
Db 394 GCTGTACTGGAAGTGGCTTGGCTTCTATTATTTCTCTGATCTGTGATCTGTG 453
QY 422 gactacccaacctatgaacaaca tgaatgacatcttccataataaagcctgtcctc 481
Db 454 GAGCTACCCACCTATGACAAACATGAATGCAATTTTCAAAATTAAGCCATGGCCCTGC 513
QY 482 aggaacacttccctgtgtgttcaagggatlatctgtatgtcaacaacacccctgttctg 541
Db 514 AGGAACACTTCTGCTGGGTTCAGGGGATTAATCTGTAATGCCAACAAACCCCTGTT 573
QY 542 cccgactcctgaggagctcccgagtgctgtgaacttaacaatctgtgtctg 601
Db 574 CCGACCTCTGGGAGGCTCCCGGAGTGTGTAATTTAACAATTAATCAATTTGCTGC 633
QY 602 cctgtctcagaatgctgagagctcttatacagccagaagaacacagatgaaga 661
Db 634 CCTGTCTCAGATCTCTGGAGGCTTTTATACGCCAGCAAGACCCGATGAAAGA 693
QY 662 catgcgaagttcttgagaacattacagcagatcaagaataatcagctcaacttgaagct 721
Db 694 CATGCGCAAGTTCTGGAACATTACGACGATCAAGAAATCCAGCTCAAACTTGAAGCT 753
QY 722 tcaagattcctgtgtgacaatgaagaacctctctgtgttcttatalacacacctctct 781
Db 754 TCAAGATTCTCTGGTGAACAATGAACCTTCTGAGTCTCTATACCAACCTCTCT 813
QY 782 cccaaagtctactgtgagacaagatgctgagagctgctgctatcttccaaagatttt 841
Db 814 CCAAAAGCTACTGTGGAACAAGATGCTGAGGGCTGAGTGTATTTCTCCACAAAGGATTTT 873
QY 842 gcaagctacagttacatttgaacaagctcgtgtcaatgatacaaaatcagaagaatgtat 901
Db 874 GCAAGCTACAGATTACATTGTAACAAGTGTGCAATGATGATCAAAATCAAGAGATGAT 933
QY 902 tcaacttggtagcaagaagtttctgtgcttctgtgtcctaccaaaggaagaactgtgtc 961
Db 934 TCAACTTGTGACCAAGAAAGTTTCTGAGCTTTGTGGCTTACCAAGAGAACTGGCTGC 993
QY 962 agcagagcagttactcgttccacaatgacatctcgtgaagcgaactctgaagacataa 1021
Db 994 AGCAGAGCAGTACTTGTGTTCCAAAGATGACATCTGAAACCAATCTGAGAACATTA 1053
QY 1022 ctctaatctcccttcccgagcaagagctgtgtgaagcccaaaaaatctgtcatag 1081
Db 1054 CTTTACATTTCTCCCTTCCCGAGCAAGAGCTGTGTAAGCCACAAACAAATTTGCTCAT 1113
QY 1082 tcttggagactctggcccaagagctgttcaagcatgaaagctgaagatgaatgtgaaga 1141
Db 1114 TCTTGGAGCTCTGGCCCAAGAGCTGTTCAAGATGAAGAGTGAAGTGAAGTGAAGAGGA 1173
QY 1142 ggtgatgttcttgaaccaatltgaacagctcgaactcctccacccaataatctacagctgt 1201
Db 1174 GGTGATGTTTCTGACCAATGTAAGACGCTCAGCTCTCTCCACCAAAATGATACAGCTGT 1233
QY 1202 gtctcgtattgtctgtgagacatcccgaggaaggggtgtgaagatcaagctctcaactg 1261
Db 1234 GTCTCGATTGTTCTGCGGGATCTCCGAGGAGGGGGGTGAAGATCAAGTCTCTCAATG 1293
QY 1262 gtaagagacaacaactacaaagccctcttgaagcaatgtgacatgtgaagatgtcgtga 1321

D	1294	GTATGAGGACACAACTACAAAAGCCCTCTTTGGAGGCATATGGCACTGAGCAATGCTCA	1355
Q	1322	aacttctacgaacaactctacaactcctctactgcaatgatattgaaagatttggagtc	1381
D	1384	AACCTTATGACAACTCTACAACTCCCTTACTGCATATGATTTGATGAAATTTTGGAGTC	1413
Q	1382	taagcctcttcccgattatcttgaaagctctaaagccgtgtctgttggaaagtcct	1441
D	1414	TAGTCCTCTTCCCGATTATCTGGAAAGCTGTGAAGCCGCTGCTCTTTGGAAATCCT	1473
Q	1442	gtatacccttgacaactccacgcagcaaaagcaggtcattgcttgaagtgaacaagacttcca	1501
D	1474	GTATACACCTGACACTCCAGCCACAAGCAGAGTCAATGCTAGGTGAAACAAACTTCCA	1533
Q	1502	ggaacgtgcctgttccatgatcttgaaagcattgtggaaagaacttgcccgaagcttctg	1561
D	1534	GGAACTGGCTGTCCATGATCTGGAAAGCATGTGGGAGGAACTCGACCCCAAGATCTG	1593
Q	1562	gacctatgagaacaagccaagaatactgaccttccgcgatgtctgttggacagcagga	1621
D	1594	GACCTTATGGAACACGCGCAAAATGSACTTGTCCGGATGCGTTTGGACAGCAGGGA	1653
Q	1622	caatgaccactcttgggaacagcagttggaatgcttgaattggacagcccaagacatcgt	1681
D	1654	CAATGACCACTTTTGGGACAGCAGCATTTGATGATTTGATGGACAGCCAAACATCGT	1713
Q	1682	gggctttttggcaagcaccccaaggaattccagtcagaaatgtcttctgtgaacactg	1741
D	1714	GCGCTTTTGGCCAGACGCCCAAGAGATTTCCAGTCCAGTATGTTTGTGTACACTG	1773
Q	1742	gagagaagcttccaacgagacttaccaggaacaaatccgcagacatatcgcctcatggaag	1801
D	1774	GAGAGAAAGCTTTCAACAGACACTAACCGGCAATCCGGACCAATCTCGCTCATGAGAGT	1833
Q	1802	tgtaacctgaacaagctagaaccctaaagctaaagatctggtcctatcaacaagtccat	1861
D	1834	TGTCAACTGGAACAAGCTAAGAACCCATATCAACAAAGAGCTGCGTCATCAACAAGTCCAT	1893
Q	1862	ggaagctgtgtgataagagaagatcttcgggctgtgatttgttcaacttgaattaccag	1921
D	1894	GGAGCTGCTGATGAGAGGAAGTTTGGGCTGATATTGTTCACTGGAATTAATCCAGG	1953
Q	1922	cagcaatgagctgtcccatcatgttcaaatgaagaatccgaatggacattgcaaatgtgga	1981
D	1954	CAGCTTGTAGCTGCCCATCATGTCTCAAGTACAAGATCCGAATGGACATTTGACATGTGGA	2013
Q	1982	gagggacaataaatactaaagatgtggaatcgggaacccctgttccatgaagctggcccttga	2041
D	2014	GAGGACAAATTAATTCAGAGATGGGTACTGTGGACCTGGTCTCGAGCTGACCCCTTTGA	2073
Q	2042	gagacatgcygtaacgtctctgggggggcttgcgtacttgcagaatgtgtgtggagcagcaat	2101
D	2074	GGACATGTGTGTAAGCTGTGGGGGGGCTTCCGCTACTTGCAGGATGTGGGGAGCGCAAT	2133
Q	2102	catcaaggttgttcgcgggcaaccgagaagaactgtgtctatataggaaagatggcccta	2161
D	2134	CATTCAGGCTGTGACGGGCAACCGAAGAAATAATGATGTCTATATGCAACAGATGCCCTA	2193
Q	2162	tcccgcttaacgttbatagacatcttctcgggggtgataggaacgggtacaatgccccttcat	2221
D	2194	TCCCGTATTACCTGTATGACATCTTCTCGGGGTGATGAGACCGCGTCAATGCCCTCTTCAT	2253
Q	2222	gaacgtgcgcctggaattactcaatgtgctgtgatacacaagggacatcggtatgagaaga	2281
D	2254	GACGCTGGCCGTGGAATTACTACAGGCTGTGATCATCAAGGGCATATGTTATGAAAGGA	2313
Q	2282	ggcagcgcttgaagaagaccatgcygatacgtgggcctgggaacaacagataactctgttttag	2341
D	2314	GGCAGCGCTGAAAGAGACATAGCGGATCATAGGGCCTGCAACACAGATTACTTGSTTTAG	2373
Q	2342	ctggttcaatlagtagcctcatctctctctctgtgagcgttgcctgtctagtgtgcatcct	2401
D	2374	CTGGTTCAATATGATACCTCATATCCCTTTCTTGTGAACGCTGGCGCTGCTAGTGTGATCCT	2433

Oy	2402	gaadtaggaaacctgctccctccacagtgatcccaagcgtggtgtgtgtcttcctccgtccgt	2461
Db	2434	GAAGTTAGGAAACCTCGTGGCCACAGTATCCACAGCGTGGTGTGTCTTCCTGTCCGT	2493
Oy	2462	gttcgtctgtgtgacaactccctcaagtgctctccgtatcgaactctctccagagccaa	2521
Db	2494	GTTTGTCTGTGTGACATCTCTGCAGTGTCTTCGTGATTACACAGCTTCTCCAGAGCCAA	2553
Oy	2522	ccctgacagcagccctgttgggggacatcatctactcaqctgtactcctgtccctaaqctctgt	2581
Db	2554	CCCTGCACACACCCCTGTGGGGGCATCATCTACTTCAACGCTGACGTCCCTTACGTCTCTGG	2613
Oy	2582	tgtagcctgaggaaggaacagcttgaggtctcaaaccaagatccttcgactaagcctgtctccc	2641
Db	2614	TGTGGCATGGGAGGAACTACGTGGGCTTACACATCAAGATCTTCGCTAGCTGTCTGTCC	2673
Oy	2642	tgtgaccttttggtctgttgctgtgtgaagtaactttgaccttttgagagcagggacttgsagt	2701
Db	2674	TGTGGCTTTTGGTGTGGCTGTGTGAGTACTTGTGGCCCTTTTGTGAGAGCCAGGGCATTTGGAGT	2733
Oy	2702	gcagtgaggacaacctgttttagagatctctgtgggggagaagtgtgtctcaactctcaacactc	2761
Db	2734	GCAGTGGGACAAACCTGTTTGAAGATCTGTGGAGGAAGATGCTTCAATCTACCACTTC	2793
Oy	2762	gattcccaatgactgttcttgacacctccctccctatcttgagtgatbaaccttgatcatctgaagc	2821
Db	2794	GATCTCCATGATGCTGTTTGAACACTTCTCTATGGGGTATATACCTGCTACATTGAGGC	2853
Oy	2822	tgctcttccagagccagtaacggaaltcccaagccctggtatcttctcttgacaagatccta	2881
Db	2854	TGTCTTTTCAGGCGCAGTACGGAATTTCCAGAGCCCTGTGATTTTCTTTGACCAAACTCTTA	2913
Oy	2882	ctgagtttggcagagaagaatgtatgagaagagccaccctggtctccaaccaagaagagatgctc	2941
Db	2914	CTGGTTTGGCGGGAATGTATGAAAGAGCCACCTCGTTTCCAAACCAAGAGATGTTC	2973
Oy	2942	agaaatcttgcatyhgagaggaagaaaccaccacacttgaagcttgggcgtgtccatccagaact	3001
Db	2974	AGAAATCTTGCATGAGGAGAGAAACCCACCTTGAACCTGGGCTGTCCATTTCAGAACT	3033
Oy	3002	ggttaaaagtctcacccagataggaatggaagtggtcgtctgactatgagcttgagacttaatttta	3061
Db	3034	GGTAAAGTCTACCCGATGGGATGTAAGTGGCTGTGATGGCTGTGGCATGTAAATTTTAA	3093
Oy	3062	tgaagggccagatcaactcctctccctgggcccacaaatggagccggggaagaagcaaccaactgctc	3121
Db	3094	TGAGGGCCAGATCACCTCTCTTCTGTGGGCACAAATGGAGCGGGGAAGCAGCCACCATGTC	3155
Oy	3122	aatcctgacccgggtgtgtcccccgaactcgggacacccgctcatactcttgggaagaagact	3181
Db	3154	AATCTGCACCGGGTGTGTCTCCCCGCACTCTGGGCAACCGCTACATCTGTGGAAAAACAT	3211
Oy	3182	tgcgtcttgatgtgaagcaacatcccgcaaaaccttgggggtctgtctcccagaataaagtgtct	3241
Db	3214	TGCTCTTGATGATGACACCAATCCCGGACAGAACTTGGGGTCTGTCTCCAGATTAAGCTGCT	3277
Oy	3242	gtttgacatgctgacactgtctcgaagaacaacatctgttctatgtccogcttgaagggtcctc	3301
Db	3274	GTTTGACATGTGACGTGCTGCGAAGAACACATCTGTTCTATGCCCGCTTGAAGAGGCTCTTC	3333
Oy	3302	tgaagaagcagtggaaggcgggagatgtaggcacatagtcgccttgatagtgtgtttgacataag	3361
Db	3334	TGAGGAAGCAGTGAAGCGGAGATGAGACAAATGAGCCCTGATGTTTGTTGTGCATCAAG	3393
Oy	3362	caagctgaaagaacaanaaagccagctcttcaagtgagatlcagaagaagctacatctgtggc	3421
Db	3394	CAAGCTGAAAGAAACAAACAGCCACACTCTTCAGGGTGAATGAGAGAAAGCTATCTGTGAC	3455
Oy	3422	cttgaccttgttcgggggagatctaaagttgtcatatctcttgatgaaccaacagctgtgttga	3481
Db	3454	CTTGGCCTTTGTTCGGGGGATCTTAAGGTTGTGATTTCTGGATTAACCAACACACTGTGTGGA	3511

[illegible]

Dh 5674 CAOCCTTGTGCTGAGAGCTGTTCACCGACAAATPAGCTGAATATATATCATPAGATTCCTGAA 5733
Qy 5702 gtccgtgttcttgatcctcccaatltttgctgggaaggaaggtcctacgcagatgtgttaa 5761
Dh 5734 GTCCGCTGTCTGATCTTCCACATTTTTTGTGCTGGAGAGGGCTCATCGAATGTGTAA 5793
Qy 5762 aaacaggaatgctgctgagcccttggaaggtttgggagaaatgcttctgtaccatt 5821
Dh 5794 AAACCAAGGAATGCTGATGCTCCGTAAGGTTTGGGAGAAATCCCTTTGTCTACCAT 5853
Qy 5822 atcttggaacttggttggaagcaacctctctgcacatggccgtggaaggggtgtgtctt 5881
Dh 5854 ATCTTGGAGCTGTGTGGAGCAAACTCTTGCCATGCGCGTGGAAAGGGGTGTGTCTT 5913
Qy 5882 cctcatctgttcttgatccagtaacagatctcctcagggccagacctgtataatgcaa 5941
Dh 5914 CCGATTTACTGTTCTGATCCACTACAGATTTCTCATCAGGCCCAACCGTAAATGCAAA 5973
Qy 5942 gctatctctctgaaatgaaatgaaatgtgaagcggaaggaaggaaggaatcttga 6001
Dh 5974 GCTATCTCTCTGATGATGAAGATGAAGATGAGGCGGGAAGACAGAAATTCCTTGA 6033
Qy 6002 tggtagaagccagaaatgacatcttaagaaatcaagaggttgacgaagataatagaagaa 6061
Dh 6034 TGSTGAGGCGCAAGATGACATCTTAGAAATCAAGGAGTTGACGAAGATATAGAAGAA 6093
Qy 6062 ggggaagcctgtctgtgacagaattggtaggcatctcctcgtgtgagtgcttgggct 6121
Dh 6094 GCGGAAGCCTGTGTGACAGGATTTGCGTGGGCAATTCCTCTGGAGATGCTTTGGGCT 6153
Qy 6122 cctggagaatgaatggggctggaataatcatcaacttcaagatgttgaagaggaatacc 6181
Dh 6154 CCGGAGATTAATGAGGCTGGAATAATCATCACTTTCAAGATGTTTACAGGAGATACAC 6213
Qy 6182 tgtaccagaaggaatgtcttcccttaacaaaataglatcttaacaaatccatgaagt 6241
Dh 6214 TGTACCAGAGAGATGCTTCTTCAACAAAATAGTATCTTATCAACATCCATGAAAT 6273
Qy 6242 aactcagaacatgagtgctacgcctcagtttgaatgcatacagaagcttgaagggag 6301
Dh 6274 ACATCGAAGATGAGCTACTGCTCCTCAGTTTGATGSCATACAGACCTGTGCTGGAG 6333
Qy 6302 agaacagtggaatgtcttcttgccttggagagagccccaagaaaggttggcaagt 6361
Dh 6334 AGAAGACGTGATCTTCTTCCCTTTGAGAGAGAGTCCCAAGAAAGAGTTGGCAAGT 6393
Qy 6362 tggtagtgaggcagatccgaagaactgggctcgtgaaatgaatgaagaaatgaatgctgtaa 6421
Dh 6394 TGGTAGTGGGCGATTCGGAACCTGGGCTCTGAAGTATGAGAAATATGCTGTAA 6453
Qy 6422 ctatagtaggaagaaagaaagcgtcttaccagcaatggttgaatgggggctcc 6481
Dh 6454 CTATAGTGGAGCAACAAAGCAAGCTCTTACAGCCATGCTTTATGCGCGGCTCC 6513
Qy 6482 tggtagtcttctgatacccaacacaggaatgatacccaagcccggtgtcttgg 6541
Dh 6514 TGTGAGTCTTCTGATGAAACCAACAGGATGATCCCAAGCCCGGCTTTCTTGG 6573
Qy 6542 gaatttgccctaaagtgttcaagagaaggaatgaatgagtgcttaccatctaatat 6601
Dh 6574 GAATTTGCGCCCTTAAGTGTCTCAAGGAGGAGATCATAGTCTTACATCTATAGTAT 6633
Qy 6602 ggaagaatgtgaagcctcttgacactagaatggaatcatgataatgaaaggttcaagtg 6661
Dh 6634 GGAAGATGTGAAGCTTTTGCACCTAGATGGCAATCATGCTCAATGGAAGGTTCAAGTG 6693
Qy 6662 ccttgagagtgccagcatctaaataataggttggagaatgtataaataatgttaag 6721
Dh 6694 CCGTGGAGTGTCCAGCATTAATAAATAGTTGGAGATGTTATACAAATAGTGTAGC 6753
Qy 6722 aatgagaggttcaaccggagcctgaagcctgtccagagatcttcttgagcttccatcc 6781
Dh 6754 AATAGCAGGGTCCAAACCGGACCTGAAGCCTGTCCAGGATTTCTTTGACTGTGATTC 6813

Qy 6782 tggagtgcttctaaagagaacacccggaacatgctacaaataccagcttccatcttcat 6841
Dh 6814 TGGAAAGTCTTAAAGAGAAACCGGAACATGCTCATATACAGCTTCATTCAT 6873
Qy 6842 atctctctggccagatattcagatctctcccaagagaacaaagcagctccacataga 6901
Dh 6874 ATCTTCTGTGCGAGATATTCAGCATCTCTCCCAAGAGCAAAAAGCGATCCCATAGA 6933
Qy 6902 agactactctgttctcagaacaaacttgaccagaatgttgaacttgcgaagacca 6961
Dh 6934 AGACTACTCTGTTCTCAGACACACTTGACCAAGTATTTGTGAATTTGCCAAGACCA 6993
Qy 6962 aagtgatgagcaacttaagaacccctcaatlaacaaaaacagacagtagtggagct 7021
Dh 6994 AAGTATATATACCACTTAAAGACCTCTCATTTACAAAAAACGACAGATGAGGAGT 7053
Qy 7022 tgcagttccacatcttcttaccagatlgaaagatgaagaagctatgtatgaagat 7081
Dh 7054 TGCAGTCTCAGATCTTCTTACAGATGAGAAAGTAAAGAAAGCTATGTATGAAAT 7113
Qy 7082 cctgttcaacgggtgtgctgaaagtaagaagaaactagacttctcttcacacatgta 7141
Dh 7114 CCGTTCTATAGCGGGTGGCTGAAAGTAAAGGAACTAGACTTTCCTTGACCATGTA 7173
Qy 7142 agtgtgtggaagaagagccagaagtgatgtggaagaatgaactggaatgactact 7201
Dh 7174 AGTGTGTGGAGAAAGAGCCAGAAAGTATGTGGAAAGAAAGTAACTGGATGATGACT 7233
Qy 7202 galactatcaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 7261
Dh 7234 GATACTATTAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 7293
Qy 7262 tgccttgaactgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 7321
Dh 7294 TGCCCTTGTAGCTATGCTGTATGCTCTCAAGTGAAGAACTTGAATTTAGTTTAA 7353
Qy 7322 cctatacctatgtaaacatctatitgaagcccaatgagacataggttgaactcaac 7381
Dh 7354 CCTATACCTATGTAAGAACTATATGAGAACCAATGAGCATATGAGGTTGAACTCAC 7413
Qy 7382 ttt 7441
Dh 7414 TTTTGT 7473
Qy 7442 aatcagccagcagatitgatcaaatcaaatgaatgaatgaatgaatgaatgaatgaatgaat 7501
Dh 7474 AATCATGGCCAGCGATTATGATCAAAATCAAAAGTAAATGCACATCCTCATTCAGTAAG 7533
Qy 7502 ccatgcagatgcccagagagactgttcccggtgacacatccatgtgcaagtgagtg 7561
Dh 7534 CCATGCGATGCCAGAGAGACTGTTCGCGGTGACATCATGCTGCAATAGATGAGTGTG 7593
Qy 7562 ccaagatattatgtgccaggttctccagaagtgtgaagccatgtgtgtgtgtgtgtgtgt 7621
Dh 7594 CCAAGATTATGTCACAAAGTTTTCAGAAAGTTTGAAGCCACATGATGTGATGCTCA 7653
Qy 7622 ctttgtagaagctgtcgtcagagatctacaaatgaatgaatgaatgaatgaatgaatgaat 7681
Dh 7654 GTTGTGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7713
Qy 7682 tgcagtgctgtaacatcctgtctgtatctccctcgtataagctgtctgtgtgtgtgtgtgt 7741
Dh 7714 TGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7773
Qy 7742 aatgcaacaaaatgt 7801
Dh 7774 ACATGCAAAAAAATGTGGGT 7833
Qy 7802 tccatgtctgagccatgaggttcaacaggttcaacatccatgaagactcttaataactta 7861
Dh 7834 TCGTATGCTTGCAGGCATGTGGTGTGACAGGTCATCTTATGAGACTCTTAATATACTTA 7893

Db 10054 CAATAATGTCATCCCTTAATAANGTCTATTTCATTAAGATTAGTCTGTTATCC 10113
Qy 10082 ttcttataccctaagaatgaagctgttttgyctcttltgtlcaatcattgagccctatcc 10141
Db 10114 TTTCTATACCTTAAGATGAAGCTGTTTGTGCTCTTTGTCATCATTAAGCCCTCATCC 10173
Qy 10142 aagcaattgaagctgtctgtatgtgattatltttgcactgtgaatattctgtgaattga 10201
Db 10174 AAGCATTATACCTGCTCTGTATGAGATCTATTGTCATGCACTGAATATCTGAAATGCA 10233
Qy 10202 aaactgacaaaagtctcaacaagaattctaaatcaatcattcaataaagaanaa 10261
Db 10234 AACTGTGACAAAAGTTTCACACAGTTTCTAGTTAATCATTTTTCATTAAGGAAA 10293
Qy 10262 aagaaaaaaatttltatgtcaataacttataatgaaglatlaaagcatatttctat 10321
Db 10294 AAGAAAAAAATTTTGTATGTCAATTAATTAATGAATTAATAATCAATATTTCTAT 10353
Qy 10322 gtgtataataatgagtcacaaataaagctgtgacagctgtttaaataaataaataa 10381
Db 10354 GTTGTATATTAATGAGTCAAAAATTAAGCTGTGACAGTTCTGTAAATAAATAAATAA 10413
Qy 10382 aaaaaaaataaataaataaataaataaataaataaataaataaataaataaataa 10441
Db 10414 AA 10473
Qy 10442 a 10442
Db 10474 A 10474

RESULT 6
AX060898 10474 bp DNA linear PAT 22-JAN-2001
LOCUS AX060898 Sequence 7 from Patent WO0078971.
DEFINITION AX060898
ACCESSION AX060898
VERSION AX060898.1 GI:12406275
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Law, R.M., Wade, D., Oram, J.F. and Garvin, M.
TITLE Atp binding cassette transporter protein abci1 polypeptides
JOURNAL Patent: WO 0078971-A 7 28-DEC-2000;
CY THERAPEUTICS, INC. (US)
FEATURES
source location/Qualifiers
1..10474
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others
ORIGIN

Query Match 99.9%; Score 10429; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10436; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 214 CAATAATGTAAGATTAATGACACAGCCAGGCGTCCCTGCTGAGCTCTGCGCGCT 273
Qy 242 gcttccagggctccgagccacacgctgagcgctgctgagctgagagacatgagctgttg 301
Db 274 GCTTCCAGGGCTCCCGACGACACGCTGGGCGTGGGCTGAGGGAACATGGCTTGTG 333
Qy 302 gcccaagctgagctgtcgtctgtgaaagaacctcaacttcaagaagaacaaatgtca 361
Db 334 GCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTACCTTCAAGAAAGAACAAATGTCA 393
Qy 362 gcttactgtaagtgtgagcgtgctcattatctccctgactgactgtctgtgct 421
Db 394 GCTGTACTGGAAGGCGCTGCTTATTTATCTTCCTGATCCTGATCTCTGTGTCGGCT 453
Qy 422 gagctacccaccatagacaacatgtaatgtccatttccaaataaagccatgccctgc 481
Db 454 GAGTACCCACCTATGTAACAACATGAATGTGCAATTTCCAAATTAAGCCATGCCCTTGC 513
Qy 482 aggaacacttctgtggtctcagaggaatattctgtaatgccaacaacccctgttccgta 541
Db 514 AGGAACACTTCTTCTGCGTTCAAGGGATTAATCTGAATGCCAAGCCCTGTTCGCTTA 573
Qy 542 cccgactcctggggagctcccgaggtgtgtgaaacttcaacaatccatgtgtgctcg 601
Db 574 CCCGACTCCTGGGGAGCGCTCCCGAGTGTGGAATCTTAAACAAATCCATTTGTGCTCG 633
Qy 602 cctgtctcagatgtcggagagcttcttatacagccagaagaacccaagacgaaga 661
Db 634 CTTGTTCTCAGATGCTCGGAGGCTTCTTTATACAGCCAGAAAGACACACATGAAAGA 693
Qy 662 catgcaaaagttctgaaacattacagcagatacaagaatccagctcaaaactgaagct 721
Db 694 CATGGCAAAAGTTTGAAGACATTAACAGACATCAAGAAATCCAGCTCAAACTGAAGCT 753
Qy 722 tcaaatcttctgtgtgagacaatgaaccttctgtgttccatatacaaaccttctct 781
Db 754 TCAAAATTTCTGTTGGAACAAATGAACCTTCTGTGGTTCTATATACAACTCTCTCT 813
Qy 782 cccaagctactctgagcaagaatctgagagctgtatgtcattctccaaagatattt 841
Db 814 CCCAAAGTTACTGTGACCAAGATCTGAGGGCTGATGTCATTTCCCAAGGATATTTT 873
Qy 842 gcaaggtacacagttacatttgaacagctgtgtgcaatgataaatacaagaagatgat 901
Db 874 GCAAGGCTACCGATTGACATTTGACAAAGCTGTGCAATGATCAAAATGAGAAGATGAT 933
Qy 902 tcaactgtgtgagcaagaagttctgagctgtgtgtgcttaccaaagagaaactgtgtc 961
Db 934 TCAACTGTGTGACCAAGAGATTTCTGAGCTTTGTGGCTTACCAAGAGAAACTGGCTGC 993
Qy 962 agcagagcagttactcgttccaaatgacatccctgaagcccaalccctgagaacataa 1021
Db 994 AGCAGAGCAGTACTCTGTTCCATCATGACATCTGAAAGCCCAATCTGAGAACCTAAA 1053
Qy 1022 ctctacatctccctcccgagcaagaagctgtgtgtgaagcccaaaacatctgtcatag 1081
Db 1054 CTTCAATCTCTCTTCCAGCAGAGAGCTGTGCTAAGCCACAAAACATTTGCTCATAG 1113
Qy 1082 tcttggagctctggcccgagagctgttcaagcatgaaagctgtgaatgtgacatgcagaga 1141
Db 1114 TCTTGGAGACTGTGGCCAGAGACTGTTCAGCATGAAGAACTGTGATGACATGCGACAGA 1173
Qy 1142 gttatgttcttgaacatgtgaacagctccagctccaccacaatctacagagctgt 1201
Db 1174 GTGATGTTTGTGACCAAGTGAACAGCTCCAGCTCTCCACCAAACTTACAGAGCTGT 1233
Qy 1202 gtctgtatgtgtgtgagcatcccgagagagagagagagagatcaagtctcctaactg 1261
Db 1234 GTCTGTATTTGTTGTGGGCATCCGAGGAGAGGGGCTGAAGATCAAGTCTCTCAACTG 1293
Qy 1262 gttagagacaacatacaagccctcttggagagcaatgtgacatgtgaaagatgtcga 1321
Db 1294 GTATGAGACAACTACTACAAGCCCTTTTGGAGCAATGACATGAGAGATGCTGA 1353

QY 1322 aacctlcatgacactctcaactccttactctgaatgattgataaagatttgagatc 1381
Db 1354 AACCTTCTATGACAACTCTCAACTCCTTACTGCAATGATTTGATGAAGATTGGAGTC 1413
QY 1382 taatccctctcccgagctctcgtgnaagctctgaagccgctcgtcttggaagatcct 1441
Db 1414 TAGTCTCTTCCCGCAATATCTGGAAGAGCTGGAAGCCGCTGCTGTTGGGAAGATCT 1473
QY 1442 gtatacaactgacactcacaagccaaagcagtlcagtcgagtgtaacaagccttca 1501
Db 1474 GTATACACCTGACACCTCCACCAAGGAGGTCATGGCTGAGAGTAAACAGACCTTCCA 1533
QY 1502 ggaactgagctgctgctcagatctctgaagagcaatgaggaagaaactcagcccaagatctg 1561
Db 1534 GGAACCTGCTGCTGCTCATGATCTGGAAGGCAATGTCGAGGAATCTGAGCCCAAGATCTG 1593
QY 1562 gaccttcagtagaagacagccaaagaaatggaactctgctcggatgctgttgagaagagga 1621
Db 1594 GACCTTCATGAGACACAGCCAAAGAAATGACCTTGTCCGATCTGTGACAGCAGGGA 1653
QY 1622 caatgacactcttggaagacagcaatgagtgatgagatgagacagcccaagacatcgt 1681
Db 1654 CAATGACACACTTTTGGGAACAGCAGTTGATGCTTAGATTGGACAGCCCAAGACATCTGT 1713
QY 1682 ggcgttttggaagacagccaaagagagatgctcagctcagtaagtgtctgtgtaacatg 1741
Db 1714 GGCCTTTTGGCCCAAGCACCACAGAGATGTCCAGTCACTAATGTTCTGTATACCTG 1773
QY 1742 gagaagactcttcaagagactaacaagcaatccgagacatactcgtcttatgagatg 1801
Db 1774 GAGAGAAGCTTTCAACGAGACTAACCAGCAATCCGACCATATCTCCGTTTATGAGAG 1833
QY 1802 tgtcaacctggaagactgaagcccaatagcaacagaagctcgtgtcaatcaaatgcaat 1861
Db 1834 TGCAACCTGGAACCACTGAAACCCATACCAACAGAACTGCTGATCAACAACTGCAT 1893
QY 1862 ggaactgctgagtagaaggaagatctcgtgctgattgtgttcaactgagataatccag 1921
Db 1894 GGAAGCTGCTGATGAGAGAGAAAGTCTGGGCTGTGATTTGCTTCACTGGAATTTACTCCAG 1953
QY 1922 cagcatgagctgcccacatcagtaagtaacaagatccgaatggaatggaatggaatgga 1981
Db 1954 CACCATTTGAGCTGCCCCATCATGTCAAGTACAAGATCCCAATGGACATTCGAAATGTGGA 2013
QY 1982 gagaacaaataaatacaagatgagtgactgagacccctggtctcagctcagctccttga 2041
Db 2014 GAGGAAATTAATAATCAAGATGGGTACTGGGACCTGTGCTCGAGCTGAGACCCCTTTGA 2073
QY 2042 ggaacatgagctgctcgtggaagagctcgtcactctgcaagatgagtgaggaagcaat 2101
Db 2074 GGAACATGCGCTGAGCTGCGGGGGGCTTCGCTACTTGGGGATGTGGTGGAGACAGCAAT 2133
QY 2102 catcagagtgagtag 2161
Db 2134 CATTCAGAGTCTGAGAGGAGACCGAGAGAGAACTGTGTATATGAAACAGATGCCCTTA 2193
QY 2162 tccctgttactgtgatacgtatctctcgtgagtgatacagcagtgcaatgagcccttcat 2221
Db 2194 TCCCTGTATACGTTGATGATCTTTCTCGGGGTGATGAGCCGGTCAATGCCCTTCTAT 2253
QY 2222 gacgtgagcctgagatctcagtgagtgagtgatcaacaagagagacgtgtaagaagga 2281
Db 2254 GACGCTGAGCTGAGATTTACTAGTGTGTATCATCAAGGCAATCCGTATGAGAAAGA 2313
QY 2282 ggcacgagctgaagaagacatgagatcatgagcctggaacaagacatcctgtttag 2341
Db 2314 GGCAGAGCTGAAGAAGACATGCGATATAGGCTTGAGAACAGCATACCTGTGTTAG 2373
QY 2342 ctggttcatctagtagcctcaatctctctctctgtgagcagctgagctagtgatcact 2401
Db 2374 CTGCTTCAATAGTAGCCATTCCTCTTGTGAGCGCTGGCCGTAGTGGTCAATCCT 2433

QY 2402 gaagttagaanaacctgctccctacagtgatccagcgtggtgtgtgtcttctgtccgt 2461
Db 2434 GAAGTTAGAAACCTGCTGCCCTACAGTATGCCAGCTGGTGTGTCTTCTGCTCCGT 2493
QY 2462 gtttgcctgtagtgaacatccctgacgtgctccctgattagcaacatctctccagaagca 2521
Db 2494 GTTTCCTGTGGTGAACATCTGACAGTGTCTTCATATGACACTCTTCTCCAGAGCAA 2553
QY 2522 cctggaagcagcctgtggaagacatcacttaactgaactgaactgaactgaactga 2581
Db 2554 CTTGACAGCAGCTGTGAGGACATCATTTACTTACAGCTGATGCTGACGCTGCTG 2613
QY 2582 tgtgcatgagagactaactgagccttcaacatcaaatctctgtagcctgtgtctcc 2641
Db 2614 TGTGCTGATGAGAGCACTGAGGCTTACACTCAAGATCTTCCCTAGCCGTGCTCC 2673
QY 2642 tgtgcttctgt 2701
Db 2674 TGTGCTTGT 2733
QY 2702 gcaatgagacacactgtgtgagatcctgtgaggaagatgagctcaatccactc 2761
Db 2734 GCAGTGGGACAACTGTTTGAAGTCTCTGTGAGAGAGATGCTTCAATCTCACCACTTC 2793
QY 2762 gatcctcaatgagctgt 2821
Db 2794 GATCTCCATGATGCTGT 2853
QY 2822 tgtcttccagcag 2881
Db 2854 TGTCTTTCAGGCGCATGAGAGATTCAGAGCTCTGTGATTTTCTGTGACCAAGTCTTA 2913
QY 2882 ctggtttgag 2941
Db 2914 CTGCTTGTGCGAGGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2973
QY 2942 agaatctgagtagaag 3001
Db 2974 AGAATCTGCAATGAG 3033
QY 3002 gataaagcttcaag 3061
Db 3034 GGTAAAGTCTACAGAGATGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3093
QY 3062 tgaagccagatcaactcctctcctgtggaacaaatgagagagagagagagagagagag 3121
Db 3094 TGAAGGCCAAGTACCTCTTCTGCGGCACAAATGAGCGGGAGAGAGAGAGAGAGAG 3153
QY 3122 aatcctgacagagtggttctcccccagacctcggaacacagcctacatcctggaagagat 3181
Db 3154 AATCTTACCGGGTGTGTCTCCCGGAGACTGAGGACCGCTACATCTGGGAAAGACAT 3213
QY 3182 tgcctctgagtagaagacatcccgagagagagagagagagagagagagagagagagag 3241
Db 3214 TCGCTTGAAGATGAGCACTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3273
QY 3242 gtttgaatctgactgtggaag 3301
Db 3274 GTTTGACATCTGACTGTGCAAGAGACATCTGTGTATGATGCCCTTGAAGAGGCTTC 3333
QY 3302 tgaagaacagtgagagcag 3361
Db 3334 TGAGAAACAGTGAAGGCGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3393
QY 3362 caagctgaaag 3421
Db 3394 CAAGCTGAAG 3453
QY 3422 ctgagccttctgctgag 3481
Db 3454 CTGAGCTTGTGTGAGGAGATCTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3513
QY 3482 cccttactcccgag 3541

|||||
Db 3514 CCCTTACTCCGAGGGGAAATGAGAGCTGCTGTAATATCCGACAAAGCCGACCAT 3573
Oy 3542 taticctctacacacacacatgatgaagcggagcgtccctggggagcaagatgcatcat 3601
Db 3574 TATTTCTCTTACACACACATGATGATGAAGCGGAGCTCCGGGGAGACAGATGGCATCAT 3633
Oy 3602 ctcccatgggaagctgctgctgctgctgctccctgcttctggaagaacccgctgggaac 3661
Db 3634 CTCCCATGAGGAAGCTGTGCTGTGTGGGCTCCCTGTTTCTGAAGAACACACCTGGGAAC 3693
Oy 3662 aagctactacccgagccttgctgaagaagaatgtggaatccctccctcaagtctctgagaa 3721
Db 3694 AGGCTACTACTGACTTGTGTGAAGAAATGTGGAATCTCCCTCAGTTCCTGACAGAAA 3753
Oy 3722 cagtagtagactgctgctacccgaaaaaaggagagcagtgcttctcagagcagcttctga 3781
Db 3754 CAGTAGTAGCAGCTGTGTCTACTCTGAAAAAGAGAGACAGTGTCTCAAGACAGTTCGA 3813
Oy 3782 tctgtgctgggagagagacatgagagtagacagctgacacatcgatgctctgcatctc 3841
Db 3814 TGCTGGCTGGGACGACCATGAGAGTACACGCTGACCATGATGTCTTGCTATCTTC 3873
Oy 3842 caaccctacaggaagaacatgctgctgaagccgagctgctggaagacatagggacatgagct 3901
Db 3874 CAACCTCATCAGGAAGACATGTGTCTGAAGCCGCTGTGGAAGACATAGGCGCATGAGCT 3933
Oy 3902 gacctatgtgctgacatagaagctgctgaagagagagccttctggaactcttcataga 3961
Db 3934 GACCTATGTGCTCCCATATGAAAGCTCTTAAGGAGGAGGCTGTGTGAAGCTCTTTCATGA 3993
Oy 3962 gattgtgacagcctctcgaagccttgagcattctgaattatgcatctcgaagacagcct 4021
Db 3994 GATTGATGACCGGCTCTCAGACCTGGGCAATTTCTAATGATGATCTCAGAGACGACCT 4053
Oy 4022 ggaagaataatctcctaaggtgagcgaagaagatggggtggaatgctgagacccataga 4081
Db 4054 GGAAGAAATATTCCTCAAGGTGGCCGAAAGAGAGTGGGGTGTGATGTGAGACCTCAATG 4113
Oy 4082 taacttgcgaagcaagcaagcagcgagcctctcgaggcaagcagaagctgtcttgccc 4141
Db 4114 TACCTTGCAGCAAGAGAAACAGCGGCTTTCGGGGACAAACAGAGTGTCTTGGCCC 4173
Oy 4142 gtctacgaagatgctgctgctgctacccaatgatactctgacatagaccagaatccagaga 4201
Db 4174 GTTACCTGAAGATGATGCTCTGATCCAAATGATGTGATGATGACCCCAATCCAGAGA 4233
Oy 4202 gacagactgctcagtgagatgagatggaagggctctacccaggtggaagctggaact 4261
Db 4234 GACAGACTTGTCTCAGTGGATGATGATGCAAAAGGCTCTTACAGGTGAAAGCTGGAAC 4293
Oy 4262 taacacgaacaaagtgtgtgccccttgttggaagaagacatctaattgcccgaagggatg 4321
Db 4294 TACACACAAACAGTTTGTGGCCCTTGTGTGAGAGAGACTCTAATATGCCAGAGCGAGTGG 4353
Oy 4322 gaaaggaatttttgcataatgctgctgacagctgctgctgctgcaattgcccctgtgt 4381
Db 4354 GAAAGGATTTTTCCTCAGATGTGTGTGCGCAGCTGTGTGTGCGCATTCGCCCTTGTTGT 4413
Oy 4382 cagcctgactgctgacaccccttggcgaagtaccccaagcctggaactctcagccctgagatga 4441
Db 4414 CAGCCTGATGCTGACCCCTTGTGGCAAGTACCCAGGCTGGAACCTTACAGCCCTGGAGTGA 4473
Oy 4442 caaagaacagtaacatattgtcgaagcaatgatagtcctcgaagaaacaggaacccctggaact 4501
Db 4474 CAAGGAACAGTACATTTTGTCAAGCAATGATGTCTCTGAGAGACAGGGGAACCCCTGGAGCT 4533
Oy 4502 cttaaacgcccctcaacaaagccctgctcctggaacccgctgtaatggaaggaaccccaat 4561
Db 4534 CTTAAAGCCCTTCAACCAAAAGCCTTGCTTGGGAGCCCGCTGTATGGAAGAAACCCCAAT 4593
Oy 4562 cccagacagccctgcaagcaggaaggaagatggaacatgcccagttcccagac 4621
|||||

Db 4594 CCCAGACAGCCCTGCCAGGCGAGGGAGAGAGTGGACCACTGCCCCAGTCTCCAGAC 4653
Oy 4622 catatgacctcttccaagatgggaactggacaatgcaaaccttaccctgcatgca 4681
Db 4654 CATATGAGCCTCTTCCAGATGGGAACTGGACATGACAAACCTTACCTGCAATGCCA 4713
Oy 4682 gctgagcagcaaaaatccaagaagatgctgctgctgtgtctccccaaggaggagggct 4741
Db 4714 GTGTAGCAGCGCAAAATTCAGAAAGATGCTGCCCTGTGTGTGCCCAAGGGGAGGGCT 4773
Oy 4742 gctctctcacaaagaaaacaaacactgcaagatactcctcagagactgacgaagaaa 4801
Db 4774 GCCTCTCTCCAAAGAAAGAAACAACTGCAAGATATCTTCAAGGACCTGACGAGAAAA 4833
Oy 4802 cattcgatattctgtggaagcgtatgtgcagatcatagccaaagcttaagaacaa 4861
Db 4834 CATTTCCGATTTATCTGTGGAGAGCGTATGTGCATATCATACCAAAAGCTTAAAGAACAA 4893
Oy 4862 gatctgggtgaatgagtttaagttatgagctcttccctgggtgctcaagtaactcaagc 4921
Db 4894 GATCTGGGTGATGAGTTAGTATGGGCGCTTTCCTGGGTGTCAGTATCTCAAGC 4953
Oy 4922 acttctccgagtgtaagaagatgtaatgagcatcaaaaatgaagaacacccaaagct 4981
Db 4954 ACTTCTCCGAGTCAAGAGTTAATGATGATGCCATCAACAAATGAAGAACCTAAAGCT 5013
Oy 4982 ggcgaagacagctctgcagatcgatcttccaacagcttgggaagattatgacagact 5041
Db 5014 GGCCAAAGACATTTGTGCAGATGCATTTCTCAACAGCTTGGGAAGATTTATGACAGGACT 5073
Oy 5042 ggaacacgaagaataatgctcaaggtggttcaataaagaagcctggcaatgaatcagctc 5101
Db 5074 GGACACCAAGAAATATATGCAAGGTGTGTTCAATTAACAAAGGGCTGGCTGAATCAGCTC 5133
Oy 5102 ttctctgagatgcatcaacaatgcatctcccgagcccaactgcaaaaggagagaaccc 5161
Db 5134 TTTCTGATGATGATCAACAAATGCAATTCCTCGGGCCAACTGCAAAAGGAGAGAAACC 5193
Oy 5162 tagccatlatggaatctactgcttccaatcaatccctgaaatcccaagcagcagctctc 5221
Db 5194 TTAGCATTTATGAAATTACAGTTTCAATCAATCCCTGATCTCAACAAAGCAGCAGCTCTC 5253
Oy 5222 aagagtgctctctgatagacacaaatgaatgagtgatctctgtccatctgttcatcttgc 5281
Db 5254 AGAGGTGCTCGATGACCAATCAATGATGATCTTGTGTGCATCTGTGTGCATCTTGTGC 5313
Oy 5282 aatgtctctgctcccaagcagccttgcgtatctctgatactcgaagcgggtcgaagaaagc 5341
Db 5314 AATGTCTTGTCCGACGACGCTTGTGTCTGATCCAGAGGCGGTCAGCAAAAGC 5373
Oy 5342 aaaaacactgcaatcaatcagtgagatggaagcctgcaatctactgctgctctaaattgtc 5401
Db 5374 AAAACACCTGCAAGTTCAATGATGATGAGTGAAGCTGTCAATCTACTGGCTCTAAATTTGT 5433
Oy 5402 ctgggataatgcaatgaatgctgtccctgcaacactggtgcatatcatcttaactgtct 5461
Db 5434 CTGGGATATCTGCAATTAAGTTGCTTCCCTGCAACACTGGGCAATTAATATCTTATCTGCTT 5493
Oy 5462 ccaagcaagatcctatgtgtctcccaacaaatctgctgctgctgctagcccttcaacttgtc 5521
Db 5494 CCAAGCAAAAGTCTTATGTCTCTCCACCAAAATCTGCTGTGTGACGCTTCTACTTTTGTCT 5553
Oy 5522 gtaatggtgtaataacacactctcaatgtaaccagcctctcttgtgttcaagaatcccaag 5581
Db 5554 GTATGGGTGTGAATACACACCTCTCATATGACCAAGCTCTTGTGTGTCAAGATCCAG 5613
Oy 5582 cacagcctatgtgtgctcaacaggtgaaactcttcaatctgcatatgaaaggtggc 5641
Db 5614 CACAGCCTATGTGTCTCTACCAAGCGTGAACCTTTCATTTGACATTAAGCGAGGCTGGC 5673
Oy 5642 caacttggctgagagctgttcaacgacaataagctgaataataatcaatgatatctgaa 5701
Db 5674 CACCTTGTGTGAGCTGTTCACCGCAATTAAGCTGAATTAATATCAATGATATCTCTGAA 5733
|||||

QY 5702 gtccgtgtctcttgatctccacatcttctgctggaacgaggtcatcgatgtgaa 5761
|||||
Db 5734 gtccgtgtctcttgatctccacatcttctgctggaacgaggtcatcgatgtgaa 5793
|||||
QY 5762 aaaccgagcaatgctgagatgcttgaagaaggttgggaggaatcgcttctgtaacatt 5821
|||||
Db 5794 aaaccgagcaatgctgagatgcttgaagaaggttgggaggaatcgcttctgtaacatt 5853
|||||
QY 5822 atcttgggaacttggtggaacaaactcttcgcacatgagcgttgaagaaggttcttct 5881
|||||
Db 5854 atcttgggaacttggtggaacaaactcttcgcacatgagcgttgaagaaggttcttctt 5913
|||||
QY 5882 ccccatctatgcttctgataccagatcttcatcaagagcccaagcctgttaatgcaaa 5941
|||||
Db 5914 cctcatattactggttctgataccagatcttcatcaagagcccaagcctgttaatgcaaa 5973
|||||
QY 5942 gctatctcctctgataagatgaagatgtgagcggaagaagaagaatctcttga 6001
|||||
Db 5974 gctatctcctctgataagatgaagatgtgagcggaagaagaagaatctcttga 6033
|||||
QY 6002 tgggtgagagccgaatgacatcttgaataaacaagagatgacgaatataagaagaa 6061
|||||
Db 6034 tgggtgagagccgaatgacatcttgaataaacaagagatgacgaatataagaagaa 6093
|||||
QY 6062 ggcgaagcctgctgttgaagaagattggtgagcattcctcctgtgagtgcttgggct 6121
|||||
Db 6094 ggcgaagcctgctgttgaagaagattggtgagcattcctcctgtgagtgcttgggct 6153
|||||
QY 6122 ccttggaggttaatggggtggaataacatcaacttcaagaatgttaacagagatatacc 6181
|||||
Db 6154 ccttggaggttaatggggtggaataacatcaacttcaagaatgttaacagagatatacc 6213
|||||
QY 6182 tcttaccagaagagatgcttcttcttaacaaataagatcttcaacaacatcaatgaat 6241
|||||
Db 6214 tcttaccagaagagatgcttcttcttaacaaataagatcttcaacaacatcaatgaat 6273
|||||
QY 6242 acatcagaacatgaggtactgctcctcagtttgaatgacatcagagcgttgaagagag 6301
|||||
Db 6274 acatcagaacatgaggtactgctcctcagtttgaatgacatcagagcgttgaagagag 6333
|||||
QY 6302 aagaacgtgagagcttcttcttgaagagaggtcccaagaagaagaagttggaagag 6361
|||||
Db 6334 aagaacgtgagagcttcttcttgaagagaggtcccaagaagaagaagttggaagag 6393
|||||
QY 6362 tgggtgagtgagcgttgaagaactgagcgttgaagatgaagaagaataatgctgttaa 6421
|||||
Db 6394 tgggtgagtgagcgttgaagaactgagcgttgaagatgaagaagaataatgctgttaa 6453
|||||
QY 6422 ctatagtgagaggaacaaacgaagctctcaagacatgagcgttgaagcgtgagcctcc 6481
|||||
Db 6454 ctatagtgagaggaacaaacgaagctctcaagacatgagcgttgaagcgtgagcctcc 6513
|||||
QY 6482 tgggtgttcttctgataacccaacagagatgatacccaagaagcgtgagcgttctgtg 6541
|||||
Db 6514 tgggtgttcttctgataacccaacagagatgatacccaagaagcgtgagcgttctgtg 6573
|||||
QY 6542 gaattgtgacctgaagtgttgaagaagagagatcaagtagtgccttatacatcattat 6601
|||||
Db 6574 gaattgtgacctgaagtgttgaagaagagagatcaagtagtgccttatacatcattat 6633
|||||
QY 6602 ggaagaatgataagcttctgacatgataagatgataatgataatgataatgataatg 6661
|||||
Db 6634 ggaagaatgataagcttctgacatgataagatgataatgataatgataatgataatg 6693
|||||
QY 6662 ccttggcagtgatcagacatcttaaaaaataggttggagatgataatgataatgataatg 6721
|||||
Db 6694 ccttggcagtgatcagacatcttaaaaaataggttggagatgataatgataatgataatg 6753
|||||
QY 6722 aatggcaggtgcaaacaccgagacctggaagcctgctcagagattcttggacttgatctcc 6781
|||||
Db 6754 aatggcaggtgcaaacaccgagacctggaagcctgctcagagattcttggacttgatctcc 6813
|||||

QY 6782 tggaaagtgtcttaaaagaagaacccggagacatgataacatcagagttccattcttatt 6841
|||||
Db 6814 tggaaagtgtcttaaaagaagaacccggagacatgataacatcagagttccattcttatt 6873
|||||
QY 6842 atcttcttggccagatattcaagatccttcccaagaagaagaagaacgacatccataga 6901
|||||
Db 6874 atcttcttggccagatattcaagatccttcccaagaagaagaagaacgacatccataga 6933
|||||
QY 6902 agactactctgttctcagaacaacatctgacaaagtatttggacttgcgaagacca 6961
|||||
Db 6934 agactactctgttctcagaacaacatctgacaaagtatttggacttgcgaagacca 6993
|||||
QY 6962 aagtgatgatacacttaaaagacccctccttcaacaaaaacagaacagtagtgaagcgt 7021
|||||
Db 6994 aagtgatgatacacttaaaagacccctccttcaacaaaaacagaacagtagtgaagcgt 7053
|||||
QY 7022 tgcagtttccatccttcttcaagatgagaagtgaaagaagcctatgataagaat 7081
|||||
Db 7054 tgcagtttccatccttcttcaagatgagaagtgaaagaagcctatgataagaat 7113
|||||
QY 7082 cctgttcaatgaggttgggtgaagaatgaagaagacatgacttcttgcacatgta 7141
|||||
Db 7114 cctgttcaatgaggttgggtgaagaatgaagaagacatgacttcttgcacatgta 7173
|||||
QY 7142 agtgcttgggaagaagaagcgaagtgatgagtggaagaagtaaaactgatactgact 7201
|||||
Db 7174 agtgcttgggaagaagaagcgaagtgatgagtggaagaagtaaaactgatactgact 7233
|||||
QY 7202 gatatacttaatgacatgataatgataatgataatgataatgataatgataatgataatg 7261
|||||
Db 7234 gatatacttaatgacatgataatgataatgataatgataatgataatgataatgataatg 7293
|||||
QY 7262 tgccttgaagcctatgcttctgataagcttcaagtgaaagacttgaatttatttla 7321
|||||
Db 7294 tgccttgaagcctatgcttctgataagcttcaagtgaaagacttgaatttatttla 7353
|||||
QY 7322 cctataccatgtaagaactatattatgaaacccaatggaatgttggattgaactaac 7381
|||||
Db 7354 cctataccatgtaagaactatattatgaaacccaatggaatgttggattgaactaac 7413
|||||
QY 7382 ttttttttttttttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 7441
|||||
Db 7414 ttttttttttttttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 7473
|||||
QY 7442 aatcatgagcgaagatattatgatacaaaatgaagaatgaacatccatcactaaag 7501
|||||
Db 7474 aatcatgagcgaagatattatgatacaaaatgaagaatgaacatccatcactaaag 7533
|||||
QY 7502 ccatgcatgcccgaagagactgttcccggtgaacatccatctgtcgaatgaagtg 7561
|||||
Db 7534 ccatgcatgcccgaagagactgttcccggtgaacatccatctgtcgaatgaagtg 7593
|||||
QY 7562 ccagagttatgagtgccaaagtttccagaagaagttgaagacacatgagtgatcatg 7621
|||||
Db 7594 ccagagttatgagtgccaaagtttccagaagaagttgaagacacatgagtgatcatg 7653
|||||
QY 7622 ctttggtaagaactgtcttgcagagcttcatcaaatggaatataatgagtgagaagtg 7681
|||||
Db 7654 ctttggtaagaactgtcttgcagagcttcatcaaatggaatataatgagtgagaagtg 7713
|||||
QY 7682 tgcacatgcttgcataacatcctgcttgaatctcctctgaagcgttcttgcagagta 7741
|||||
Db 7714 tgcacatgcttgcataacatcctgcttgaatctcctctgaagcgttcttgcagagta 7773
|||||
QY 7742 acatgcaacaaaatgttgggtgtctcctgaagcgaagaactgttgcatttattatg 7801
|||||
Db 7774 acatgcaacaaaatgttgggtgtctcctgaagcgaagaactgttgcatttattatg 7833
|||||
QY 7802 tccatgcttgcagccatgagcttcaagagtgatccttcaatgagatcttaaatataacta 7861
|||||
Db 7834 tccatgcttgcagccatgagcttcaagagtgatccttcaatgagatcttaaatataacta 7893
|||||
QY 7862 gatccgtgtaagaagcaagaatcaacagccaactgtctgggctgcgaagcgtctgaagc 7921
|||||

|||||
 Db 7894 GATTCGTGTAAGGCAAGAAATCAACAGCCAACTGCTGGGCTGCAAGCTGCTGAAGC 7953
 Qy 7922 caggccatgaggatlaaagaatgctgctgctcaaacctagaagagctgctgccaattgctc 7981
 Db 7954 CAGGGCATGGGATTAAGAGATTTGCGTCAACCTAGGGAAAGCCCTGGCCATTTGTC 8013
 Qy 7982 ctgaactgctgctaacatggtacacgtcactcaagaagttatctgacacaaagtctatc 8041
 Db 8014 CTGACTGCTGCTAAGATGTAACACTGATCTCAAGATGTTATCTGACACAAAGTGTAT 8073
 Qy 8042 attctgagcttttgaatcaatctagaagaatgagaatgagttgttcttttgaacaaa 8101
 Db 8074 ATTTCGGCTTTTGAATTAATCTGAAAATGAAAAGATGGATGTATTTTGACAAAAA 8133
 Qy 8102 tgtttgacttttaagttaatttgaatlttaagttctatcaatgacttctgaactcctt 8161
 Db 8134 TGTGTGACTTTTAAATGTTATTTGGAATTTTAACTTCTATCAGTACCTTCTGAATCTT 8193
 Qy 8162 agaattgaccttttgaagaccttggtatagagagatgagccactgccccactattt 8221
 Db 8194 AGAATGGCTCTTTGTAAGACCTGTGGTATAGAGAGATGAGCCACTGCCCCACTATTT 8253
 Qy 8222 ttaatttctaatgaaagtttgacatacaagtcagtcagtagctgctagaagaagcaatgtag 8281
 Db 8254 TTAATTTCTATGTAAGTTTGACATACATGACTGACTGCTGAAAGCAATGTGATG 8313
 Qy 8282 gtcaagatctcatgacataatatttgaagttctctcaagatcttaagatcttaac 8341
 Db 8314 GTCAGATCTCAATGACATTAATTTGAGTTTCTTCAGATCAATTAAGATTAATCTTAAC 8373
 Qy 8342 tcaacttcaatcaataatlttttgaagtgtatgctgtagcagaagaatgagtagctac 8401
 Db 8374 TCCTTCATCAACAAATTTTGTGAGTATGCTGATAGCTGAAAGATATGTACGTAC 8433
 Qy 8402 gtaaaagacagagagataatgaagtcagtaacttccgtgctgcaatgctatcagctca 8461
 Db 8434 GTATAGACTAGAGAGATTAATTAAGTCTCAGTACACTTCTGTGCCATGTTATTAACCTCA 8493
 Qy 8462 ctggtttcaacaataatgctgctgctgctgctgtagagagccactgtacaataattgagca 8521
 Db 8494 CTGTGTACAAATATATGTTGCTGCTGTGAGAGGCCACTGTACAAATATTTGGGCA 8553
 Qy 8522 gaccttttttttttttaattgcaaatgcaaatgcaagaagaatgaaaggtcac 8581
 Db 8554 GCGTTTTTTTTTTTTTTTATTTGCAACATGCAAAAGCCAAAGAACTTAAGGGTCAAA 8613
 Qy 8582 agttaacaatgaatcttctcaacagggaaacagcctaagcttgaacaaactgtctgaacaa 8641
 Db 8614 AGTTTAAACAATGAATTTCTCAACAGGGAACAGCTAGCTGAAACCTTGCTGAACAAAC 8673
 Qy 8642 acaactgtgtttatagcatttagtaaccttcaataataggtcttgcaatattgatac 8701
 Db 8674 ACAACTGTGCTTTATGGCATTTATGATCTTCAATTAATTTGCTTCAAGATTAATTTGATAC 8733
 Qy 8702 cccatttaactctgacagctcacaatttttcatctcttcaactagtcagtaagaacaaat 8761
 Db 8734 CCCATTAAATCTGACAGCTCAAAATTTTTCATCTTTCATATCACTAGTCAAGAAAAATAT 8793
 Qy 8762 aaaaaacaactactcocalatgtagagcattttcagagtttctaaaccagttctattt 8821
 Db 8794 AAAAACAACAATTTCTCCATATGAGACATTTTTCAGAGTTTCTTAACCCAGCTCAATTT 8853
 Qy 8822 ttctagcagtaaacatttgaataaatactgcttcaactaatacttcttcaacttctt 8881
 Db 8854 TTTCTAGTCACTAAACATTTTGAATAATCTGTTTCACTAATTAATCTGTTAACTGCTTT 8913
 Qy 8882 gagagaaagaaaaataatgagagaaactatgttttgggaaagtcaagtgaacttctcaata 8941
 Db 8914 GAGGAAAGAAAAAATATGAGAACTATTTGTTGGGAAGTTCAAGTGAATTTTCAATA 8973
 Qy 8942 tcaatctaactcttcaacttttccaataattgaataataacgtcaaaaggtgtagac 9001
 |||||

Db 8974 TCATTACTAATCTTCTCAGCTTTTCCAAATTTGAATATTAACGCTAAAGGTATAGAC 9033
 Qy 9002 ttcaagattcaaatatcttctctataatltttaaattacagaatataataaacccac 9061
 Db 9034 TTTCAATTTCAAAATTAATCTTTCTATATTTTAAATTTACAGAAATTTATATACCCAC 9093
 Qy 9062 tgcgaaaaaagaaaaatgattgtttttagaagttlaaagtcacaaatattgattttaaata 9121
 Db 9094 TCGTCAAAAAACAAAAATATGATTTTACAGTTAAAGCAATATATGATTTAAATATA 9153
 Qy 9122 agtaagagagacatacttccaataactagtagatagtagccatgctgcaattcaagatctc 9181
 Db 9154 AGTATATAGGCAATATTTCCAAATTAATGATATGACATGCTGCAATTTACAGATCT 9213
 Qy 9182 tcaaaaatacagaatttataagaataatlttccctcaactaataatlttccaataaaga 9241
 Db 9214 TCAAAATATACGAATTTATAGAAATATTTCTCCATTTATATTTTCAAAATCAAGT 9273
 Qy 9242 tatgtttccctcaatttactaanaatcgtatcttaattctcaatlaagtaaatctatgag 9301
 Db 9274 TATGTTTCCATTTTACATTAATTCGAATTCATTTCTATATATATGTAATCTATGAG 9333
 Qy 9302 caactcctactcgtgctcctcgtatctcaagagccatattttaaataaagaagcact 9361
 Db 9334 CAACTCTTACTTCTGCTGCTCTGATTTCAAGGCCATATTTTAAATAATCAAAAGGCACT 9393
 Qy 9362 gtgaactatttgaagaagaacagacatltttaaataagatgaaagagcctctgaag 9421
 Db 9394 GTGAATCTTTTGAAGAAACACGACATTTTAATACAGATTGAAGAGACCTTCTGAAG 9453
 Qy 9422 ctgaagaacatctatagtlacalactcaatlaactgaatgtagtcttcaataatgaa 9481
 Db 9454 CTAGAAACAACTATAGTTATATACATCTTCAATTAATAGCTGATTAATTAATTAATA 9513
 Qy 9482 ttttttcaatttctcgtgtagaaactaaatgtgtgtagaagaatttttaccactcactc 9541
 Db 9514 TTTTTCATATTTTCTGTAACCTTAATTTGTGAGAAATTTTACCAACTCTATATCTC 9573
 Qy 9542 aatcaagaacaaattctgtatattccctgtagaagtagtaagtttgaagtttcagaatctc 9601
 Db 9574 AATCAAGCAAAATTTCTGTATATTTCCCTGTGAATGTATGATGTGAGTTCACAAAATTC 9633
 Qy 9602 tcaaaatagtgltcaaaaatlttctgcttltgcaatlttgggacactcagaacattat 9661
 Db 9634 TCAAAATAGCTGTCAAAATTTCTGTTTGCATCTTTGGAGACCTCAAAAACTTAT 9693
 Qy 9662 taacaactgtagatattgagaataacagaagaacaaataaagccctctataataatagcc 9721
 Db 9694 TTAACAATCTGTGAATTTGAGAAATTAACGAAGAAATTAATTAACCCCTTATTAATTAATGCC 9753
 Qy 9722 cagcaaatctatgtttaaacaacacacacactacactactglatlctatctgta 9781
 Db 9754 CAGCAACANTTCATTTTAAAAAACAACCAACCTCACACTGATTAATTCATTTCTGTA 9813
 Qy 9782 ctgaagaacaaatgcttggactatlaaagtgtgcaatcaatcaatctcactgtagtaa 9841
 Db 9814 CTGAAGCAAAATGCTTTGACTATTAATATGTTGACATCTTCACTTCACTGTAATGTA 9873
 Qy 9842 tcaattgactaaagcatttgcgtgttttctctcgtgtggnatataatcaagtaaaata 9901
 Db 9874 TCAATGACTAAAGCAATTTGCTGCTGTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9933
 Qy 9902 ttctcagaagacatgltgcaatgaactgaaccccttgatatttgaacataatttg 9961
 Db 9934 TTTTCCAAAGACCATGCTCATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9993
 Qy 9962 gaccttggtatatactactaataaataaagtaataatgagaaataatgcttaattctt 10021
 Db 9994 GACCTTGTATTAATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10053
 Qy 10022 caaatgtgcatcccccataaangtctatatttcaataaggaattagctgctatccc 10081
 Db 10054 CAAATGCTGATCCCTTAAANGTCTATTTCCATTAAGATTTACTGCTATATCC 10113
 |||||

QY	10082	ttctctacccttaagaatgaagctggttttggctctttgttcaatcttgccctaatcc	10141
Db	10114	ttcttttacccttaagatgaagctggttttggctctttgttcaatcttgccctaatcc	10173
QY	10142	aagcaattacgctgctgtaatggatcatatttgcactggaaatctcgagaattgca	10201
Db	10174	aagcaatttaccgctgctgtaatggatcatatttggcaactggaaatctcgagaattgca	10233
QY	10202	aaactagacaaagtttccaaacagatttctaagttaaatcatlctcatlaaaggaaaa	10261
Db	10234	aaactagacaaagtttccaaacagatttctaagttaaatcatlctcatlaaaggaaaa	10293
QY	10262	aagaaaaaaaatttggtagtcaataactttatatgaagtattaaatgcaattctat	10321
Db	10294	aagaaaaaaaatttggtagtcaataactttatatgaagtattaaatgcaattcttat	10353
QY	10322	gttgttaataatgagtcacaaataaagctgtgacagctgtgttataaaaaa	10381
Db	10354	gttgttaattattgacttcacaaatttaacgctgtgacagctgtgttataaaaaa	10413
QY	10382	aaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa	10441
Db	10414	aa	10473
QY	10442	a 10442	
Db	10474	A 10474	

	RESULT	7			
LOCUS	AX060900				
DEFINITION	AX060900	10474 bp	DNA	linear	PAT 22-JAN-2001
ACCESSION	Sequence	9 from Patent WO0078971.			
VERSION	AX060900				
KEYWORDS	AX060900.1	GI:12406276			
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 10474)				
AUTHORS	Lawn,R.M., Wade,D., O'rm,J.F. and Garvin,M.				
TITLE	ATP binding cassette transporter protein abci1 polypeptides				
JOURNAL	Patent: WO 0078971-A 9 28-DEC-2000;				
	CV THERAPEUTICS, INC. (US)				
FEATURES	Location/Qualifiers				
source	1..10474				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
BASE COUNT	2907 a	2304 c	2415 g	2844 t	4 others
ORIGIN					

Query Match	99.9%	Score 10429;	DB 6;	Length 10474;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 10436;	Conservative	0;	Mismatches 5;	Indels 0;
			Gaps	0;

QY	2	gcgaggaaacccgaagacgcgaagccgaacccctctctcccgagctgcgcaaggcaaggcggg	61
Db	34	GGCACGAGACCCCAAGAGCCGACCCACCCCTTCTCCCGGCGTGGGAGGGGACGGCGGG	93
QY	62	gagtcgcgcgcagcaacacagagccggtctctaaaggcgccttgcgcctgctttttccccgg	121
Db	94	GAGCTCGCGCGCACCAAGAGCCGGTTCTCAGGGCGCTTTGCTCTTGTTTTTCGCCGG	133
QY	122	tctcgtttctctccctctctccggaagcctgtcaagggtgaaggaaagaagacgcaaca	181
Db	154	TTCTGTTTTCTCCCTCTCTCCGGAAGGCTTGTCMAAGGGGTAGGAGAAAGACGCAACA	213
QY	182	caaaagtcggaaaacagttatgacacacacacgggcgcctctgctgtgagctctgcgcgc	241
Db	214	CAAAAGTCGAAACAGTTTATGACCAACACAGGGCGTCCTCGCTGTAGCTCTTGCGCGCT	273

QY	242	gacctcagaagctcccgagacacacgcgtgagcgcgtgctgaggaagacatgctgttg	301
Db	274	GCCTTCAGAGGCTCCCGAGCCACACGCGTGGCTGCTGAGGGAACTGGCTTGTTG	333
QY	302	gacctcagctgtaggtctgctgtctgtgtggaagaacctcaacttcaagaagaacaaacatgtca	361
Db	334	GCCTCAGCTGAGAGTGTGCTGTGTGGAAACCACTTCATTTGAGAAAGAACATGTGCA	393
QY	362	gcctttactggaagtagcctgagccctattatcttcgatacctgatacctcgttlcgct	421
Db	394	GCTGTTACTGGAAAGGGGCGCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTTGCGCT	453
QY	422	gaagctacccacccctatgacacacatgaaigtcatcttccaaataaagcccatgcccctcgc	481
Db	454	GAGCTACCCACCCCTATGAAACAATGAAATGCCATTTCCAAAATTAAGCCATGCCCTGCG	513
QY	482	aggaacactcctctgtgtgtcaggggataatctgtatgacccaacacccctgltccgtta	541
Db	514	AGGAACACTTCCTTGTTGGTTACAGGGATATCTGTAAAGCCCAACACCCCGTTTCCGTTA	573
QY	542	cccgagctcctgtagagctcccgagatgtgtgtggaaccttaacaatatctgtgctcg	601
Db	574	CCCGACTCCTGGGGAGGCTCCCGGAGTGTGTGGAACCTTTAACAAATCCATTGTGGCTCG	633
QY	602	cctgtttccagatgctcgtggaagctctttatcacgcagagaagacccagcatgaaga	661
Db	634	CCGTGTTTCAGATGCTCGGAGGCTCTTTTATACAGCCAAAGAACACCGATGAGAGA	693
QY	662	catgagcaaatgtctggaacattacacagcaatcaagaataacagctcaaaccttgaagt	721
Db	694	CATGGGCAAAAGTCTGAGAACATTACAGCAGATCAACAAATCCAGCTCAAACTTGAACT	753
QY	722	tcaagaattcctgltgagcaatgaacacctctcctggtlccctalatacaacctctctc	781
Db	754	TCGAATTTCCGTGGTGCAATGAAACCTTCTCGGTGCTTATCACAACTCTCTCT	813
QY	782	cccaagaactcactgtgagcaagatgctcgaagagctgatacttcacaaagtatlttt	841
Db	814	CCCAAAAGTCTACTGTGGCAAGATGCTGAGGGGCTGATGTATTTCTCACAAAGGATATTTT	873
QY	842	gcaagagctacagttacatttgaacaatctgtgcaatgataccaatcgaagaagatgat	901
Db	874	GCAAGGCTACCAAGTTACTATTGACAACTGTGCAATGATCAAAATTCAGAAAGATGAT	933
QY	902	tcaacttggtagccaagaagtttctgagcttltgtgctcctccaaagagaactgctgc	961
Db	934	TCGAATTTGGTACCAAGAGTTTGTGAGCTTGTGGCTTACCAAAAGAACTGGCTGCG	993
QY	962	agcagaagtagtactcgtcttccaacatgagacatccgtgaagccatccttagaacactaa	1021
Db	994	AGCAAGAGGAGTACTGTGTTCCAAATGAGACATCTGGAACCCAAATCTTAGAACACTTAA	1053
QY	1022	ctctacatctcccttcccgagcaagagagctgtgcttgaagcccaaaaaacatgtctgcatag	1081
Db	1054	CTCTACATCTCCCTTCCCGAGCAAGGAGCTGCGTGAAGCCACAAAACATTTGCTCATAG	1113
QY	1082	tcttggagacttggcccaagaagctgttcagcatggaagaagctgagtgatcatctgcagga	1141
Db	1114	TCCTTGGGACTGTGGCCCAAGGAGCTGTTCACATGAAACGCTGGAGTGAATCTCGACAGSA	1173
QY	1142	ggtatggttcttgacaagtltgaacagctcacgtcctccaccaatctacacagctgt	1201
Db	1174	GGTGATGTTTCTGACCAATGTGAACAGCTCCACTCTCTCACCCCAATTTACCAAGCTGT	1233
QY	1202	gtctcgtattgtctgtcgggcatcccgaggaggagggtcgaagatcaagltctcactag	1261
Db	1234	GTCCTGATTTGCTGCGGGCATCCCGAGGAGGGGGGCTGAAGATCAAGTCTCTCAACTG	1293
QY	1262	gtatgaagaacaacatacaaaagccctcttttgaaggaacatgacatctgggaagatgctga	1321
Db	1294	GTAATGAGACAACAATCAAAAGCCCTTTTGGAGGCAATGCACTGAGGAAGATGCTGGA	1353

1322 aacctctatgacaactctacactccttactgcatgalttgatgaaagaaatttgagtc 1381
1354 AACCTTATATGACACTGTACAACTCCTTACTGCAATGATTGATGAAGAAATTTGAGACT 1413
1382 tagtccctcttccgcatatcttgaaagctctgaaagccgtctgcttgaggaaagtcct 1441
1414 TAGTCTCTTTCCCGCATTTATCTGGAAAGCTCTGAAAGCCGCTGCTGCTTGGGAAATCT 1473
1442 gtaacacactgacactccagacagagcaggtctatgctgagtgagaaagaaacttcca 1501
1474 GTATACACTGTGACACTCCAGCCCAAGCAGAGTCAATGGCTGAGTGAAACAAACACTTCCA 1533
1502 ggaactgagctgctgctcactgcatctgaaagcaatgctgaggaagaaactcaagcccaagatctg 1561
1534 GGAACCTGGCTGTGTTCCATGATCTGAAAGGCAATGTGGGAACTCAGCCCAAGATCTG 1593
1562 gacctcaatgagaagaaagcaagaaatggacctgtccggaatgctgttgaaagcaagga 1621
1594 GACCTTCATGGAGAACAGCAAGAAATGGACCTTGTCCGATGCTGTGGACAGAGGA 1653
1622 caataacacacttttggaacacagcagttgagtgagtgagtgagagcccaagacatcgt 1681
1654 CAATGACCACTTTTGGAGACACAGTGGATGGCTTAAATTGGACAGCCCAAGACATCTGT 1713
1682 ggcgtttttgccaagcaccagagagatgctcagctccagtaaagttctgtgtacactg 1741
1714 GGGGTTTTGGCCAAAGCACCCAGAGATGTCCAGTCCATATATGGTGTCTGTATACACTG 1773
1742 gagaagaacttccaacgagacttaacaggaatccgagacatatctgcttcaatgagatg 1801
1774 GAGAGAGAGCTTTCACAGACACTAACCGAGCAATCCGACCATATCTCCGCTTATGAGAG 1833
1802 tctcaacactggaacaaactctgaaacccatagcaacagaagctctgctcatcaacagctcat 1861
1834 TGTCACCTGTGAACAACTGTGAACCCATACCAACAGAACTGTGCTCATCAACAAGTCCAT 1893
1862 ggaagctgctgagatgaaagaaagtlctgagctgtgtatgtgttcaactggaacttaactcag 1921
1894 GGAGCTGTGATGAGAGAAAGTTCTGGGCTGTATTGTTCACATGGAATTAATCTCAAG 1953
1922 cagcatgagctgagcccatcatgtaacatgtaacagatccgaatgagatctgaaatgtgga 1981
1954 CACCATTTGAGCTGCCCATCATCTCAATGTAACAAATCCAAATGAGCAATGACAAATGTGA 2013
1982 gaagaaataataaataaagagatgagtaactgagagacccctgttccctgagctgaaaccccttga 2041
2014 GAGGACAAATAAATAATCAAGATGGGTACTGGAGACCTGTGCTCGAGCTGACCCCTTTGA 2073
2042 ggaacatgaggtacgctctgagggagctctgacacttgcagagatgagtgagagcaggaat 2101
2074 GGACATGTGTGTACTGTGGGGGGCTTCGCTACTTTCAGAGATGTGTGTGAGAGGCAAT 2133
2102 catcaagagtgctgagcaggaacaggaagaagaactgtgtctatatacaacagatgacctca 2161
2134 CATCAAGGTGCTACGAGGACCGAGAGAAACTGTGTCTATATCAACAGATGCTCCCTTA 2193
2162 tccctgttactgagatgacactctctgagggatgagatgagcaggttcaatgcccccttcat 2221
2194 TCCCTGTATGATGATGACATCTTTCTGGGGGTGATGAGCGGTCAATGCCCTTTTCAAT 2253
2222 gacgctgagctgagatctactcaatgagctgtgatacatcaagagcaatcggtatgagaagaa 2281
2254 GAGCGTGGCTGTGATTTACTCACTGTGCTGTGATCATCAAGGCGATCGTGTATGAGAAGA 2313
2282 ggaacgctgaagaagacacatgagatcatgagcctgagcaacagacatactactggtttag 2341
2314 GGCACGGCTGAAGAGACATGCGGATCATGGGCTGTGAAACAGCATACTCTGGTTTAA 2373
2342 ctggttcaatagtagcctcatctctcttctgtgagcgtctgagctagtgatcct 2401
2374 CTGTTTCATATGATGCTCATCTCTCTTCTTGTGAGCGCTGCGCTGATGTGTCATCTCT 2433
2402 gaagttgaaacacctgctgctcactaagtgatcccaagcgtggtgttgttctctctgctgcgt 2461

2434 GAACTTGGAAACCTGTGCTTACAGATGATCCAGGCTGTGTTGTCTCTGTCCGT 2493
2462 gtttgcgtgtgacaactcctgacagtgcttccctgattagcacactcttccagagccaa 2521
2494 GTTTCCTGTGTGACAACTCTGCACTGCTTCTGATATGACAACTCTTCCAGAGCCAA 2553
2522 cctgacagcagcctgtgagggacatcactactcaacgctgtaactgacctagcctgtgt 2581
2554 CCTGACAGACCTGTGGGGCATCATCTTACCTTACCTTACTGCTCCACAGCTCCGTG 2613
2582 tgtgcatgagaaacacatgctgagcttcaacatcaaatcttgcctagcctgtgtctcc 2641
2614 TGTGACATGGAGGACATACGCTGCTTACACTCAAAATCTGCTAGCTGCTGTCTCC 2673
2642 tgtgacttctgtgtgtgctgtgagtaacttgcctcttctgagagcaggtgcatltgagt 2701
2674 TGTGCTTTTGTGGTTTGGCTGTGATCTTTGCCCTTTTGAAGAGCAGGCAATTTGAGT 2733
2702 gcaatgagacaacctgtttgagagctcctgtgaggaagatgagctcaatcacaacttc 2761
2734 GCAGTGGGCAACCTGTTTGAAGTCTGTGAGAGAGATGGCTTCAATCTCACACTTC 2793
2762 gatctcaatgagctgtgttgacaccttccctctataggggtgatacctggtacattgagc 2821
2794 GATCTCCATGATGCTGTTTGAACCTTCTCTATGGGGTGTATGACCTGTGATCATTTAGG 2853
2822 tgtcttccagagcaatgcaatctccagccctgtgtatcttccctgacacaaactcta 2881
2854 TGTCTTTCCAGGCCATGACGAATTTCCAGGCCCTGTGATTTTCTTCCACAAAGTCTTA 2913
2882 ctggttctgaggaagaaatgatagaagaagcaccctggttccaacagaagaagatgtc 2941
2914 CTGTTTGGCAGGAAATGATGAGAAAGAGCCACCTGTGTTCCAAACGAGAAAGATGTC 2973
2942 agaactctgcagtgagagagaaacccacttgaactgaggtgagtgatctcaactcaagcct 3001
2974 AGAAATCTGATGAGGAGGAAACCCACTTGAAGCTGGGCTGTGTCATTCCAGAACT 3033
3002 gataaagctcaacagatgagatgagatgagtgagctgagctgagccttggcaactgaaatttca 3061
3034 GSTAAAGTCTAACCGAGATGGGATGAAGTGGTGTGATGGCTGGGACATGAATTTTAA 3093
3062 tgaaggccaagatcaactccttccctgagcccaatagagcgggagaaagacacacatgtc 3121
3094 TGAGGCCACAGATCACCTCTTCTGGGCCAAATGAGACGGGGAGAGACACCATATGTC 3153
3122 aatcctgacgggtgtgttcccccgaactgaggaacgacctacactctgaggaagaagcat 3181
3154 AATCTTGACGGGTTGTTCCCCCGCACTCGGGCAACGCTACATCTGGGAAAGACAT 3213
3182 tgcctctgagatgagacacatccgagcaagacctgggggtctgtcccaagataagtgct 3241
3214 TCGCTCTGATGAGACACCATCCGGCAGAACCTGGGGGTGTGTCGCCAGCATAGTGCT 3273
3242 gtttgaatgtctgactgtctgagaaacacatctgtgttcatgtcccggttgaagggctctc 3301
3274 GTTTACATGTGCTGATGTCGAAACACATCTGTTCTATSCCGCTTGAAAGGGCTCTC 3333
3302 tgaagaacacgtgaaaggcagatgagacagatgagcctgtgagtgtgttgcatacaag 3361
3334 TAGAAGACCGTGAAGGCGGAGATGAGACAGATGGCCTGTGATGTTGGTTCATCAAG 3393
3362 caagctgaagaagcaaaacagcagctgtcaggttgaaatgcaagagaagaactatctgtgc 3421
3394 CAAGCTGAAACCAAAACCAAGCACCTGTCAAGTGAATGAGAGAAAGCATATCTGTGC 3453
3422 ctgtgacctgtgctggggatctaaaggtgtgcatcttgatataacccaagctgtgtgga 3481
3454 CTGTGGCTTTGTGGGGATCTTAAGTGTGTATTTGATGAAACCAACACTGCTGTGGA 3513
3482 ccttactcccgagggagataaggagctgctgtcgtgaataacagcaagccgacacat 3541

[illegible]

QY 5702 gtccgtgtctcttgatctctccacatttttgccttgagcagagagctcatcgtacatgtgtaa 5761
|||||
Db 5734 gttccgtgttttgatcttccacatttttgccttgagcagagagctcatcgtacatgtgtaa 5793
|||||
QY 5762 aaaccaggaatgtgtctgtatgccctggaaaagtttggggaataatcgcttttgcacacatt 5821
|||||
Db 5794 aaaccaggaatgtgtctgtatgccctggaaaagtttggggaataatcgcttttgcacacatt 5853
|||||
QY 5822 atcttgagactgtgtggaagaaacctcttcgcctatgagccgttgaaaggggtgtgtctt 5881
|||||
Db 5854 atcttgagactgtgtggaagaaacctcttcgcctatgagccgttgaaaggggtgtgtctt 5913
|||||
QY 5882 cctcatcgttcttgatcagtaacagattcttcatcagagccagacctgttaattgcaa 5941
|||||
Db 5914 cctcatcgttcttgatcagtaacagattcttcatcagagccagacctgttaattgcaa 5973
|||||
QY 5942 gttatctctctgaaatgtaagatgtaagatgtgagcgggaaaagaaagaaatcttga 6001
|||||
Db 5974 gttatctctctgaaatgtaagatgtaagatgtgagcgggaaaagaaagaaatcttga 6033
|||||
QY 6002 ttgttgagccagaaatgacatctttagaaatcaagagtttgcagaaatataatagaagaa 6061
|||||
Db 6034 ttgttgagccagaaatgacatctttagaaatcaagagtttgcagaaatataatagaagaa 6093
|||||
QY 6062 gcggaagcctgtcttgacagagattgcgtgagcaatccctccgtgtgagtttgagct 6121
|||||
Db 6094 gcggaagcctgtcttgacagagattgcgtgagcaatccctccgtgtgagtttgagct 6153
|||||
QY 6122 ccttgagagttatgaggtctggaanaatcaacttcaagaatgttatacagagaaatacac 6181
|||||
Db 6154 ccttgagagttatgaggtctggaanaatcaacttcaagaatgttatacagagaaatacac 6213
|||||
QY 6182 ttttaccagagagagatgtcttcttcaacaaaatagtaatcttatacaacatcagaaagt 6241
|||||
Db 6214 ttttaccagagagagatgtcttcttcaacaaaatagtaatcttatacaacatcagaaagt 6273
|||||
QY 6242 aaatcagaacatgaggtctactgacctcagtttgatgacatcaagaagctgttgacttgag 6301
|||||
Db 6274 aaatcagaacatgaggtctactgacctcagtttgatgacatcaagaagctgttgacttgag 6333
|||||
QY 6302 agaacacgtgagatgttcttgccttcttgagagagatcccaagaaagaaagtttgcaaggt 6361
|||||
Db 6334 agaacacgtgagatgttcttgccttcttgagagagatcccaagaaagaaagtttgcaaggt 6393
|||||
QY 6362 ttgttgagttgagatgttgcgaataatcggtcgttgaaatgtaagaaataatgtctgttaa 6421
|||||
Db 6394 ttgttgagttgagatgttgcgaataatcggtcgttgaaatgtaagaaataatgtctgttaa 6453
|||||
QY 6422 ctatagttgaggaacaacaacgcaagctctctacagcaatggttgcagcggccctcc 6481
|||||
Db 6454 ctatagttgaggaacaacaacgcaagctctctacagcaatggttgcagcggccctcc 6513
|||||
QY 6482 ttgtgtgttcttgatgtaacccaacgaagcatgtaatcccaaaagccggcggttctgtg 6541
|||||
Db 6514 ttgtgtgttcttgatgtaacccaacgaagcatgtaatcccaaaagccggcggttctgtg 6573
|||||
QY 6542 gaatttgccttaagatgtgttgcaagagagagatcagtaagtgcttaactcctcatagat 6601
|||||
Db 6574 gaatttgccttaagatgtgttgcaagagagagatcagtaagtgcttaactcctcatagat 6633
|||||
QY 6602 ggaagaatgtgaagcctcttgcactagaatggcaatcaatgtaatgaaatgaaagttcagtg 6661
|||||
Db 6634 ggaagaatgtgaagcctcttgcactagaatggcaatcaatgtaatgaaatgaaagttcagtg 6693
|||||
QY 6662 ccttgagagttgcagatccttaaaaaatagtttgagagatgttatcaaatgtgtgtacg 6721
|||||
Db 6694 ccttgagagttgcagatccttaaaaaatagtttgagagatgttatcaaatgtgtgtacg 6753
|||||
QY 6722 aatagcagagttgcaccccggaactgaaagcctgtcagagattcttcttgagcctgcattcc 6781
|||||
Db 6754 aatagcagagttgcaccccggaactgaaagcctgtcagagattcttcttgagcctgcattcc 6813
|||||
QY 6782 ttggaagtgttcttaaaagagaacacggaacatgctatacaatccagcttcatcttcat 6841
|||||

Db 6814 ttgaaagtgttcttaaaagagaacacccgaacatgcttcatctaccagcttccatcttcatt 6873
|||||
QY 6842 atctctcttgccagatatacagatcctctccagagcaaaaagcagctccacataga 6901
|||||
Db 6874 atctctcttgccagatatacagatcctctccagagcaaaaagcagctccacataga 6933
|||||
QY 6902 agactacccgttctctcagaacaacatcttgacaaagtatttgtaactttgcaagagca 6961
|||||
Db 6934 agactacccgttctctcagaacaacatcttgacaaagtatttgtaactttgcaagagca 6993
|||||
QY 7022 tgcagttctcacatcttcttctacagatgtaagaatgtaagaagctatgtatgaagat 7081
|||||
Db 7054 tgcagttctcacatcttcttctacagatgtaagaatgtaagaagctatgtatgaagat 7113
|||||
QY 7082 cctgttcaataggggtgtgtgtaagaagagagacttcttcttccacatgtga 7141
|||||
Db 7114 cctgttcaataggggtgtgtgtaagaagagagacttcttcttccacatgtga 7173
|||||
QY 7142 agtgtgtgtaagaag 7201
|||||
Db 7174 agtgtgtgtaagaag 7233
|||||
QY 7202 gatactatcaatgtaagatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaat 7261
|||||
Db 7234 gatactatcaatgtaagatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaat 7293
|||||
QY 7262 tgccttttgagctatgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7321
|||||
Db 7294 tgccttttgagctatgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7353
|||||
QY 7322 cctatacctatgtgaacatctatatagaacccaatgtaacatggttgaactcac 7381
|||||
Db 7354 cctatacctatgtgaacatctatatagaacccaatgtaacatggttgaactcac 7413
|||||
QY 7382 ttt 7441
|||||
Db 7414 ttt 7473
|||||
QY 7442 aatcagtcagcagatctatatagaacccaatgtaacatggttgaactcac 7501
|||||
Db 7474 aatcagtcagcagatctatatagaacccaatgtaacatggttgaactcac 7533
|||||
QY 7502 caatgcaatgccaag 7561
|||||
Db 7534 caatgcaatgccaag 7593
|||||
QY 7562 ccaagatttatgttgccaagtttttcaagaagttggaagccaatggtgtgtgtgtgt 7621
|||||
Db 7594 ccaagatttatgttgccaagtttttcaagaagttggaagccaatggtgtgtgtgtgt 7653
|||||
QY 7622 ctttttgaaagcgtctgtctgaagatctatcaaatgtaatcagttgacagaatg 7681
|||||
Db 7654 ctttttgaaagcgtctgtctgaagatctatcaaatgtaatcagttgacagaatg 7713
|||||
QY 7682 ttgcaatgctgt 7741
|||||
Db 7714 ttgcaatgctgt 7773
|||||
QY 7742 acatgcaacaaaatgt 7801
|||||
Db 7774 acatgcaacaaaatgt 7833
|||||
QY 7802 tccatagcttgcagacatggtgtctacaggttcaatccttatgagactcttaataacta 7861
|||||
Db 7834 tccatagcttgcagacatggtgtctacaggttcaatccttatgagactcttaataacta 7893
|||||
QY 7862 gatcctgttaagaggaagaatcaacagccaactgtgtgtgtgtgtgtgtgtgtgtgtgt 7921
|||||

Db	7894	GATCCTGGTAAAGAGCCAAAGATACAAAGCCAAACCTGCTGGGGCTGCAGACTGCTGAAGC	7953
Qy	7922	caaggcatlgygataaagagaatlgcgtltaaaactlaagggaagccctgtgccatttgc	7981
Db	7954	CAGGGCAATGGATTTAAAGAGATTTGGCGTTCAAAACCTAGGGAAGCCGTGTGCCATTTGTC	8013
Qy	7982	ctgactcttcgtctacactlgyaacctcgcacatcctaagaatglttactctgcacaaglytatt	8041
Db	8014	CTGACTGCTGCTAACATGAGTACACTGCTATCTCAAGATGTTATCTGCACACACTGTAAT	8073
Qy	8042	attctcgcttlttgaaatlaactagaanaatlgaaaagaatggagtlgtatatttggcaaaa	8101
Db	8074	ATTCTGGCTTTTGAATTTAATCTAGAAANATGAAAGATGGACCTTGTAATTTTGACAAA	8133
Qy	8102	tglttgcacttlttaatglttatttggaaatttlaagtcctatcagtgactcttgaactcct	8161
Db	8134	TGTTTGACTTTTAAAGTTAAAGTTAAAGTTTAAAGTTCTATCACTGACTGACTCTGAACTCT	8193
Qy	8162	agaatgcccctcttgytagaacccttgytlatagagagatgagccactgtccccccttct	8221
Db	8194	AGAAATGCCCTTTGTAGAAACCCGTGTATACAGAGATATGGCCACTGCCCACTATTT	8253
Qy	8222	ttatttctctatglaagtttgcacatacgaatcgaatgagctagtgagaaagcaatgylatg	8281
Db	8254	TTATTTTCTTATGTAAAGTTTGCAATATGCAATGCAATGACTAGTGGCTTAGAAGCAATGTATG	8313
Qy	8282	gtcaagatctcagacatlatatttggatttcttcttcaagatcattagataacttcaatc	8341
Db	8314	GTCAGAGTCTCATGACATTTATATTGAGTTCTTTCAGATCATTTTACGATATCTTTATCT	8373
Qy	8342	tcaactlcaatcaataatatttllgagtgatgctgatgctgaagaaagatgacgtac	8401
Db	8374	TCACTTCATCAATCAATATTTTGTGAGTATGCTGTACTGTAAACAGATATGACTTAC	8433
Qy	8402	gtatagactcaagagatataatgaatcagtaactctctgtgccatgltattcaagctca	8461
Db	8434	GTAATAAGACTAGAGAGATATTAAGTCTCACTACACTTCCGTGCCATGTAATTCAGCTCA	8493
Qy	8462	ctlggttlaaatalatagtgltgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	8521
Db	8494	CTGGTTTACAAATATATAGT	8553
Qy	8522	gaccttltt	8581
Db	8554	GCCTTT	8613
Qy	8582	agtltaacaatgaatcttctcaacagggaaacagactagcttgaanaactgtcgcgaaaac	8641
Db	8614	AGTTTAAACATGSAATTTCTTCAACAGGAAACAGTACGTTAAAACTTGCTGAAAAAC	8673
Qy	8642	acaaacttgtgttataggcatattgaactcctcaaatatttggcttgcagatalgtgatac	8701
Db	8674	ACAACTTGTGTTTATGSCATTTAGTACCTTCAAAATTAATTTGGCTTGCAGATATTGCATAC	8733
Qy	8702	ccaatlaaatctgacagctcacaatttctcaactctctcaactcagtgatlaaagaaatat	8761
Db	8734	CCCATTAATATGAGAGTGTCAAAATTTTTCATCTCTTCAATCACTAGTCAAGAAATATAT	8793
Qy	8762	aaaaacaacaactctccatatagagacatttctcagagtttctlaaccaggtctattt	8821
Db	8794	AAAAACAACAAATACTTCCATATGAGCAATTTTTCAGAGTTTCTTAACCCAGTCTTATTT	8853
Qy	8822	ttctagtagtaaacatttggataaanaacttcttaacttaacttaacttgaactgtctt	8881
Db	8854	TTCTAGTCACTTAACATTTTGTAAAAATGCTGTTTCACTATATCTTAACTGTTAACTGCTT	8913
Qy	8882	gaagagaaaagaaatalatagagaaactatglttgggagagttcaagttatcttcaata	8941
Db	8914	GAGAGAAAAAGAAATATAGAGAGAACTATTTGTTGGGAGAGTTCAAGATGATCTTTCAATA	8973
Qy	8942	tcattactaacactctctcaacttcttccaaatattgaatatataagctaaagtgtaagac	9001
Db	8974	TCATTACGTAACCTCTTCCACTTTTCCAAATTTTAAATATTAATTAACCTTAAAGCTGTAAAGAC	9033
Qy	9002	ttcaagttcaaatlaactcttctctatatttlttlaaatlaagaattlatataccac	9061
Db	9034	TTCAATTTCAAAATTAATCTTTTCTATATTTTAAATTTTAAAGATATTAATTAACCCAC	9093
Qy	9062	tgctgaanaagaaanaaatalgtatgttctagaagttlaagttlaaactatgtatttlaataata	9121
Db	9094	TGCTGAAAAAAGAAAAAATGATTTGTTTGAAGTTAAAGTCAATATGATTTTAAATATA	9153
Qy	9122	agtaataagagcatatttccaatctacagtgatataatgtgcattgttgaatttaagttatc	9181
Db	9154	AGTATGAGGCAATATTTCATATACATAGATATGATGCAATGCTTGCAATTTTACAGTATCT	9213
Qy	9182	tcaaaaaatacgaattlatagaatatttcccccattiaaialtttcaaaatcaaatg	9241
Db	9214	TCAAAAATPACGAATTTATAGAAATATTTGTCCTCATTTAATTTTTCAAAATCAAAAGT	9273
Qy	9242	tatggttctctcaatttctactaaatcgtatctcaattcttcaatlatagtaactatagac	9301
Db	9274	TATGTTTCCATATTTTTACTTAAATTCGATATTCATATTCATATATGTAATCTATAGAC	9333
Qy	9302	caactccttaactgctgtctccctcgtatctcaagagcataltttlaaanaataaagacact	9361
Db	9334	CAACTCCTTACTTGCTGGTTCCCTGATTTTCAAGGCAATTTTAAAAATCAAAAGGCACT	9393
Qy	9362	gtgaactatttggagaanaacagacatlttlaacagattlgaaagagacctcttctgaag	9421
Db	9394	GTAACATTTTAAAGAAAAACAGACATTTTAAATACAGATTTGAAGAAAGACCTCTTGAG	9453
Qy	9422	ctagaanaacatlatagttlaaactcttcaatcttgaatctgtgtaacttlttaanaatgtaa	9481
Db	9454	CTGAAACAAATCTATATATTAATTAATCTTCAATTAATCTGTTATCTTTTAAATATGTA	9513
Qy	9482	tttttcaacttctcgt	9541
Db	9514	TTTTTACATTTTCCGTGTGAACCTAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	9573
Qy	9542	aatcaagaaaatttctgatalatccctgtggaaatgtaactatgtgaatttgaatc	9601
Db	9574	AATCAAGCAAAATTTCTGATTTATTCCTGTGGAATGACTATGTGAATTCAGAAATTC	9633
Qy	9602	tcaaaatagctgttcaaaaatttctcgttltgatacttlttgagacacctcagaaaactat	9661
Db	9634	TCAAAATAGCTGTCAAAAATTTCTGCTTTTGATCTTTTGGACACTCGAAGAAACTTAT	9693
Qy	9662	taacaacttgtatataatgagaataacagaaanaataaagacccctatacaataatgcc	9721
Db	9694	TAAACACTGTAATATGAGAAATACGAAGAAATATATAAGCCCTTATATACATTAATATGC	9753
Qy	9722	cagcaaatlcatgtttaaanaacaaacaaactcaactcaactgtatattcaatctgtga	9781
Db	9754	CAGCAATATCATTTGTAAAAAAACAAACCAAACTCACTACGTAATTTCTATATCTGTA	9813
Qy	9782	ctgaaagcaaatgcttlttgaactatataatgltgacaatcattcaactcaactglatagtaa	9841
Db	9814	CTGAAAG	

QY	10082	tttataacctagaatgaacgtctttttgtgcctttgttcacatcatgtggccctcatcc	10141
Db	10114	ttcttatncccttaagatgaactgtttttgtgctttttgttcacatcatgtggccctcatcc	10173
QY	10142	aagaccttaagcgtctcgttaatgysgatctattttgacctgysaatatcysgaatgca	10201
Db	10174	AAGACCTTATGAGCTGTCTGTATGGAGCTATTTTGTGACATGGAATATCTGAAATTGCA	10233
QY	10202	aaactagacaaaagtttcacacacagatctcgaagttaaatcaattttcaattaaagga	10261
Db	10234	AAACTAGACAAAAGTTTCACACACAGATTTCTTACGTTAAATATTTTCATTTAAAGCA	10293
QY	10262	aagaaaaaaaattttgtatgtcacaacttatatgaagatlttaaatgcatatttcac	10321
Db	10294	AAGAAAAAAAATTTTGTATGTCAATACCTTTATATGAGCTTTTAAATTCATATTTCTAT	10353
QY	10322	gtctgataataatgagtcacacaaataaagcgtctgacagttcgtttaaaaaa	10381
Db	10354	GTTGTAAATATATATGATGCTCACAAATTAAGCTGTGACAGTCTGTTAAAAA	10413
QY	10382	aaa	10441
Db	10414	AAA	10473
QY	10442	a	10442
Db	10474	A	10474
RESULT	8		
LOCUS	AX127831	9854 bp	DNA
DEFINITION	Sequence 70 from Patent WO0130848.		Linear
ACCESSION	AX127831		
VERSION	AX127831.1	GI:14134478	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 9854)		
	Deneffe,P., Rosler-Montus,M.F., Arnold-Reguigne,I., Prades,C.,		
	Naudin,L., Lemouine,C., Duvergier,N., Jaye,M., Searfoss,G.H.,		
	Remaley,A., Brewer,H.B. and Dean,M.		
TITLE	Nucleic acids of the human abcl gene and their therapeutic and		
JOURNAL	diagnostic application		
	Patent: WO 0130848-A 70 03-MAY-2001;		
FEATURES	Aventis Pharma S.A. (FR)		
source	Location/Qualifiers		
	1..9854		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
BASE COUNT	2665 a 2219 c 2334 g 2635 t	1 others	
ORIGIN			
Query Match	93.6%;	Score 9777.8;	DB 6; Length 9854;
Best Local Similarity	99.8%;	Pred. No. 0;	
Matches 9810; Conservative	0;	Mismatches 18;	Indels 2; Gaps 2
QY	1	ggccggaccgcgacgagccgagccgaccccttctcccgagctcgagggcagggcgag	60
Db	9	GGCGGGGACCCCGAGCCGAGCCGACCCCTTCTCCCGGGCTGGCGGAGGGGCGG	68
QY	61	ggagctcgcgcgaaccaacagagccgagttctcagggcgcttgctccctgtttttcccg	120
Db	69	GGAGCTCCGCGACACAGAGCGGGTTCTCAGGGGCGTTGTGCTTGTGTTTTCCCG	128
QY	121	gtctgttttctccctctccggaagcgtgtcgaagggttagagaaagagacgcaaac	180
Db	129	GTTCTGTTTCTCCCTCTCCGGAAGCGTTGTCGAAGGGGTAGAGAAAGACGCAAC	188
QY	181	acaaaagtgaacacgttaatgaccagccagcgagcggtccctgctgtgagcttgccgcg	240

Db	189	ACAAATATGGAAACAGTTAATGACACAGCCAC - GGCCTCCTCGCTGTGAGCTCTGGCGGC	247
QY	241	tgccttcaggagctcccgagcccaacgctcgggcgctgctgcgtctggaggaatggttgtt	300
Db	248	TGCCTTCACAGGGCTCCCGAGCCACACAGCTGGGGGTGGCTGTGAGGAACTGGCTTGTT	307
QY	301	ggctcagcgtgaggttgcctgcgttggaanaaacctcaacttcagagaagaacaaacatgctc	360
Db	308	GGCTTCAGCTGAGGTTGCTCTCTGTGSAANAACCTCACTTTCAGAAAGAAACAAACATGTC	367
QY	361	agctgttactgtgaagtgccctgagcctctatlatctccctgatccgtatctctgttcgcg	420
Db	368	AGCTGTGCTGTGAAGTGGCCTGCGCTCTATTATCTTCCTGATCTGATCTCTGTTGGCC	427
QY	421	tgaagtaaccaacctatgaaacaacatgaaatgacatttccaaataaagccagtcgacctg	480
Db	428	TGAGACTCCACCACTATGAACAACAAGAAATGCCATTTCCTCAATAATMAACCATGCGCTCG	487
QY	481	caggaaacacttcccttggtgttcagaggatattctgtaatgccaacaacccctgattccgtt	540
Db	488	CAGGAACACTTCCTTGGGTTCAAGGGATTATCTGTAAATGCCAACACACCCCTGTTCCGTT	547
QY	541	accgcactccctgaggaggtcccgagatgtgttgaaacttlaacaalcatgttgctc	600
Db	548	ACCCGACTCCTGGGGAGGCTCCCGAGTGTGTGSAAACTTTCATMAAAATCCATTTCTGCTC	607
QY	601	ggctgttctcagaatgctcggagctctcttctaagcccgagaagaacccagcatlagg	660
Db	608	GCTGTGTTCTGAGATGCTGGAGGCTTCTTTATACAGCCAGAAACACACGACTGAGGG	667
QY	661	acatgcgcgaaggtctbagaacatlaacagcaatcaagaalacagcctcaaaccttgaagc	720
Db	668	ACATTCGCCAAAGTCTCTGAGAACATTTACAGAGATCAAGAAATCCAGCTCAAACTTGAAGC	727
QY	721	tccaagatttccctggttggaacatgaaacctctctggtgttcctatatcaaacctctctc	780
Db	728	TTCAAGATTTCCTGCTGTGAGAACATGAACCTTCTCTGGTTCCTGTATACAACTCTCTC	787
QY	781	tcccaagttctacgtgtggaagaatgcttgaaggctgtatctgaattccacaaggtattt	840
Db	788	TCCCAAACTCTACTGCTGTGACAAAGATGCTGAGGCTGTATCTCATTTCTCCAAAGTATTTT	847
QY	841	tgcgaagcttacaatltacattltgacaagtctgtagcaatgtagcaacaaatcagaagaatga	900
Db	848	TGCNAAGCTACCACTTACATTTTGCAAGAAGTCTGTGCAATGATATCAAAATCAGAGAGATGA	907
QY	901	ttcaactctgtgacccaagaagttcttgaagcttctgagcctacccaaggagaactgctg	960
Db	908	TTCAACTGTTGTAACCAAGAAATTTCTGAGCTTGTGTGCTTACCAAGGGGNAACCTGCTG	967
QY	961	cagcagagcgaatctcgttcccaacatgaaactcctgaagccaactccctggaacacaa	1020
Db	968	CAGCAGACCGAGTACTTCGTTCCAAATGACATCTGGAAGCCATCTCGAAGAACACTTAA	1027
QY	1021	actctaacctcccttcccgagaagaaggttgctgaagccaaacaaacatctgctgcta	1080
Db	1028	ACTCTACTCTTCCTCTCCCGACGACAGAGCTGGCCGCAAGCCAAACAAATCTGCTGATA	1087
QY	1081	gctcttggaactctgcccgaagagctgtcttcagcaatggaagcttgaagtgcacatgcaag	1140
Db	1088	GTCTTGGGAGCTCTGGCCAGSAGCTGTTCAAGCATGAAGAAGCTGAGATGCATGACGACAGG	1147
QY	1141	agggtatgcttctgcaccaagtgtgaacagctccagctccctccacccaactatccaggtg	1200
Db	1148	AGGTATGTTCTTGACCAATGTGAACAGCTCCAGCTCTCCACCAAAATCTACAGGCTG	1207
QY	1201	tctctcgtatgtctcggcggaatcccgaaaggaggggctgtaagatcaagctcttccaact	1260
Db	1208	TCTCTCGTATGTTGCTCGCGGATCTCCAGGAGGAGGGGCTGAAAGATCAAGTCTCTCAACT	1267
QY	1261	ggatagagacaacaactacaaagccctcttggagagcaatgacctgagaagatgtgct	1320

Db 1268 GGTATGAGCAAACTACAAAGCCCTTTGGAGGCAATGGCACTGAGGAAGATGCTG 1327
QY 1321 aaacctctatgacaactctacactctactgcaatgattgataagaatcttgagat 1380
Db 1328 AAACCTTCTATGACAACCTACAACTCCTTACGCAATGATTGATGAAAGATTGTGGAGT 1387
QY 1381 ctgctctctctccgcattatctgaaagctctgaaagccgctgctctgttggaagatcc 1440
Db 1388 CTATGCTCTTTCCCGATTTATCTGAAACCTCTGAAGCCGCTGCTGTTGGGAAGATCC 1447
QY 1441 tgatataacctgacaactccagcacaagagatgcatgctgagtgatgaaagaaccttcc 1500
Db 1448 TGATATACCTGACACTCCAGCCACAAGAGAGTCAATGGCTGAGGTGAACAAACCTTCC 1507
QY 1501 aggaactgctgtgtccatgcatctgaaagcaatgtggaagaaactcaagcccaagatct 1560
Db 1508 AGGAACCTGGCTGTGTTCCATGATCTGGAAGGCAATGTGGAGGAACACACCCCAAGATCT 1567
QY 1561 ggaacctctatgagaacacgcaagaaatgacctgtccgagatgctgttggaagagag 1620
Db 1568 GGACCTTCAATGAGAACAGCCAAAGAAATGACCTTGTCCGAGATGCTGTGACACAGAGG 1627
QY 1621 acaatgacctcttttggaacagcagctgagatgcttgaattgagacagcccaagacatcg 1680
Db 1628 ACAATGACCACTTTTGGGAACACAGATTGGATGGCTTACATTGCAAGCCCAAGACATCG 1687
QY 1681 tggcgttttttgccaagcaccacagagagatgtccagtcagtaatgctctgttacaact 1740
Db 1688 TGGCGTTTGTGGCCAAAGACCCAGAGATGTCCAGTCAGTAATGCTTGTGTACACT 1747
QY 1741 ggaagaaagcttccaacgaactcaacagcaatccgagcaatctgcttcaatgagat 1800
Db 1748 GGAGAGAGAGTTTCAACGAGACATAACAGCAATCCGAGCAATCTGCTTCAATGAGAT 1807
QY 1801 gttcaactctgaacaaagctagaacccaatagcaacagaatgtctgctcatcaacaagtcca 1860
Db 1808 GTGTCAACCTGAAACAAGCTAGAACCCATAGCAACAGAACTGTGGCTCATCAACAAGTCCA 1867
QY 1861 tggagctgtgagatgagaagaaattctgagctgtgattgttctcaatgaaatctcaag 1920
Db 1868 TGGAGCTGTGATGAGAGAACTTCTGGGCTGTGATTTGTGTTCACTGAAATTAATCCAG 1927
QY 1921 gcaagcatgagctgtcccaatcatgtcaatgataagaatccgaaatggacatctgaaatgtgg 1980
Db 1928 GCGACCTTATGAGCTGCCCCATCATGTCAATACAGATCCGAATGAGCAATGCAATGTGG 1987
QY 1981 aagagacaataaaatcaagagatgtgacttgggaacctgtgctcgaagtggaccctttg 2040
Db 1988 AGAGGCAAAATAAATCAAGATGGTACTGGGACCTGTGCTGAGCTGACCCCTTTG 2047
QY 2041 aagacatcgatgactgtgagggggcttgcctacttgaagaaatgtgtgagacagcaaa 2100
Db 2048 AGGACATGCGGTACGCTGTGGGGGGGCTTGCTACTTGCAGAGATGTGGGAGAGCA 2107
QY 2101 tcatcaggtgtgtaagggcacccgagaagaacatggtgtctatctgaacagatgtccct 2160
Db 2108 TCAATCAGGCTGCTGACGGGACCCGAGAAATACTGTCTATATGCAACAGATGCCCT 2167
QY 2161 atccctgttaagctgtatgacatcttctgaggtgtgataagacggatcaatgcccccttca 2220
Db 2168 ATCCCTGTAGCTGATGATCATCTTCTGCGGGTATGAGCGCGGTCANTGCCCTCTTCA 2227
QY 2221 tgaagctgtgctggatctactcaatgagtgctgtgataatcaagggacatgtatgaaag 2280
Db 2228 TGACGCTGGCTGTGATTTAATCAGTGGCTGTGATCATCAAGGGCATCGTGTATGAGAGG 2287
QY 2281 aggaacggtgtaaaagagacatcgagatgataagggcttggaacaaagcactactctgttta 2340
Db 2288 AGGACAGGCTGAAGAACACATGCGGATCATGGGCTTGACAAACAGCATCTCTGTTTA 2347
QY 2341 gctgttcaattagtagcctcatctctctgtgagcgttggcctgtatgtgtcatcc 2400
Db 2348 GCTGCTTCAATATGATGCTCATCTCTCTTCTGTGAGCGCTGGCTGTATGATGATCC 2407

QY 2401 tgaagttgaaacactgtctgcctcaagtgatcccaagtggtgtgtctctctgcg 2460
Db 2408 TGAAGTTAGAAACCTGCTGCCCTTACAGTGAATCCAGCGTGTGTGTCTCTGTCG 2467
QY 2461 tgttgcctgtgtgacaalccctgcagtgctctcctgattgaacacactctctccagaagca 2520
Db 2468 TGTGTGCTGTGGTACATCTCGCAGTCTTCGTGATTAGACACTCTTCCAGAGCA 2527
QY 2521 accbgaagcagcctgtgtggggcatctactcaatcaagctgttactgcctcaagctctgt 2580
Db 2528 ACTGGCAGACCTGTGGGGCATCATCTTACGTGTACTCTCCCTACGCTCTGT 2587
QY 2581 gttgtgcaatggcagactacg tgggtctcaacactcaagatctctgtagcctgtctc 2640
Db 2588 GTGTGGCATGCGAGACTACGTGGGCTTCAACATCAAGATCTTGATAGCCTGTGTCTC 2647
QY 2641 ctgtggtcttgggttggctgtgagtaacttgccttcttgaagagcagggcatgtgag 2700
Db 2648 CTGTGGCTTTTGGGTTTGGCTGTGAGTAATTTGCCCTTTTGAAGAGACAGGCAATGGAG 2707
QY 2701 tgcagttggaacactgtttgaagctctgtgagaagatgagcttcaatccaaact 2760
Db 2708 TGCAATGGGAACACTGTTTGAAGTCTCTGTGAGGAAGATGCTTAATCTCAACACTT 2767
QY 2761 cgaatccatgatactgttllgacacctctactatggtgtatgatacctgttataatgag 2820
Db 2768 CGTCTCCATGATGCTGTGTGACACTTCCCTATGTGGGGTATGACTGTGATATTAGG 2827
QY 2821 ctgtcttccagagcagatgagaaatcccaagccctgttcttcttgaacaaagtct 2880
Db 2828 CTGTCTTTCAGGCGCAGTACGAAATCCAGGCTCTGTGATTTTCTTGAACCAAGTCT 2887
QY 2881 actgttgtgagaaagtatgataagaagccacccctgttctccaaacagaagaatgt 2940
Db 2888 ACTGTTTGGAGAAAGTATGAGAAGGCCACCTGTGTTCAACCAAGAGATAT 2947
QY 2941 cagaatctgataagagagagaaacccaacttgaagctgtggcgtgtccatcaagacc 3000
Db 2948 CAGAAATCTGATGAGAGAGAACCCACCACTTGAAGCTGGGGGTGTCTCATTCAGAAC 3007
QY 3001 tgttaaaagtctaacaggatgagatgagaatgtgtgtctgataagccctgtgacatgtttc 3060
Db 3008 TGTAAAAAGTCTACCGAGATGGATGAAAGGAGGCTGTGATGGCTGGGCACTGAATTTT 3067
QY 3061 atgagggccaagatcact 3120
Db 3068 ATGAGGGCCAGATCACTCTCTCTGAGCCACAAATGAGAGCGGGAAGAGACACCATGT 3127
QY 3121 caatctgaacgggtgtgttcccccagcctcgggcaacggcctcaatctcttggaaaagaca 3180
Db 3128 CAATCTGACCGGGTGTTCCTCCCGGACCTCGGAGACCCGCTACATCTGCGGAAAAGACA 3187
QY 3181 ttgcctctgagatgagacacatccggcagaaactgtgggtgtgttctcccaagataatgttc 3240
Db 3188 TTGCTCTGAGATGAGACCATCCGGCAGAACCTGGGGGTGTGTCTCCACGATAAAGTGTG 3247
QY 3241 tgttgaatgctgtgactgtgtgaagaacacatctgtgttctatgcccgttgaagaggtctc 3300
Db 3248 TGTTTGACATGTGACTGTGGAAGAACATCTGTGTTCTATGTCCCGCTTGAAGGGCTCT 3307
QY 3301 ctgagaagcagtgaaagcggagatggaagcagatgtggccctgtatgttgttgcataa 3360
Db 3308 CTGAGAAGCACGTGAAGGCGAGATGAGCAGATGGCCCTGTGATGTGGTTGCCATCA 3367
QY 3361 gcaagctgaaagaagaacaaagccagctgtcaggtgtgaatgtcagagaagaagctatctgttg 3420
Db 3368 GCAAGCTGAAGAAAGCAAGCCAGCTGTCAAGTGTGAAGTGAAGCAAGAAAGCTATCTGTGG 3427
QY 3421 ccttggccttgtcggggagatcctaaggtgtcattctgtgataagaccacaagctgtgtgg 3480
Db 3428 CTTTGGCTTTGTGCGGGGATCTAAGTTGTCTATCTGTGATGAACCCACAGCTGTGTGG 3487

Db 5648 CCACCTTTGCTGAGAGCTTCAACGACAAATAGCTGAATTAATATCATGATATCTCTGA 5707
QY 5701 agtcgctgttcttgatcttcccaatcttctcgtggaagagagcctcatcgaatgagta 5760
Db 5708 AGTCGGTCTTCTGATCTTCCACATTTTTCCTGGGACAGGAGCTCATGACATGATGTA 5767
QY 5761 aaaaacggagaaatgagctgagcttgaagaaggttggggagaaatcgcttctgacat 5820
Db 5768 AAAACCAAGGAATGAGTGGAGCCCTGGAAAGTTGGGGAAATCCCTTTGTCACCAT 5827
QY 5821 tatcttgagacttggtgagagaaacctctcgcacatgagcgtggaaggggtgagtc 5880
Db 5828 TATCTTGGAGCTTGGTGGAGCAACCTCTTCCGACATGGCGGTGGAAGGGGTGCTTCT 5887
QY 5881 tcccatctactgttcttgatccaglacagatcttctcatcagggccagacctgttaagca 5940
Db 5888 TCCCATTAATCTGTTGATCCAGTACAGATTTTCATCAAGGCCCAACCTGTAATGCA 5947
QY 5941 agctatctccttgaatgaaatgaagatgagatgagcggagaaagagagatctctg 6000
Db 5948 AGCATCTCTCTGAATGATGAGATGAATGAATGAGGCGGGAAGACAGAGATCTTG 6007
QY 6001 atggttgagagcgaatgacatcttgaagaatgaagagttgacgaatataagaaga 6060
Db 6008 ATGGTGAGGCCCAAGATGACATCTTAGAAATCAAGAGATTGACGAAGATATATAGAA 6067
QY 6061 agcgaagacctgctgttgacagagattgagtgagcaltctcctgtggtggttgagc 6120
Db 6068 AGCGGAAGCTGCTGTTGACAGATTTGCTGGGACATCTCTGCTGAGTGGCTTTGGGC 6127
QY 6121 tccctgagagttaaatgagcctgaanaatcactcaacttcaagatgcttaacagagataca 6180
Db 6128 TCTCGGAGATTAAATGGGGCTGGAAATCATCACTTTCAAGATTTTAAACGAGATACCA 6187
QY 6181 ctgttccagagagatgcttcttcttaacaaatagtatcttaacaacatcagaag 6240
Db 6188 CTGTATACCAAGAGAGATGCTTCTTACAGAAATAGTATCTTATCAACATCCATGAAG 6247
QY 6241 tacatcagaacatgagctactgcccctcagtttatgcatcacaagagcgttgaagta 6300
Db 6248 TATCATGAGACATGGGCTACTGCTCAGTTGATGCCATCAAGAGCTGTGACGGGA 6307
QY 6301 gaaagacgtagagcttcttgccttgaagagagtcaccaagaagaagttgagcaag 6360
Db 6308 GAAACACGAGGAGCTTCTTGGCCCTTTGAGAGAGTCCCAAGAAAGATGGGCAAG 6367
QY 6361 ttgttgatgagcagatcgaanaatgagcctgagcctgtagatgagagaatctgctgta 6420
Db 6368 TTGTTAGTGGGAGATTCGAAACTGGGCTGCTGAAGTATGAGAGAAAATATGCTGTA 6427
QY 6421 actatagtgagagcaaaacgcaagcctctacagcaatgagcttgatcagcagcctc 6480
Db 6428 ACTATAGTGAAGCAACCAACGACACTCTCTACACCATAGCTTGATCGGCGGCCCTC 6487
QY 6481 ctgttgatggttgagatgaaccacacagagatgaatcccaagccggcggtctctgt 6540
Db 6488 CTGTGATGTTCTGATGTAACCCACACAGCATGATGCCAAAGCCGCGGCTCTTCTT 6547
QY 6541 ggaatctgcccctaaatgcttgaagaagagagatcagtagtcttaccatcagta 6600
Db 6548 GGAATTTGCCCCCTAATGTTGTCAGAGAGGAGATCACTAGTGTCTTACATCTCATAGTA 6607
QY 6601 tggagaatgtgaagctcttgcactaggatgagcaatcagtagtcaatggaagttcaggt 6660
Db 6608 TGGAAATATGTGAACCTTTTGGACTAGAGATGCAATCATGTGCAATGAAAGTTCAAGT 6667
QY 6661 gacttgagcagttctcagcatctaaanaaaggttggagagatggttatacatagttgac 6720
Db 6668 GCGTTGGCAGTGTCAACGATCTTAAAAAATAGGTTGGAGATGTTAATCAATAGTTGTAAC 6727
QY 6721 gaatacagagttcaaacccggagcctgaagcctgacagagcttcttggacttgatctc 6780
Db 6728 GAATACAGAGGTTCAACCCGGACCTGAAGCTGTCCAGGATTTCTTTGAGCTGCAATTC 6787
QY 6781 ctggaagtggttctaaagaagaacacccggaacatgctcaacatcagcttccatctcat 6840
Db 6788 CTGGAAGTGTTCAAAGAAAGAAACCGGAACATGCTCTCAATACAGGTTCCATCTTCAT 6847
QY 6841 tatcttctctggcagagatatacgaatcctctcccaagcaaaaagcagctccacatag 6900
Db 6848 TATCTTCTCTGGCCAGGATATTCAACATCTCTCCCAAGCAAAAAGGACTCCACATAG 6907
QY 6901 aagactactcgttctcagaacaacactggaacagatattgtgaacttgcgaagacc 6960
Db 6908 AAGACTACTCTGTTCTCAGACACACTTGACCAAGTATTTGTGAATCTTCCCAAGAGAC 6967
QY 6961 aagatgatatgaaccaatlaaagaacctctcaatcacaaaaaccagaacagtagtgaag 7020
Db 6968 AAAGATGATGATCACCTTAAAGACCTCTATTACAAAAACCAAGACAGTACTGAGACG 7027
QY 7021 ttgcagttctcaatcttcttcaagagatgaggaagttgaagaagctatgatgaaga 7080
Db 7028 TTGCAGTCTCAGATCTTTCTACAGATGAGAAAGTAAAGAAAGCTATGTATGAAGAA 7087
QY 7081 tccgttcaacaggggtgagctgaagaatgaagaagtaagacttctccttgcacatgag 7140
Db 7088 TCTCTTATACGGGGGTGCTGAAGATTAAGAGAGTACACTTCTTCCACCATGTG 7147
QY 7141 aaggttgtagaagaagaagcagagatgtagtgggaagaagtaactgatactgac 7200
Db 7148 AAGTGTGAGGAAGAAAGCCAGAGTGTGATGGGAAGTAACTGATACTGTAC 7207
QY 7201 tgatactatcaatgaaatgaatcaatgaaatgaagaacaaatccatcagagagca 7260
Db 7208 TGATCTATTCATGATGCAATGCAATTCATGCAATGAAGAAATTCATATACAGGGCA 7267
QY 7261 gtgccttgtgagcctatgcttctgtagtgcctcgaatgaagactgaaattagtttct 7320
Db 7268 GTGCTTTGTAGCCATGATGCTGTATGCTCAAGAGAAAGACTTAAATTAATTAATTTT 7327
QY 7321 accataccctatgaaacatctatcattagaaacccaatgagacatatggttgaactaca 7380
Db 7328 AACTATACCTATGTAACACTTATTATGAAACCAATGAGATATGAGTTGAACCTACA 7387
QY 7381 ctcttcttcttcttcttctcctgtagtctcattgaggttgaacaaatlaatcacaag 7440
Db 7388 CTTTTTTTTTTTTTTTGTCTCTGTATCTCATTTGGGGTGTGAACAATTAATCATCAAG 7447
QY 7441 taatcagtcagcagatattgatacaaaatcaaaagttaagacatcccatcactaa 7500
Db 7448 TATCATGAGCCAGCATTTATGATCAAAATCAAAAGTAAATGACATCTCATCTAA 7507
QY 7501 gccatgcaatgccagagagactggttcccggtgacacatccatctgctgcaatgagttg 7560
Db 7508 GCATGCGCATGCCAGAGAGACTGTTCCCGGTGACACATCCATGCTGGCAATGATGT 7567
QY 7561 gccagagttatagtgccaaagtttctcaagaagtttgaagacacatggtgtgcatgctc 7620
Db 7568 GCCAGAGTTATTAATGTCACAAATTTTTCAGAAAGTTTAAGCACCATGATGTCATCTC 7627
QY 7621 acttttgaaagctgctcctcagagatcattacaatgaaatgaatgaatgagtaag 7680
Db 7628 ACTTTTGGAAAGCTGCTCTGCTCAGAGTCTATCAATTAATGATATGAGTTGACAGATG 7687
QY 7681 gtgcagtgctggttcaacatccttcttgaatccctctgaatgaagctgttctggtgag 7740
Db 7688 GTGCGATGCGGTGCTTAACATCTCTTGTGATTCCTCTGATTAAGCTGTCTGGTGGAGT 7747
QY 7741 aacatgcaacaaaatggtggtgtctcctgaagcagggaaactggttcaatgttatatt 7800
Db 7748 AACATGCAACAAAATGTTGGGTGTCTCTAGGCAAGGGGAAACTGTTGCTATTTATAT 7807
QY 7801 gtccatagcttcagagcagatggtctacaggttaaccttaagagcttaataatactt 7860
Db 7808 GTCTTATGCTTGCAGCATGAGGTCTACAGGTCATCTTATGAGACTCTTAAATATACCT 7867

QY 7861 agatccgtgtaagagcaagaatcaacagccaaactgctgggctgcgaagctgcgaag 7920
 |||||||
 Db 7868 AGATCTGCTTAAGAGCAAGCAATCAACAGCCAACTGCTGGGCTGCAGCTGCTGAAG 7927
 |||||||
 QY 7921 ccagggcatgaggaattaaagagattgctgcttcaaacctlaaggggaacgctgtgcccattgt 7980
 |||||||
 Db 7928 CCAGGGCATGAGGATTAAAGAGATTGGCTTCAAACTGAGGAGACCTGTGCCATTGTT 7987
 |||||||
 QY 7981 cctgactgtctcctaacaatgtaacatgcaatcctcaagatgttattcctgaacaagtgtat 8040
 |||||||
 Db 7988 CCGAGCTGCTCTCTAACAAGTACACATGCATCTCAAGAGTATTATCTGCACAACTGTAT 8047
 |||||||
 QY 8041 tatlctgcttcttgaatlaactcagaanaatgaaaagaatggagttgtatcttggcaaaa 8100
 |||||||
 Db 8048 TATTCTGGCTTTTGAATTAATCTAGAAAATGAAAAGTGGAGTTGTATTTTGACAAAA 8107
 |||||||
 QY 8101 atgttgtaacttcttlaattgtaatttgaatttlaagtlcatalcaatgtaacttgcattcct 8160
 |||||||
 Db 8108 ATGTTGTACTTTTAACTTATTGGAATTTTAAAGTTTATCTATCACTGACTTCTGAATCCT 8167
 |||||||
 QY 8161 tagaatgacctcttgtaagaacctgtggtatagaaggaatgagccactgcccactatc 8220
 |||||||
 Db 8168 TAGAAAGGCTCTTTGTAGAACCTGTGTATAGAGAGTATGCGCACCTGCCACTATT 8227
 |||||||
 QY 8221 ttatttcttctgtaagtctgcatatcagtcataagctagtgccctgaagaagaatgtgat 8280
 |||||||
 Db 8228 TTTATTCTCTTATGAGTTTGGATATACATGATGATGCTAGTGCCTTGAAGAAAGTGTAT 8287
 |||||||
 QY 8281 gctcaggaatcctcagcatatatttgaatttcttctcagatcatattagataacttlaatt 8340
 |||||||
 Db 8288 GGTGACAGATCTCATGACATTTATTTAGAGTTTCTTCAATCATATTAGATTAOTCTTAAT 8347
 |||||||
 QY 8341 ctcaactlcaatcaataatttcttgagtgtaactgtctgtagctgaagaagtatgtatgta 8400
 |||||||
 Db 8348 CTCACTTCATCAATCAAAATATTTTGAAGTATGCTGATGCTGAAAGGATATGATACGTA 8407
 |||||||
 QY 8401 cgtataagactagaagatatlaagctcagtaacacttctcgtgcagatgttattcagctc 8460
 |||||||
 Db 8408 CGTATAGACTAGAGATATTTAGTCTCAGTACACTTCTGCTGCTCATTTTTCAGCTC 8467
 |||||||
 QY 8461 acctgttcaacaatalagttgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8520
 |||||||
 Db 8468 ACTGTTTACAAATATAGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8527
 |||||||
 QY 8521 agcccttt 8580
 |||||||
 Db 8528 AGCC-TTTTTTTTTTTTTTAAATTTGCAACATGCAAAAGCCAAAGAAATTAAGGCTCAC 8586
 |||||||
 QY 8581 aagtttaacaatgaattcttcaacagggaaaacagctagcttgaagaacttgcgtgaaaa 8640
 |||||||
 Db 8587 AAGTCTTAACATGAATTTCTTCAACAGGAAACACCTAGCTTGAATACTTGTGAAAA 8646
 |||||||
 QY 8641 cacaactgtgttcttgcagctttagtaacttcaaatatgtgcttgcagataatgtgata 8700
 |||||||
 Db 8647 CACAACCTGTGTATGAGCTATTAGTACCTTCAATTAATTTGGCTTGCAGATTTGTGATA 8706
 |||||||
 QY 8701 ccccatlaaatctgcagacgtctcaaatcttcaactccttcaatcactcagtcagaagaaaaa 8760
 |||||||
 Db 8707 CCCCATTAAATCTGACAGTCTCAAAATTTTTCATCTTCAATCAATGTCACAAAAAATA 8766
 |||||||
 QY 8761 taaaaaacaataacttccataatgagagcaatttccagagtttccaaoccatcttatt 8820
 |||||||
 Db 8767 TAAAAACAACTACTTCTCATATGAGCAATTTTTCAGAGATTTCATACCACTCTTATT 8826
 |||||||
 QY 8821 ttcttagtcagtaaacattgttaaaaaatactgttctcaactaactactactgttactgtct 8880
 |||||||
 Db 8827 TTTCTACTAGTAAACATTTGTAAAAAATCTGTTTCACTAATCTACTGTTAACTGTCT 8886
 |||||||
 QY 8881 tggagagaagaagaaaaataatgagagcaactatgtttggggaagtccaagtgatcatcaat 8940
 |||||||
 Db 8887 TGAAGAGAAAAGAAAATATGAGAACTATTTGTTGGGGAAGTTCAAGTGATCTTTTCAAT 8946
 |||||||
 QY 8941 atcaactaacttcttccacttttccaaaattgtaataatgaagtaagtgtaaga 9000
 |||||||

Db 8947 ATCAATTACTACTCTTCCACTTTTCCAAAATTTGAATTAACGCTAAGGCTGTAAGA 9006
 |||||||
 QY 9001 ctcaagatttcaaatlaattcttctataatttctttaaatttcaacgaatatataataacca 9060
 |||||||
 Db 9007 CTTGAGATTTCAAAATTTATCTTCTATATTTTAAATTTTACAAATATTTATATACCCA 9066
 |||||||
 QY 9061 ctgctgaagaagaagaaatgatgtcttgaagttlaaagtlcaatlaattgaatttlaaat 9120
 |||||||
 Db 9067 CTGCTGAAAAAGAAAAATATGTTTGTGTAAGTTTAAAGTCAATATTTGATTTTAAATAT 9126
 |||||||
 QY 9121 aaglaattgaagcatatttccaaactagtagatagatgcatgctgtgcaattcagatc 9180
 |||||||
 Db 9127 AAGTATGAAGGCAATTTTCCAAATACAGTATGATGCAATGCTGATTTTACAGTATC 9186
 |||||||
 QY 9181 ttcaaaaatagagaattatagaataatttccctcaattatatttccaaatcaag 9240
 |||||||
 Db 9187 TTTCAAAAATATACGAATTTATGAAATTAATTTCTCATTTTAAATTTTCAAAATCAAG 9246
 |||||||
 QY 9241 ttatggttccctcaatttactaaactgattcctcaatttctcattatagataatcactga 9300
 |||||||
 Db 9247 TTATGTTTCTCATTTTACTTAAATGCTATTTCTTATTTCTTATATGTAATCTATGA 9306
 |||||||
 QY 9301 gnaactccttactcgtgtcctcgtatctcaaggccatatttlaaaaaatcaaaaggcac 9360
 |||||||
 Db 9307 GCAACTCCTTACTTCTGCTGCTGCTGATTTCAAGGCCATATTTTAAATAAAGCAC 9366
 |||||||
 QY 9361 tgtgaactatttgaagaagaacagacatttlaacagattgaagaagcctctcgtga 9420
 |||||||
 Db 9367 TGTGAACATTTTGTGAAGAAACACMACATTTTAAATACGATTTGAAGAGACCTCTTCGAA 9426
 |||||||
 QY 9421 gctagaagaactatagttatlaacttcaacttaactgtgtacactttaaataatga 9480
 |||||||
 Db 9427 GGTAGAAAACATATATGATTTATCTTCAATTTATGCTGTTTAAATATGTA 9486
 |||||||
 QY 9481 atttttcaatttctcgtgtlaaactlaattgtgtgaagaatttccaaactcactact 9540
 |||||||
 Db 9487 ATTTTTCATTTTCTGTTAAACCTAATTTGTGTGAATTTTAAACCACTCTATACT 9546
 |||||||
 QY 9541 caatcaagaagaattctcgtatatactcctgtggaatgtaactatgtaagtttcaagaat 9600
 |||||||
 Db 9547 CAATCAACCAAAATTTCTGATATTTCTGTAATGCTGTAATGCTGTTTGAATAAT 9606
 |||||||
 QY 9601 ctcaaatagcgtgtcaaaaatttctgttcttgcacttgggaacactcagaagaactia 9660
 |||||||
 Db 9607 CTCAAAATACGTTTCAAAATTTTGTCTTTTGCATCTTTTGGACACTCGAAAACTTA 9666
 |||||||
 QY 9661 ttaacaactgtgataatagagaatcagaagaataatlaaagccctctatacataatgac 9720
 |||||||
 Db 9667 TTAACACCTGTAATATGGAATATGAGAAATATTAAGCCCTATATCAATAATGC 9726
 |||||||
 QY 9721 ccagcaaatatcattggttaaaaaaacaacaaactcacaactacgtatattatattcgt 9780
 |||||||
 Db 9727 CCAGCACAATTCATTTTAAAAAACMAACCAACCTCACACACGTATTTTATTTATCTGT 9786
 |||||||
 QY 9781 actgaagcaaatgcttctgtactaattaaatgttgcacatcatcatca 9830
 |||||||
 Db 9787 ACTGAAGCAAAATGCTTTGTGACTATTTAAATGTTTGCACATCATTCATCA 9836
 |||||||
 QY 9836 ACTGAAGCAAAATGCTTTGTGACTATTTAAATGTTTGCACATCATTCATCA 9836
 |||||||

RESULT 9

AXI39818 9854 bp DNA Linear PAT 30-MAY-2001
 LOCUS
 DEFINITION Sequence 70 from Patent EP1096012.
 ACCESSION AXI39818
 VERSION AXI39818.1 GI:14275400
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
 1 (bases 1 to 9854)
 REFERENCE

Naudin, L., Lemoine, C., Duverger, N., Jaje, M., searfoes III, G.H.,
Remaley, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
Journal
Aventis Pharma S.A. (FR)
Patent: EP 1096012-A 70 02-MAY-2001;

FEATURES
source
1.9854
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 2665 a 2219 c 2334 g 2635 t 1 others
ORIGIN

Query Match 93.6%; Score 9777.8; DB 6; Length 9854;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 9810; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

QY 1 ggcggagaccgagagaccgagaccctctctccggggtgagcgagagagcg 60
Db 9 GGC GGAGACCCGAGAGCCGAGCCGACCCCTTCTCTCCGGGCTGGCGAGGGGCG 68
QY 61 ggaagctcgagcaacagagagcggtctcaaggcgcttgctcctgttttcccg 120
Db 69 GGAGCTCCGGGCAACAAGAGCGGCTTCAAGGCGCTTGCTCTGTTTTCCTCCG 128
QY 121 gtctgtttctccctctccggagagcttgcaagggttagaagaagaagcgaaac 180
Db 129 GTTCTGTCTCTCCCTCCCTCTCCGGAAGGCTTGCAAGGGGTAGGAAGAGCGCAAC 188
QY 181 acaaaagtggaaaaacagtaataaccagacagcgagcgctcgtgcttgagctcagc 240
Db 189 ACAAAAGTGAAGAAACAGTTATGACCAAGCCAC - GGGGTCCCTCTGTGAGCTCTGGCCG 247
QY 241 tgccttcagaggtcccgagcaacgcgtgagcgctgctgagggagacaagcttct 300
Db 248 TGCTTTCAGAGGCTCCCGAGCCACACGCTGGGGGCTGCTGAGGGAACATGGCTTGT 307
QY 301 ggcctcagctgaggttgctgctgtggaagaacctactctcaagaagaacaacatgc 360
Db 308 GGCCTCAGCTGAGGTTGCTCTGTGGAAGACCTCACTTTCAGAGAAACAACATGTC 367
QY 361 agctgtactggaagtggcctgagctctatcttctcctgacatcctgcttgcgc 420
Db 368 AGCTGTGCTGGAAGTGGGCTGCTCTATTATCTTCTCGATCCGATCTCGTTCCG 427
QY 421 ttagctaccacacctgaacaacatgaatcatcttcaataaagcagcagctctg 480
Db 428 TGAGCTAACCAACCTATGAACAACATGAAGCCATTTCCAATAAAGCCATGCCCTTG 487
QY 481 caggaaacctctctggttcagaggatctatctgaatgcaacaacccctgttcgct 540
Db 488 CAGGAACACTCTCTGGGTTCAAGCGATTATCTGTAATGCCAAACAACCCCTGTTCCGT 547
QY 541 acccgactcctgggagagctcccgaggttgctggaacttaacaaatccattgagctc 600
Db 548 ACCCGACTCCTGGGAGGCTCCCGAGTGTGGAACCTTTAAACAATCCATTGAGGCTC 607
QY 601 gactgttccagatgctgagagctctcttatacagcagagaagaacacacacagag 660
Db 608 GCGTGTTCAGATGCTCGAGGCTCTTTTATACAGCCAGAAAGACACCAACATGAAG 667
QY 661 acatgcaagaagttctgagaacattacagcagatcaagaatccagctcaaaactgaaac 720
Db 668 ACATGGGCAAAAGTTCTGAGAACATTACAGCATCAAGAAATCCAGCTCAAACTTGAAGC 727
QY 721 ttaagaattcctgtgagcaatgaacactctctgaggttctctatatacaacactctc 780
Db 728 TTCAAATTTCTCGGTGGCAATGAACCTTCTGGGTTCTGTATCAACAACCTCTCTC 787
QY 781 tcccaagctactgtgagcaagatgctgaaggtcgaatctctcccaagctattt 840
Db 788 TCCCAAGCTCTACTGTGAGCAAGATGCTGAGGCTGATGTCTCTCCCAAGGATATTTT 847

QY 841 tgcagagctaccagttacatttgacaagctctgtgcaatgatacaaatcagaagatga 900
Db 848 TCCAAAGCTACAGTTACATTGACAACTCTGTGAATGATCAAAATCAACAAGATGA 907
QY 901 ttaacattgggagcaagaagttcttgagcttctgtgctatacaagaagaactgctg 960
Db 908 TTCAACTTGCTGACCAAGAGTTCTGAGCTTGGGCTTCCCAAGGAGAAATGGCTG 967
QY 961 cagaagagagtaacttgcttccaaactgagcaatcctgaagcaatccttgagcaactaa 1020
Db 968 CAGCAGAGAGTAATCTGTTCCAAATGACATGCAATCCTAAGCAATCTGGAACACTAA 1027
QY 1021 actatacatctccctcccgagcaagagctgctgtaagccacaanaacattgtcata 1080
Db 1028 ACTTACATCTTCCCTCCCGAGAGAGCTGGCGGAGCCACAAAACATTTGCTGATA 1087
QY 1081 gctctggagacttgcccgagagctgttcagcatgagaagcttgagatgacatgacag 1140
Db 1088 GTCTTGGGCTTGACCCAGAGCTGTTCAGCATGAGAGCTGAGATGACATGCGACAG 1147
QY 1141 aggtgagtttctgagcaatgtaacagctccacccctccccaacaaatctaccagctg 1200
Db 1148 AGGTGATGTTCTGTACCAATGGAACAGCTCCAGCTCTCCACCAATCTACAGGCTG 1207
QY 1201 tctctcgatgctgagcgacatcccgagagggagggctgaaagatacaagctctcaac 1260
Db 1208 TCTCTGTAATTTGCTGGCGGATCCCGAGAGGGGGCTGAATCAAGCTTCTCAACT 1267
QY 1261 gtaagagacaacaacatacaagaacctcttgagagcaatgagacatgagaagaatg 1320
Db 1268 GSTATGAGAGACACACATCAAAAGCCCTTTTGAAGCAATGACATGAGAAATGCTG 1327
QY 1321 aaacttctatgaacaactcaaacctccttaactgcaatgattgaaagaattgagat 1380
Db 1328 AAACCTTCTATGACACACTCAAACTCTTACTCAATGATTTGATGAAGATTTGGAGT 1387
QY 1381 ctgactcctctcccgacatctcgaagaagctcgaagccgctcctgttggaagaatgc 1440
Db 1388 CTAGTCCCTTTCGCCGATTATCTGGAAGCTCTGMAAGCCCTCTGTTGGAGATTC 1447
QY 1441 tgaataccctgagacactcgaacccaagagcagatgagctgagatgaaagaactctc 1500
Db 1448 TGTATACACTGAGACACTCCAGCCACAAGCGATGATGGCTGAGGTGAACAAGACTTCC 1507
QY 1501 aggaactgagctgttctcatgatactgagaagcagtgaggaggaactgaagcccaag 1560
Db 1508 AGGAACCTGGCTGTTCATGATCTGGAAGGCAATGGAGGAATCCAGCCCAAGATCT 1567
QY 1561 ggaactcattgagaagaacagcaagaatgagactctgacgagatgcttgagagcaggg 1620
Db 1568 GGCCTTCTATGAGAGACAGCAAGCAAAATGACCTTTGTCGGATCTGTTGGACAGCGG 1627
QY 1621 acaatgacactcttggaacagcagttgagttgattagatlgagacacccaagaatcg 1680
Db 1628 ACAATGACCACTTTTGGGAACAGCAGTTGATGAGTTAGATGGACAGCCCAAGACATCG 1687
QY 1681 tggagtttttgccaagcaccagagagatgtccagctcagtaatggttctgttacaact 1740
Db 1688 TGCGGTTTGTGGCCAAAGCAACCAAGAGATGTCAGTCCAGTAATGAGTTCTGTATACCT 1747
QY 1741 ggaagaagacttcaagaagactaacaagcaatccggagacatatctcgcttcaatgag 1800
Db 1748 GAGAGAGAAGCTTTCAGAGACTAACAGCAATCCGGACATATCTCCGCTTATGAGAG 1807
QY 1801 gttctcaactggaacaagctgaacccaatgacaacaagaatctgtgtcatcaacaagt 1860
Db 1808 GTGTCAACCTGGAACAACCTGGAACCCATAGCAACAGAAAGTCTGGCTATCAACAAGTCA 1867
QY 1861 tggagctgagcagatgagaagaagctcggagctgattgttctcaactgagaaatccag 1920
Db 1868 TGGAGCTGTGATGAGAGAGATTTGGGCTGGTATTGTTCACCTGGAATTAATCTCCAG 1927

```
QY 1921 gcaagcattgagctgccccatcatgtaagtaacaagatccgaatgagcatgtgacaatgtg 1980
D 1928 GCAGCATTTGAGCTGCCCCATCATGATCAAGTACAAAGATCCGAATGACATTTGCAATGTG 1987
QY 1981 agaggaacaataaatacaagatggtgactgagacccctgtccctgagctggcccttg 2040
D 1988 AGAGGACAAATTAATCAAGATGGGTACTGGGACCCCTGGTCTCGACGTGACCCCTTG 2047
QY 2041 agagcatgcygtaagctgctggggggcttcgactactgagaatgtgtgtgagcaagca 2100
D 2048 AGGACATGCGGCTAGCTGTGGGGGGCTTGCCCTACTTGACAGATGTGTGGAGCAGCA 2107
QY 2101 tcaatgaggtgctgagcgggagccgagaagaaactgtgtctatagcaagatgacct 2160
D 2108 TCATCAGGGGTGTGACGGGACCGAAGAAACCTGTGTATATGCAACATCCCT 2167
QY 2161 atccctgtctgctgtaagatcttctcgaggatgaagccgtaagcccttca 2220
D 2168 ATCCCTGTTCATGATGATGATCTTCTGCGGGTGAATGACCGGTCATGCCCCCTCTTCA 2227
QY 2221 tgaagctgagcctgagattactcaagtgctgtgatacaagagcatcgtgtatgaaag 2280
D 2228 TGACGGCTGGCCTGGATTACTCATGTGCTGTGATCATCAAGGGCATCGTGTATGAGAAG 2287
QY 2281 aggcacgctgtaaaagagacatatcgatcatgagccctgagcaacagcatctgttita 2340
D 2288 AGGCACGGCTGAAAGAACCATGGGATCATGGGGCTTGACAAACAGCATCTTGTTTA 2347
QY 2341 gctgtgcatatgactgactcactcctctctgtgtgagcgtgagcctgtgactgatacc 2400
D 2348 GCTGCTCATTTAGAGCCTCATTCCTCTCTGTGAGCCGTGGCTGCTGCTAGTGTATCC 2407
QY 2401 tgaagatgaagaaactgctgctcctcctacagtgatcccaagcgtgtgtgtgttcttc 2460
D 2408 TGAAGTGAAGAAACCTGCTCCTACAGTATCCACGCTGTGTGTGTCTCTGTCG 2467
QY 2461 tgtttgtgtgtgtacacatcctcgaagctcctcctgatacaacatcttccagacca 2520
D 2468 TGTTCCTGTGTGTACAAATCTCGAGTGTCTTCCTGATTAACACACTTCTTCCAGAGCCA 2527
QY 2521 acctgagcaagcctgttgggggacatcactactcaagctgtacatgacatgacatgac 2580
D 2528 ACCTGAGCAGAGCCTGTGGGGGATCATCTACTTCAAGCTGTACCTGCTGCTGT 2587
QY 2581 gtgagatgagcaagactaagctgagctcctcctcctcctcctcctcctcctcctcct 2640
D 2588 GTGTGAGTGTGAGCACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2647
QY 2641 ctgtgctcttgggttggctgtgagacttgcctcttggagagcaagggacatggag 2700
D 2648 CTGTGGCTTTGGGTTTGGGCTGTGAGTACTTGTGCTTTTGAAGAGCAGGGCATTTGAG 2707
QY 2701 tgaagtgagacaacctgttgaagatcctgttgaagaaagtgttcaatctcaacct 2760
D 2708 TGAGTGTGGGACAACTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2767
QY 2761 cgaatcctgagctgttgaacacctcctcctcctcctcctcctcctcctcctcctcct 2820
D 2768 CGGTCTCATGATGCTGTGTGACACTTCTCTATGGGGTATACCTGTGTGACTTGAAG 2827
QY 2821 ctgtctctcagcagcaagaaatcccaagccctgagatcttccctctgacaagactcct 2880
D 2828 CTGTCTTCCAGGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2887
QY 2881 actggttctgagagaaagtgtatgaagaaagcaacccctgttccaaacagaaagaaagt 2940
D 2888 ACTGTTTGGGAGAAAGTGTATGAGAGACCACTGTGTGAGTGTGAGTGTGAGTGTGAG 2947
QY 2941 cagaatctgcatgagagaaagcaaccccaactgaaagctgtgaggtgtccatcaagaa 3000
D 2948 CAGAAATCTGATGAGAGAGAACCCCACTGAAAGCTGTGGGGTGTGCTTCAAGAAC 3007
QY 3001 tgtataaagctacccagatggagatgaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3060
D 3008 TGTATAAAGCTACCGCATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 3067
QY 3061 atgagggcagaatcaacctcctcctcctcctcctcctcctcctcctcctcctcctcct 3120
D 3068 ATGAGGGCAGATCACTCTCTCTGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 3127
QY 3121 caatctgagcgggtgttcccccagcctcctgagcagccctacatccttggaaagaa 3180
D 3128 CAATCTGAGCGGGTGTTCCTCCCGGACCTGGGACCGCTTACTTCTGGGAAAGNCA 3187
QY 3181 ttcgctctgagatgagcaacatcccgagaaactgaggggtgtgtcccaagataagctgc 3240
D 3188 TTGCTGTGAGTGTGAGCAACATCCGAGAACCTGGGGGTGTGTCCCGCATGACGTC 3247
QY 3241 tgtttgacatgctgagctgtgaaagaaacatcgttctatagcccttgaagagctcct 3300
D 3248 TGTTCATGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3307
QY 3301 ctgagaagcagtgagagcagagatgagagcagatgagcctgagatgtgtgtgtgtgt 3360
D 3308 CTGAGAGCTAGTGTGAGGAGGAGATGAGAGATGAGTGTGAGTGTGAGTGTGAGTGT 3367
QY 3361 gcaagctgaaagcaaaagccagctgtgagtgagtgagtgagtgagtgagtgagtgag 3420
D 3368 GCAAGCTGAAAGCAAAACCAAGCCAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3427
QY 3421 ccttgacctgtgtggggatcaaggtgtgtatctctgagatgaacccaagctgtgtgt 3480
D 3428 CTTGGCTTTTGTGGGGATTAAGTGTGTATCTGTGATGAAACCAAGTGTGTGTG 3487
QY 3481 acccttactcccgaggggaatgagagctgtgtgataacccaagccagca 3540
D 3488 ACCCTTACTCCCGAGGGGAATATGAGAGCTGTCTGTGAAATACGACAAAGCCGACCA 3547
QY 3541 tlatctctcaacaacaatgagatgagagagagctgtgtgtgtgtgtgtgtgtgtgtgt 3600
D 3548 TTTATCTCTTACACACCAATGATGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 3607
QY 3601 tctccatgagagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3660
D 3608 TCTCCATGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3667
QY 3661 caggtactacactgagctgtgtcaagaaagtgtgaatcctcctcctcctcctcctcct 3720
D 3668 CAGGTACTACCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3727
QY 3721 acagtagtagcactgtgtatcactgagaaagagagagagtggttctcaagagcaatgt 3780
D 3728 ACAGTAGTAGCATTGTGTATACCTGAAAGAGAGAGAGTGTGTGTGTGTGTGTGTGT 3787
QY 3781 atgtgtgctgtggcagcagacatgagatgagagctgtgacatcgatgtctgtcctatct 3840
D 3788 ATGTGTGCTGTGGCAGCAGCAATGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3847
QY 3841 ccaactcactcaagaaagctgtgtcgaagcccgctgtgtgaagacatagagcaatgagc 3900
D 3848 CCAACTCCTATCAGAGAGCAATGTGTGAGCCGCTGTGTGAGAGCAATGAGGAGTGTGAG 3907
QY 3901 tgaactatgtgtgcataatgagctgtgaagaaagagagccttltgtgaagccttcaatg 3960
D 3908 TGACCTATGTGTGCTATGAGAGCTGTGAGAGAGAGAGCTGTGTGTGTGTGTGTGTGT 3967
QY 3961 agatgagcagcctcctcagacatgtgagatctcagatgagcactcagagcaagc 4020
D 3968 AGATGATGAGCGGCTGTGAGAGCTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 4027
QY 4021 tggagaataatctcctcaagtgagccgaagagagtgagtgagtgagtgagtgagtgag 4080
D 4028 TGGAAATAATCTCTCAAGGTGTGAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4087
QY 4081 gtaccttgcagagcaagcaagcagcgagccttgcggagcaagcagagctgtctgtgc 4140
```


QY	6301	gaagaaacgttgagagttctttgtcccttttgagaagagttcccaagagaaaagatttggcaag	6360
Db	6308	gagaaacacggagaggttctttgtcccttttgagaagagttcccaagagaaaagatttggcaag	6367
QY	6361	tttgtagagttggagatcttggaacctgggcccgtggaagtatgagaanaaatatctgctga	6420
Db	6368	tttgtagagttggagatcttggaacctgggcccgtggaagtatgagaanaaatatctgctgga	6427
QY	6421	actatagtgagagcaacaagcaagctctctctacaagcatgagcttgatctgctggcgcc	6480
Db	6428	actatagtgagagcaacaagcaagctctctctacaagcatgagcttgatctgctggcgcc	6487
QY	6481	ctggagtggttctcgatgtagaccacacaaggaatgagatcccaagcccggtcttg	6540
Db	6488	ctggagtggttctcgatgtagaccacacaaggaatgagatcccaagcccggtcttg	6547
QY	6541	ggaattgtgccttaagtgtgttcaaggaagggagatcaagtgtgttcaatctcatagta	6600
Db	6548	ggaattgtgccttaagtgtgttcaaggaagggagatcaagtgtgttcaatctcatagta	6607
QY	6601	tggaagaagtgtgaagctcttgacatagaatgacataatgttcaatggaaggttcaagt	6660
Db	6608	tggaagaagtgtgaagctcttgacatagaatgacataatgttcaatggaaggttcaagt	6667
QY	6661	gaccttggcagtgctccagcatctaaanaataagtttgagatgtgtatacaatagttgac	6720
Db	6668	gaccttggcagtgctccagcatctaaanaataagtttgagatgtgtatacaatagttgac	6727
QY	6721	gaatagaagaggttcaaccggagaccttgaagcctgctccagaattcttggagttgacat	6780
Db	6728	gaatagaagaggttcaaccggagaccttgaagcctgctccagaattcttggagttgacat	6787
QY	6781	ctggaagtgttcttaaaagagaanaacacccgggaataatgtcatacaccagttccatctcat	6840
Db	6788	ctggaagtgttcttaaaagagaanaacacccgggaataatgtcatacaccagttccatctcat	6847
QY	6841	tatcttctctggccagatatttagatactctctccagagaataaaggagactccacatg	6900
Db	6848	tatcttctctggccagatatttagatactctctccagagaataaaggagactccacatg	6907
QY	6901	aagacttactgtttctccaagaacaacacttgcacaaatatttgaactttgcaaggacc	6960
Db	6908	aagacttactgtttctccaagaacaacacttgcacaaatatttgaactttgcaaggacc	6967
QY	6961	aagatgatatgaccacttaaaagacctctcatatacaaaaaacagacagttatggag	7020
Db	6968	aagatgatatgaccacttaaaagacctctcatatacaaaaaacagacagttatggag	7027
QY	7021	ttgcagttctacaactcttctctacagatgagaagaatgaaaanaagcatgtatgaa	7080
Db	7028	ttgcagttctacaactcttctctacagatgagaagaatgaaaanaagcatgtatgaa	7087
QY	7081	tccgttcatcaacggggttgcctggaagtaaaaggaactagacttctccttgacacatgt	7140
Db	7088	tccgttcatcaacggggttgcctggaagtaaaaggaactagacttctccttgacacatgt	7147
QY	7141	aagtgttgtgagaanaagggccgaagttgatttgtggaagaagtaaacctgatactgac	7200
Db	7148	aagtgttgtgagaanaagggccgaagttgatttgtggaagaagtaaacctgatactgac	7207
QY	7201	tgaatacttaacatgcaatgaatctcaatgcaatgaaaacaaatctcatatacagggga	7260
Db	7208	tgaatacttaacatgcaatgaatctcaatgcaatgaaaacaaatctcatatacagggga	7267
QY	7261	gtgccttctgagcctatgtcttgtatagtgctcctaagtgtgaagacttgaatttagttttt	7320
Db	7268	gtgccttctgagcctatgtcttgtatagtgctcctaagtgtgaagacttgaatttagttttt	7327
QY	7321	accttaactaatgaaacatctatataggagaaccaatgagacataatggtttgaactaca	7380
Db	7328	accttaactaatgaaacatctatataggagaaccaatgagacataatggtttgaactaca	7387
QY	7381	cttttttttttttttttctgtgtaattcactatggggttgcacaataatcataag	7440

Db	7388	CTTTTCTTTTCTTTTGTTCCTGCTATTCATTCGTTGGGTTGGCAACATATATTCATCAAG	7447
Qy	7441	taatcagcgcaacgagttatgatcaaaatacaaaagtgatgacacatcccatctacaa	7500
Db	7448	TAATCATGCGCACCGATTTTATGATCAAAATCAAAAGGTAAATGACATTCCTCACTAA	7507
Qy	7501	gcaatgcatacccaagagactggtttcccggtgacacatccatctgctgagcaatggtt	7560
Db	7508	GCCATGCGCATGCCACAGACAGACTGTTCCCGGTGCACATCATTCGTGGCAATGAGTGT	7567
Qy	7561	gccagagattatgagccaaagttttccagaagtttgaagcacaatggtgtgtgcacgtc	7620
Db	7568	GCCGAGATTATAGTGCCAAGTTTTCAAAAGTTGAAGCACCATGCTGTGTCATGCTC	7627
Qy	7621	actttgtgaagcgctgcctgcacagatctcaaacattgaataatcaagttgacagaatg	7680
Db	7628	ACTTTGTGAACACTCTCTGCTCAACAGCTCTTCAACATTTGAATATCAGTTGACAGAAATG	7687
Qy	7681	gtgcacagcgtaggcataacatccgtcttgatattcccttcgataaagctgttcctgtgcagt	7740
Db	7688	GTCGCATGCTGGGTGCTAATCCCTGTTATTCCTCTGATTAAGCTGTTCGGTGGGAGAT	7747
Qy	7741	aacatgcaacaaaatgtggtgtgtctctaggaacgggaacacttggttccatgttatatt	7800
Db	7748	AACATGCAACAAAATGTGGTGTCCTCTGTGGCACGGGAACCTGGTTCCATGTTATATT	7807
Qy	7801	gtccatagcttgagccatctggtgtcctaaaggtcatccctatagaacctttaaataactc	7860
Db	7808	GTCCTATGCTCGAGCCATGGCTCTACAGGGTCATCCTTATGAGACTCTTAAATATCTT	7867
Qy	7861	agatcttggtgaaggagcaaaatacaacagccaaactgctgggctgcaagctgtcgaag	7920
Db	7868	AGATCTGTGTAGAGGCGCAAGATCAACAGCCAAACTGCTGGGGCTGCMACTGCTAAG	7927
Qy	7921	ccaaggcaatggagtaaaagagatttggtgttcaaaccttagggaaacccgtgtcccatgtt	7980
Db	7928	CCAGGCGAATGGGATTAAAGAGATTGTGCGTTCAACCTTAGGSAACCTGTGCCATTGT	7987
Qy	7981	actgactctgcgtcaacatagtlcaactgcatctcaagaatgttaltctgacacaagtgtat	8040
Db	7988	CCTGACTGTCGTATACATGATGTAACGTGACATCGCATCCAAGATGTTATCTGACACAAGTGTAT	8047
Qy	8041	tattctcggcttttgaattaactcagaaaaatgaaaagtgaagttgatttattttgaacaaa	8100
Db	8048	TATTTCTGGCTTTTGAATTAATCTGAAAAATGAAAAGTGAAGTTGATTTTGACAAAA	8107
Qy	8101	atggttgtaacttttaagtattttgaattgaattttaaattcacaagtgaactctgaatcct	8160
Db	8108	ATGTTTGACTTTTATGTTATTTGGAATTTAACTTATACAGTGACTTCTGAATCCT	8167
Qy	8161	tagaatgacctcttltgaaagccctgtgtgataagagatgagccaactgcccacatat	8220
Db	8168	TGAGATGSCCTTTTGTAGAACCTCTGTGTATGAGAGGATAGGGCACTGCCACATTT	8227
Qy	8221	ttattttcttaatgaattgagatgacatcagatcagctagctagtgccatagaagaatgtgat	8280
Db	8228	TTTTATTTCCTATGTAGATTGTGCAATACAGTCACTGACTAGTGCCCTTAGAAAGCAATGTAT	8287
Qy	8281	ggtcagagatcctaatactiatattagtttcttcacatcatattagatactttaat	8340
Db	8288	GGTCAGAGATCTGATGACATTTATATTGAGTTTCTTTCAGATCATTTAGATACCTTAAAT	8347
Qy	8341	ctcaactlcaatcaataatatttttgagtgatagctgtgagctgtaagaagatgataagcta	8400
Db	8348	CTTCACCTTATCATCATCAATTAATTTTGTAGGTATGCGTATGACGGAAGGATATGTACSTA	8407
Qy	8401	cgtataaagctagagagatatgaagttcagatcaactcctgtgcacagtattatcaagtc	8460
Db	8408	CGTATAGACTTAGAGAGATATTAAAGTCTCAAGTACACTTCTGTGGCATTTATTCAGCTC	8467
Qy	8461	actgtgttacaataataggtgtctgtggtgtgtaggaagccaatgtaacaatatltggc	8520

Db 2520 CTAGCCGCTGTCCTCTGCTGCTTTGGCTTTGGCTGCTGACTTGTCCCTTTTGAAG 2579
Qy 2686 agcaggcattgagtgagtgaggaacacctgtttgagagctctgtgaggaagatgct 2745
Db 2580 AGCAGGCAATTGAGTCAGTCAGTGGACACCTGTTGAGAGTCTGTGAGGAAGATGGCT 2639
Qy 2746 tcaatcaccacacttgatctcagatgatctgtttgacaccttccctctatlgggtgata 2805
Db 2640 TCATCTCACCACTTGGTGGTCTCATATGATGCTGTGTGACACCTTCTCTATGAGGATGA 2699
Qy 2806 cctgtgacattgagtgctgtcttccagccagtcaggaattccagagccctgtatttc 2865
Db 2700 CCTGGACATTTGAGCGCTGCTTCCAGCGCAGTACGGAATTCACAGCCCTGGATTTC 2759
Qy 2866 ctgtgacacagtgctctactgtgttgaggaagatgataaggaagacccctgttcca 2925
Db 2760 CTTGCACCAAGTCTCTACTGTTGGCGAGCAAGTATGAGAAGACCCCTGTGTCGA 2819
Qy 2926 accagaagaagatgtaagaatctgcatgaggaaggaacccacacttgaagctggagc 2985
Db 2820 ACCAGAAGAAGATATCAGAAATCTGCATGAGAGAGAACCCACCACTTGAAGCTGGCG 2879
Qy 2986 tctcactagaacacctgtaaaagtctacccaagatggaatgaaagtgtctcgatgac 3045
Db 2880 TGTCCATTGAGAACCTGTGPAAGTCTCCGAGATGGATGAAGGTGGCTGTGATGGCC 2939
Qy 3046 tggacattgaatttataagaggccagatcacctcctctctggccaacatgagcgagga 3105
Db 2940 TGGCACTGAATTTTATGAGGGCCAGATACCTCCTTCTGGGCCCAATGATGAGCGGGA 2999
Qy 3106 agagagacacatgtaacatctgacccaggtgtlcccccagaccctggagccactaca 3165
Db 3000 AGACGACCACTGTCATCTGACCTGACCGGGTGTCTCCCGCCGACCTGGGACCGCTTACA 3059
Qy 3166 tccaggaaagacatctgctctgagatgagaccatcccgagagacactggaggtctgtc 3225
Db 3060 TCTCGGAAGAACATTCGCTCTGAGATGAGCAACATCCGCGAAGACCTGGGGCTGTGC 3119
Qy 3226 cccagcataagtgctgtttagacatgctgtctgaaagacacatctgttctatgccc 3285
Db 3120 CCCAGATTAACGTGCTGTTGACATGCTGACGTGAGAACACATCTGTTCTATGCCC 3179
Qy 3286 gcttgaagaggtctctctgagagacactgtaagcgagagatggaatgagccctgagtg 3345
Db 3180 GCTTGAAGAGGCTCTCTGTGAAAGACGTAAGGCGGAATGAGAGATGGCCCTGAGTG 3239
Qy 3346 ttgtttgccaatcaagcaagctgaaagcaaaacaagcaagctgtcaagtgaatgcaga 3405
Db 3240 TTGATTGGCATCAAGCAAGCTGAAGAAAGCAAAACAAAGCAGCTGTGAGTGAATGCA 3299
Qy 3406 gaaagctatctgtggtctgtgacctgtctcgaggagatcaaggtgtcaatctgtgaag 3465
Db 3300 GAAACCTATCTGTGGCTTGGCTTGTGCGGGATCTAAAGTGTCTCAATTCGTGATGAC 3359
Qy 3466 ccacagctgtgtgagaccttactcccgcaagggaatataagagctgtgtgaataacc 3525
Db 3360 CCACAGCTGTGTGAGACCTTACTCCCGAGGCAATTTGGAGTGTGCTGTAATAATCC 3419
Qy 3526 gacaaagccgaacatattctctctacacacacatgtaagcaagcgagcttccgtggg 3585
Db 3420 GACAAGGCGGACCATTTCTCTCTACACACACATGATGAAGCGGAGCTCTCTGTTGGA 3479
Qy 3586 acaagattgccaatctcccatggaagcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3645
Db 3480 ACAGATTTGCCATCTCTCCATGGGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGGA 3539
Qy 3646 agaaccagctggaagaagctactacactgacctgtgtcaagaagaagatgtaaccctccc 3705
Db 3540 AGAACCAGCTGGGAAGAGCTACTACTGACCTTGGTGTGTAAGAAAGATGTGAATCTCTCC 3599
Qy 3706 tcaagtctcagaaacagtagtagcactgtgtacatcactgaaagaaagagagacagttt 3765
Db 3600 TCAGTCTCTGCAAGAACGTAGTAGCACTGTGTATACCTGTAAGAAAGAGAGACGTTCTT 3659

Qy 3766 ctcaagcagttctgagtgctgacctggcagcagccatgaagatgacacgctgacacg 3825
Db 3660 CTCAGAGCAATTTGATGATCTGCTGGCTGGCCACGACATGAAAGTGAACCTTGACCTTCG 3719
Qy 3826 atgtctctgatatctcaacctcatcaaggaagcatgtgtctgaagcccgctgttgaag 3885
Db 3720 ATGTCTCTGATATCTCCAACTCATAGGAAGCATGTGTGTGAAGCCCGCTGGTGAAG 3779
Qy 3886 aatatgagcagatgagctacatgtctgctccatatgaagctgctgaaggaagagcccttg 3945
Db 3780 ACATAGGCAATGAGCTGACCTATGTGCTGCATATGAAAGCTGCTTAAGAGAGACCTTGG 3839
Qy 3946 tgaaccttctcatgagatgataagcagctctcaagacccctggagatctgaattatgca 4005
Db 3840 TGAACCTCTTCATGAGATGATGATGACCGGCTCAGACCTGGGCAATTTAGTTATGCA 3899
Qy 4006 tctcagaagagacaccttgaaagaatattctcctcaaggtgtgcccgaaggaagtgagtgatg 4065
Db 3900 TCTCAGAGACCACTCTGGAAGAAATTTCTCTCAAGGTGGCCGAAGAGATGGGGTGATG 3959
Qy 4066 ctgagacctcagatgtaaccttgccaagcaagacgaacgaagcggtccttcggggacaagc 4125
Db 3960 CTGAGACCTCAGATGATGATCTTGGCCAGCAAGACGAAGACGCGGCTTCGGGACACAGC 4019
Qy 4126 agagctgtcttcgcccgttaactgaagatgactgtgtgtatccaatgtatctgacatag 4185
Db 4020 AGACCTGTCTTCCGCTTCACTGAAGATGATGCTGTGATCCAAATGATTTGACATAG 4079
Qy 4186 accagaatccagagagacagactgtctcagtgagatgagtggaaggttctactaacag 4245
Db 4080 ACCAGATCCAGAGACACAGACTTGTCTAGTGGATGATGGAAGGTCCTTACCAGG 4139
Qy 4246 tgaaggtctggaaccttaacacagcaacagtttgtgccccttltgtggaagagactga 4305
Db 4140 TGAAGGCTGGAACCTTACACAGCAACAGTTGTGGCCCTTTGTGGAAGAGACTCTAA 4199
Qy 4306 ttgcaagcagagagtcggaagagatltttgtcagatgtcttcgagcagctgtgtgtct 4365
Db 4200 TTGCCAGACGAGAGTGGGAAGGATTTTTCCTCAGATGTCTTGCACAGCTGTGTGTCT 4259
Qy 4366 gcaatgccccttgtgtlcaagcctgacgtgtccaccttggcaagtaecccaagctggaac 4425
Db 4260 GCATTTGCCCTTGTGTGAGCTGATGCTGACCCCTTGTGGCAAGTACCCAGCCTGGAAC 4319
Qy 4426 ttaagcccttgatgttaagaagaacagatcacatlttloagcaatgtgtctccgaagaa 4485
Db 4320 TTCAAGCCTTGATGTACAAAGAAAGTACATTTGTGACAAATGATGCTCTGAGAGACA 4379
Qy 4486 cgggaacctggaactctttaaacyccctcaacaaagacacttgctcggagaccgtgtga 4545
Db 4380 CGGGAACCTTGGAACCTTTAAACGCCCTCCACCAAGAACCTGTGCGGACCCGCTGTA 4439
Qy 4546 tgaaggaagaaacccatcccaagacacgacctgcaagcgagggaaggaagtggaacctg 4605
Db 4440 TGAAGGAACCCCAATCCAGACACGCCCTGCGAGGAGGAGGAAGTGGACACATG 4499
Qy 4606 cccagttcccagacacatataagactcttccagaaatggaactggaatgagcagaac 4665
Db 4500 CCCAGTTCGCCAGACATCATATGACCTTCTCAGAAATGGAACTGGACAAAGCAAAACC 4559
Qy 4666 cttaacctgatagcagtgtaagcagcaaaaatcaagaagatgtgtcctgtgtlcccc 4725
Db 4560 CTTACACCTGATCCAGTGTAGAGGAGCAAAATCAAGAAATGCTGTGTGTGTGTGTGTG 4619
Qy 4726 cagggcagggggtgtgtcctctccaaagaagaacaaacacgtgcagatalcctcag 4785
Db 4620 CAGGGCAGGGGGGCTGCTCTCCCAAAAGAAACAAAACACTCAGATATCTTCAAG 4679
Qy 4786 acctgacaggaagaacatctcgatctatctgttgaagagatgtgaagatcaagaca 4845
Db 4680 ACCTGACAGGAAGAAACATTTGAGATTATCTGTGTAAGACGTATGTGACGATCATAGCA 4739

QY 4846 aaagcttaagaacaagatcgtggtgaatgaattagratagcgagccttccctgggtg 4905
|||||
Db 4740 AAAGCTTTAAAGAAAGATGTGGGTGAATGATTTAGTATGGCGGCTTTTCCCTGGGTG 4799
4906 tcagtaatactcaagcactcccccagtlcaagaagtltaatgatgcatcaacaatgta 4965
|||||
Db 4800 TCAGTATATCTCAAGCAGCTTCCCGAGTCAGAAATTAATGATGCGACCAAAATAGA 4859
4966 agaaacacctaagaactgycgaagaagacagtlctgcagatcgatattctcaacagctggaa 5025
Db 4860 AGAAACACCTAAAGCTGGCCAAAGACAGTTCTGCAGATGATTTCTCAACACCTGGGAA 4919
5026 gattatgaagagactggaacacagaataatgtaaggtgtgttcaataacaaggct 5085
|||||
Db 4920 GATTATGACAGAGCTGGACACCAAAATATATCTCAAGGTGTGGTTCAATTAACAAAGGCT 4979
5086 ggcattgcaatcagctcttccctgaatgltcaacaatgccattctccggcgcaactgyc 5145
|||||
Db 4980 GGCATGCAATCAGCTCTTCTCTGAATGTCATCAACAATGCCATTTCCGGGCGCAACCTGC 5039
5146 aaaaggagagaacccatagccatlatggaattactgcttcaatcaatccctgaatctca 5205
|||||
Db 5040 AAAAGGAGAGAACCCCTAGCATTAATGAAATTAATCTCTTCAATCAATCCCTGAATCTCA 5099
5206 ccaagcagcagctctcagaggtggtcctgtagtgaacacatcaatgtagtgccttgltca 5265
|||||
Db 5100 CCAAGCAGCAGCTCTCAAGAGTGGCTCCGATGACACATCAGTGGATGTCCTTGTGTCCA 5159
5266 tctgtgcatcttgcgaatgtccctgltcccaagcagcttgcgtatctcgtatccagag 5325
|||||
Db 5160 TCTGTGTCATCTTTGCAATGTCTTGTCTCCACAGCTTGTGCTATTCCTGATCCAGG 5219
5336 agcgggttcagcaagaacaacactgcatctcaatgtagtggaggtgcctgtcatctact 5385
|||||
Db 5220 AGCGGGTCAGCAAAAGCAACCTGCAATTCATCACTGAGTGAAGGCTGTATCTACT 5279
5386 ggcctcctaattgtgtctgagatagtgcaatgaactgtgctccctgcacactgltcatla 5445
|||||
Db 5280 GGGCTCTAATTTTGTCTGGGATATGTGCAATTAACGTTGTGCTCCCTGCCACACTGTGATTA 5339
5446 tcaatctcaatctgtcccaagcaagaagtcctlatgltccctcccaaatctgctgtgtag 5505
|||||
Db 5340 TCATCTTCATCTGCTCCAGCAGAAAGTCTATGTGCTCTCCACCAATCTCTGCTAG 5399
5506 ccccttcaacttgcgtatgaggtgtgtcaatcaactcctcactgtaacccagcctcttgg 5565
Db 5400 CCGTCTCTACTTTTGTCTGTATGGTGTCAATCAACCTCTCATGTATACCGCTCTCTTG 5459
5566 tgttcaagaatcccccagcagcctatgtgtgtcaccagcgtgaaccttctcatctgca 5625
Db 5460 TGTTCAGATCCCAAGCACAGCTATGTGTGCTCACCAAGCTGCAACCTTCTTATGGCA 5519
5626 ttaatgcaagcgtgagccacttgtgtcgtgaagctgttcaaccgacaataagctgaataa 5685
Db 5520 TTAATGCGAGGTGGCCACCTTTGTGTGCTGAGCTGTACCGAACAAATTAACCTAATA 5579
5686 tcaatgatatcctgaagcgtgtgttctgtatcttcccaacttlttggcttggagcagagc 5745
Db 5580 TCAATGATATCTCGAAAGTCGTGTCTGTGATCTTCCACATTTTGTCTGGAGAGAGGCT 5639
5746 tcaatgacatggtgaanaacagcaagcaatgctgtagtgccttggaaaggttttgggagaa 5805
|||||
Db 5640 TCATGACATGCTGAAAAACAGCAAGCAATGCTGATGCCCTGAAAAAGTTTGGGAGAAATC 5699
5806 gcttgtgtcaccaatctcgtggagactgtgtggagcgaacactcttcgcaatggtcgtgg 5865
Db 5700 GCTTTGTGTACACATTAATCTTGGGACTTGTGGAGCGCAAAACCTTGTGCCATGGCCGTGG 5759
5866 aaggggtgtgttcttccatctactgttctgataccagtaagaatttctcaagcgcca 5925
Db 5760 AAGGGGTGTGTCTTCTCATTAATGTGTCTGATTCAGTCAAGATTTCTTCAATCAGGCCCA 5819
5926 gaactgttaaatgcaagatlatctcctctgaatgtaagaatgtaagaatgtgagcgggaa 5985
|||||
Db 5820 GACCTGTAATGCAAAAGCTATCTCCTGTAATGATGAATGATCAATGTGAGCGGGAAA 5879
5886 gaacagaaatctctgtgtgtgtgagggccaaatgacatcttgaataatcaaggagtgtgca 6045
Db 5880 GACAGAAATTTCTTGTGTGTGGAGGCGAGAAATGACATCTTGAATAATCAAGAGTTGACGA 5939
6046 agatataagaagaagcgaagcgcctgctgtgacagatlttgcgttggcalttccctctg 6105
Db 5940 AGATATTTAAGAAAGAAAGCGGAACCTGCTGTGTGACAGGATTTGGCTGGGCAATTCCTCTG 5999
6106 gtgagtgcttggcctcctggtgaggttaatggtgtggaataatcatcaacttcaagatgt 6165
Db 6000 GTGAGTCTTTGGGCTCTCCGAGTAAATGGGCTGAAAAATCAATCACTTCAAGAGAT 6059
6166 taacagagataaccactgttactcagagagagatgcttcttcaaaaaatagtaactat 6225
Db 6060 TAACAGAGATACCACTGTTCACAGAGAGATGCTTCTTAACAGAAATGATATCTTAT 6119
6226 caaacatccatgaagtacatcagaacaatggtactgcccactgaattgtatgcatcacag 6285
Db 6120 CAACATCTCATGAAGTATCATCAGAACATGSGCTACGCCCTCAGTTGATGCTATCACAG 6179
6286 agctgttgaactgggagagaacacgtgaggttcttgccttltgagaagatgccagaga 6345
Db 6180 AGCTGTGACGTGGAGAGAACACGTGAGTCTTCCCTTGTGAAGAGAGTCCAGAGA 6239
6346 aagaagtgtgcaaggtgtgtgaggttggagagttcgagaacttgggcccgtggaagtatgag 6405
Db 6240 AAGAAGTGTGGCAAGTGTGTGAGTGGCGATGGAACCTGGGCTCTGTAAGTATGAGAG 6299
6406 aaaaatltgctgtaactatagtgagagcaacaacgcaagctcttcaagcactgctt 6465
Db 6300 AAAATATGTGCTGTAATATAGTGAAGGCAACAAAGCAAGCTCTTACAGCATGGCTT 6359
6466 tgaatgcgagcctcctgtgtgttcttctggaatgaaccccaagagcatggtatcccaag 6525
Db 6360 TGATCGGGGCGCTCCTGCTGTGTGTCTGATGATACCCACACAGGCTATGATCCAAAG 6419
6526 cccggcggttcttggaaattgtgccttaagtgttcaagggagggagatcaatgagtg 6585
QY 6586 ttacatccatagatagtgaaagatgtgaagctcttgcactaagatgtagtgaatgltca 6645
Db 6420 CCGGCGGTTCTTGTGAATGTGCTTAACTGTTGTGCAAGAGGAGGAGATCATGATGTC 6479
6586 ttacatccatagatagtgaaagatgtgaagctcttgcactaagatgtagtgaatgltca 6645
Db 6480 TTACATCTCATAGTATGGAAGATGTAAGCTCTTGCATGAGATGGAATCATGTCA 6539
6646 atggaaggttcaagtgccctgtgaggtgtlccagcatctaaataatggttggagatggt 6705
Db 6540 ATGGAAGTTCAGCTGTGCTTGGCGAGTGCAGCATCTTAAATAATAGGTTGGAGATGTT 6599
6706 atacaatgtgtgacgaatagcaaggttccaaacccgagcctggaagcctgtlccaaatct 6765
Db 6600 ATACATATGTTGTACGAATGACAGGATCCAGCGACCTGGAAGCCGTGTCAAGATTTCT 6659
6766 ttgactgtgcatlcttcgtgaaggtgtlctbaaagaagaacacggaacatgctacaaatcc 6825
Db 6660 TTGACTTGCATTTCTCTGGAAGTGTTCAAAAGAGAAACCCGAGACATGCTCAATATAC 6719
6826 agcttcaatctcaatctctctgtgcagagatattcaacatcccttcccaagaagaaa 6885
QY 6720 ACCTTCATCTTCAATTAATCTTCTGCGCAGGATATTCAGATCTCTCCCAAGCAAAA 6779
6886 agcagctccacatagaagactactcgttctcagaaacacacttgaacaaagatattgtga 6945
Db 6780 AGCGATCTCAGATACAAAGCACTGCTGTGTCTGACAAACCTTGACCAAGTATTGTGA 6839
6946 acttggcaaggaaccaagtgtatgtagcaacttaaaagcctctcatcaaaaaaac 7005
QY 6840 ACTTTGCCAAGGACCAAGATGATGATGACCACTTAAAGACCTTCTATTCACAAAAACC 6899
7006 aagaagtagtgaaggttgaggttctcacaatcttctcaagatgtaagaatgtaagaagaa 7065
|||||

Dh 6900 AGACAGTGTGACGCTTTCACATCTTTCTACAGATGAGAAAGTGAAGAAA 6959
Qy 7066 gcatgtaagaagaatccctgttcaacagggtgagctgaagaagtaagaagtaagctatgc 7125
Dh 6960 GCTATGTATGAAGAACTCTGTTTCAATACGGGGTGGCTGAAGTAAGAGNACTAGACTTT 7019
Qy 7126 cctttgacacacatgtaagaatgctgtgagagaagaagccagaagctgtagtggaagaagta 7185
Dh 7020 CTTTGGACCCATGTGAAGTGTGTGAGAGAAAGAGCCAGAAAGTGAAGTGGGAGAGTA 7079
Qy 7186 aactgagactgtactgatactatcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaat 7245
Dh 7080 AACGGATAGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7139
Qy 7246 tccattcaaggag 7305
Dh 7140 TCCATTACAGGGGAG 7199
Qy 7306 tgaattgatttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 7365
Dh 7200 TGAATTAGTTTCTTACCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7259
Qy 7366 ggggttgaactcaacttt 7425
Dh 7260 GGGTTGAACACACCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 7319
Qy 7426 caataatcatcaatgaatcatgagcagagagagagagagagagagagagagagagagagag 7485
Dh 7320 CAATAATTCATCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7379
Qy 7486 atctcatcaactgaagcagatgagcagagagagagagagagagagagagagagagagagag 7545
Dh 7380 ATCTCATCTCACTAAGCCATGAGCCATGAGCCATGAGCCATGAGCCATGAGCCATGAGCCAT 7439
Qy 7546 gctggcaatgaagtgagcag 7605
Dh 7440 GCTGGCAATGAGTGTGAG 7499
Qy 7606 tgggt 7665
Dh 7500 TGGGT 7559
Qy 7666 tcaagtgagcagagatgagcag 7725
Dh 7560 TCAAGTGAAGAGAGT 7619
Qy 7726 tgggt 7785
Dh 7620 TGGT 7679
Qy 7786 ttcattgttataatttctctatgtctctgagcagatgagcagagagagagagagagagagag 7845
Dh 7680 TTCATTGT 7739
Qy 7846 ctcttaataataataataataataataataataataataataataataataataataataata 7905
Dh 7740 CTCTTAAAT 7799
Qy 7906 tgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 7965
Dh 7800 TGAAGCTGCTGAGAGCCAG 7859
Qy 7966 cctgtgcccatttgcctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 8025
Dh 7860 CCGTGTGCCATTGTCTGAGCTGTCTGAGCATGTGTGAGCATGTGTGAGCATGTGTGAGCATGT 7919
Qy 8026 ctgacacagtgatataattctgtgcttctgagcagcagcagcagcagcagcagcagcagcagcag 8085
Dh 7920 CTGACACAGTGTAT 7979
Qy 8086 tgtatttgaacaaagt 8145
Dh 7980 TGTATTGTGACAAAATGT 8039

Qy 8146 tgaattcctgaatccttgaatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 8205
Dh 8040 TGACTTCTGATATCTTATGATATGAGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8099
Qy 8206 caactgcccactatttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 8265
Dh 8100 CACTGCCCCACTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 8159
Qy 8266 agaaagcaatgtag 8325
Dh 8160 AGAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8219
Qy 8326 taggaactccttaactcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 8385
Dh 8220 TAGGATAGCTTATATCTCATCTTCTCATCTTCTCATCTTCTCATCTTCTCATCTTCTCATCTTCT 8279
Qy 8386 aagagatgtactgtactgtactgtactgtactgtactgtactgtactgtactgtactgtactgt 8445
Dh 8280 AAGAGATGTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8339
Qy 8446 catgtattcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 8505
Dh 8340 CATGTTATCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 8399
Qy 8506 gtaacaaatattggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 8565
Dh 8400 GTACCAATATCTGGCAGGC - TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 8458
Qy 8566 aagtaagaggtcacaagcttaacaaatgaatcttcaagagagagagagagagagagagagag 8625
Dh 8459 AAGTATTAAGGTCACAGCTTAACATGATTTCTTCAACAGGAGAAACACACTAGCTTGA 8518
Qy 8626 aaactgtcgaacaaacacacacttggttattgagcagcagcagcagcagcagcagcagcagcag 8685
Dh 8519 AAACCTGCTGAAAAACACACTGTTGTATGAGCTTGTATGAGCTTGTATGAGCTTGTATGAGCT 8578
Qy 8686 tgcagatattgagacccatcttaactcagcagcagcagcagcagcagcagcagcagcagcagcagcag 8745
Dh 8579 TGCAGATATGTGATATCCCATTAATGTGACAGTCTCAAAATTTTCAATCTTCAATCTTCAATCT 8638
Qy 8746 tagtaagaagaataataaaacaaataataataataataataataataataataataataataata 8805
Dh 8639 TAGTCAAGAAAAATATAAAACAACAAATCTTCCATATGAGAGATTTTCAAGATTTTCAAGATTTT 8698
Qy 8806 taaccagcttatttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 8865
Dh 8699 TAACCACTTATTTTCTGTGAGTAAACATTTGTAAAAATCTGTTTCACTAATATCT 8758
Qy 8866 tactgttaacgtcttgag 8925
Dh 8759 TACTGTTAACGTCTTGAG 8818
Qy 8926 aagtgatcttcaatataactactactactactactactactactactactactactactactactact 8985
Dh 8819 AAGTATCTTTCAT 8878
Qy 8986 gctaaagtgtaagactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 9045
Dh 8879 GCTAAAGGTGTAAGACTTCAGATTCAAAATTAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 8938
Qy 9046 atattataaacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 9105
Dh 8939 ATATTATATTAACCCAGTGTGAG 8998
Qy 9106 atgatttttaataataagtagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 9165
Dh 8999 ATTGATTTTAAAT 9058
Qy 9166 gcaatttaacagatcttcaacaaataacagagatataagagagagagagagagagagagagagag 9225
Dh 9059 GCATTTTACAGTATCTTCAAAATATACAGAAATTTATAGAAATTAATTTCTCTCATTAATATAT 9118

QY 9226 ttltcaaaatcaaaagttagtggcttcatttactaaatcgtatcttaatttcatt 9285
|||||
Db 9119 TTTTCAAAATCAAACTTATGTTTCTCTCATTTTACTAAATCGTATCTTATCTTCATT 9178
QY 9286 atagtaaatctatgagcaactccttacttcggttccttgatattcaaggacatattaa 9345
|||||
Db 9179 ATAGTAAATCTATGAGCAACTCTTACTCTGCTTCCCTCTGATTTCAGGACATATTTTAA 9238
QY 9346 aaatcaaaagcactgtagaactatttgaagaacaacgcacatttataacagattaa 9405
|||||
Db 9239 AAAATCAAAAGGCACTGTAAGTATTTTGAAGAAAACACAACTTTTAAATACAGATTGAA 9298
QY 9406 aggaactcttcgaagcagaacaactatagttatataccttacttaactggtta 9465
|||||
Db 9299 AGGACCTCTTCTGAGCTGAGAAACAATCTATATACATCTTATATATATCTGTGTA 9358
QY 9466 cctttaaataagtaacttttactatcttcctggtgtaaacctaatgtgtgaataattt 9525
|||||
Db 9359 CTTTTTAAATAGTATATTTTACATTTTCCGTGTAACCTAAATTTGCTAGAAATTTT 9418
QY 9526 taccacacttactcaatcaatcaaatcttcgtatatttccctggtgtaagtactatg 9585
|||||
Db 9419 TACCAACTCTTATCTCAATCAAGCAAAATTTCTGTATATCTCTGTGGAATGTACTATAG 9478
QY 9586 tgaattcagaagaattcctcaaaatacgtgtcctcaaaatttcgcttctgcatcttgagac 9645
|||||
Db 9479 TCAGTTTCAAGAAATCTCAAAATACGTGTCAAAATTTTCGCTTTTGCATCTTTGGGAC 9538
QY 9646 acccaagaagaacttatacaaacctgtgaatatgagaatacagaagaataataagccc 9705
|||||
Db 9539 ACCCTAGAAATCTTATTAACAACCTGTGAATATGAGAAATACAGAAATTAATTAAGCCC 9598
QY 9706 tctatataaattgcccagacacattcattgttaaaaaaaccaacacacttaactactg 9765
|||||
Db 9599 TCTATACATTAATGGCCAGCAATTCATGTGTAATAAACCAACCACTCACACTACTG 9658
QY 9766 tattcaatctatctgacgagaagaacatgcttctgactataatgtgtgacacatctc 9825
|||||
Db 9659 TATTTCAATATCTGTACTGAAAGCAAAATGCTTTGTGACATTAATGTTCACATCATTC 9718
QY 9826 attca 9830
|||||
Db 9719 ATTCA 9723

RESULT 11
AX139817
LOCUS AX139817 9741 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 69 from Patent EPI096012.
ACCESSION AX139817
VERSION AX139817.1 GI:14275399
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Deneffe, P., Roslier-Montcus, M.F., Arnold-Reguigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., seafloss II, G.H.,
Renaley, A., Brewer, H.B. and Dean, M.
TITLE Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
JOURNAL Patent: EP 1096012-A 69 02-MAY-2001;
Aventis Pharma S.A. (FR)
FEATURES
source location/Qualifiers
1. 9741
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2650 a 2180 c 2290 g 2620 t 1 others
ORIGIN
Query Match 92.6%; Score 9672.8; DB 6; Length 9741;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 9705; Conservative 0; Mismatches 18; Indels 2; Gaps 2;
QY 106 ctgtttttcccggttcgttttctcccttcctcgaagagctgttcaaggtataga 165
|||||
Db 1 CTTGTTTTTCCCGGTTCTGTTTTTCTCCCTTCTCCGGAAGGCTGTCAAGGGATAGA 60
QY 166 gaagagagcgaacacacaaagtgaagaacagttaagaccagccagggctccctgc 225
|||||
Db 61 GAAAGAGACGCAACACAAAAGTGAACAGTTAATGACACAGCAC-GGGCTCCCTGCT 119
QY 226 gtgagctcgtccggtcgtccttccagggctccgagcaacagctgtggtcgtcgtgag 285
|||||
Db 120 GTGAGCTCTGGCGGCTGCTCTTCCAGGGCTCCGAGCACAGCGTGGGGGTGCTGGGTGAG 179
QY 286 ggaacatggtctgttgcctcagctgtaggttgcctgtgtgtgtggaagaaccttaaga 345
|||||
Db 180 GGAACATGGCTTGTGTTGGCCCTGAGCTGAGTTGCTGCTGTGGAAGAACCTTCATGAA 239
QY 346 gaagacaacacatgctcagctgttactggaagtgtgctgtgctctatattactcctgatcc 405
|||||
Db 240 GAACACAAACATGTCACCTGCTGTGAACTGGCTTGCTCTATTTATCTTCTGATTC 299
QY 406 tgaactcgttgcgttgcgttgccttccacacacttgaacacacatgaatgcaatttccaaata 465
|||||
Db 300 TGATCTCTGTTGGGCTGAGCTACCCACCTATGAAACATGATGCAATTTTCCAAATA 359
QY 466 aagcagatgacctcgtcgaagaacacttccctgtgtgttcgaaggtatctgttaagcaca 525
|||||
Db 360 AAGCAATGCCCTTGAGGAAACATCTTCTTGGGCTGAGGGGATATCTGTAAGCCAAACA 419
QY 526 acccgttccggttaccgacactcctgtggaaggtcccggaagtgttgaactttaa 585
|||||
Db 420 ACCCTGTTCCTGTACCCTGCTCTGAGAGCTCCGGAAGTGTGGAATTTAAACA 479
QY 586 aatccattgtgctgcgtcgttctcagaatgcggaggttcttatacagccagaag 645
|||||
Db 480 AATCATTTGGGCTGGCGCTGTTCAAGATCTGAGAGCTTCTTTATACAGCCAAAG 539
QY 646 acaccagatgaagaagacatgcgaagaattctgagaacatgaacagatcaagaagaatcca 705
|||||
Db 540 ACACGACATGAAAGACATGCGCAAAATCTTGAAACATTTACGACATCAAAATCCA 559
QY 706 gctcaaatctgaagcttcaagatttccctgtgtgacaacatgaacacttccctggttccat 765
|||||
Db 600 GCTCAAACTTGAACCTTCAAGATTTCTGTGTGACATGAACCTTCTCGGGTTCTGTG 659
QY 766 atcaaaccttctctcccaagcttctacgtgtgacaagaatgtcgaaggtcgtatcttc 825
|||||
Db 660 ATCAACAACCTCTCTCTCCCAAAAGCTACTGTGACCAAGATGCTGAGGGCTGATGTCATTC 719
QY 826 tccagaaggtatttttgaaggtcaccagtttaattgaaagtctgtgaatgagatcaa 885
|||||
Db 720 TCCACAAAGTATTTTTCAGAGGCTACCAAGTTTCAATTGACAAAGTCTGTCAATGATCAA 779
QY 886 aatcagaagaatgatcaactcgttgaacaaagaatgttctgagcttgtgacctaccaa 945
|||||
Db 780 AATCAGAAGAGATGATTAACATCTGTGACCAAGAGTTTCTGTGAGCTTTGGGCTTCCAA 839
QY 946 agagaagaacgtgctgacgacgagagagtaacttggttccaaatgagaaatcttgaagcaca 1005
|||||
Db 840 GGGAGAAACTGTGCGAGCAGAGAGGAGTACTTGTTCACATGAGATCTTAAGCCAA 899
QY 1006 tctcgaagaacacttaacttcaactctcccttcccgagacagagcgtgctgagacacaa 1065
|||||
Db 900 TCTGAGAACACTTAACCTTACATCTCTCTTCCGAGACAAAGAGCTGCGGAGCCACAA 959
QY 1066 aaacattgtcagatagcttctggaactcgtgcccagaagagctgttcaagatagaagctgga 1125
|||||
Db 960 AAACATTGCTGATAGTCTGTGGAGCTGTGCGCAGAGAGCTGTTACAGATGAGAAGCTGGA 1019
QY 1126 gtgacatgacgacagaggtatgttttctgaccaatgtgacaacgtccagctcctccacc 1185
|||||

Db	1020	GTGACATGCGACGAGGATGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACACC	1079
QY	1186	aaatctacaagcgtgltctcgtatctgtctcgtgcgacatcccgaggagaggggctgtgaaga	1245
Db	1080	AAATTTACACAGCCTGTCTCGTATTTGTCTCGCGCATCCGAGGAGGAGGGCTGAAGA	1139
QY	1246	tcaagtctctcaactggtatagagacaacaactacaagccctctttggagcgatagca	1305
Db	1140	TCAAGTCTCTCACTGGTATAGAGACAACATCAAAAGCCCTCTTGGAGGCAATGGCA	1199
QY	1306	ctgaggaaagatgctgtaaacctctatgacaactacacactccttactgtcaatgttta	1365
Db	1200	CTGAGGAAGATGCTGAAACTCTATGACAACTCACTCAACTCCTTACTGCAATGATTTGA	1259
QY	1366	tgaagaatttggagctcagtcctctcttcccgattatcttgaaagcctctgaagccgtgc	1425
Db	1260	TGAAGAATTTGAGTCGTATGTCCTCTTCCGCATATCTGGAAGAAAGCTCTGGAAGCCGTGC	1319
QY	1426	tctgtgggaagaatctcgtatatacaactgacactccagccacaagcaagtcagtctag	1485
Db	1320	TGCTTGGGGAAGATCCTGTATATACCTTGACACTCCAGCCACAAGCAGTCAATGGCTGAGG	1379
QY	1486	tgaacaagaaccttccaggaactgctgtgtccatgatlctggaagcaatgtggaagAAC	1545
Db	1380	TGAACAAGACCTTCCAGAGAACGTGGCTGTTCATGATCTGGAAAGCATGTGGGAGGAAAC	1439
QY	1546	taagccccaagaatctggagccttcaatgagaagaacgaagaatagacatgttccggatgc	1605
Db	1440	TGAGCCCAAGATCTGGACCTTCATGGAAGACGCAAGAAATGCACTTGTCCGGATGC	1499
QY	1606	tgtttgacaagcaggagacaatgaccacttttggaaacagatltgatlgtgtctagattgga	1665
Db	1500	TGTTGGACAGCGGAGACATGACCACTTTTGGGAACAGCAGTTGGATGGCTTAGATTGGA	1559
QY	1666	cagcccaagacaatgtagtcgttttttggccaagcaacccagagagatgtccagtccagtaatg	1725
Db	1560	CAGCCCAAGACATCTGGCTGTTTTTGGCCAAAGCACCCAGAGATGTCCAGTCAGTAAAG	1619
QY	1726	gttctgttataccctggagagagaagcttccaagagactacaagacaatccggaccat	1785
Db	1620	GTTTGTGTGACACCTGGAGAGAGCTTTCACAGAGACTAACCAAGCAATCCGGACCAAT	1679
QY	1786	cttcgcttcaatgagtgtgttcaacctggaacaagctagaacccaatgacaacagaaatctggc	1845
Db	1680	CTCGCTTATGAGAGTGTCAACCTGAACCAAGCTAAGAACCCATATGCAACAATACTTGGC	1739
QY	1846	tcaatcaacaagtcacaatggagctgtcgtggaatgaagagaatcttggcgtgtatctgttca	1905
Db	1740	TGATCAACAAGTCCATGGAGGTGCTGGATGAGAGSAATTTGTGGCTGTGATTTGTGTTCA	1799
QY	1906	ctggaacttactccagcgacgaatltgagctgcccacatcgtcaagtatacaagaatccgaaatg	1965
Db	1800	CTGGAAATTACTCCAGGACGACATTGAGTGCCTCCCATCATGCTACAAAGATCCGAATGG	1859
QY	1966	acattgacaatgttggagaggaacaataaataccaagataggatctggagacccctgttctc	2025
Db	1860	ACATTGACATHTGAGAGAGCAATAAATCAATCAAGATGGGTACTGCGGACCCCTGTGCTCTC	1919
QY	2026	gagctgacccctttagagacatgctgtaagcttggggggcttcgctacttctgcaagatg	2085
Db	1920	GAGCTGACCCCTTTTGGAGACATGCGGTACGTCGTGGGGGGCTTGCGCTACTTGGCAGATG	1979
QY	2086	tgttggagacaggaatcatctcaggtgtgtcagcggcacaacgagaanaaactggtgtctata	2145
Db	1980	TGTGTGAGACAGCAATFCAAGGGTCTGACGGGACCGGACGAABAABAACTGTGTCTATA	2039
QY	2146	tgcacaacatgcccataccctgttlaagtttgaatcatcttcttcggtgatalgagccggt	2205
Db	2040	TTCACACAGATGCGCTATCCCTGTTACGTTGATGACATCTTTCTCGGGGTGATGAGCCGGT	2099
QY	2206	caatgcccccttctatgacgtctggcccttgagatttactcaatgtgctgtgtatatcaagagca	2265
Db	2100	CAATCCCCCTCTCAATGACGCTGTGGCTGGAATTTACTCAAGTGGCTGTATCATCTCAAGGGCA	2159
QY	2266	tctgtataagaagaagagcagcgtgaaagagacaaatgcgatatatggcctgtgaacaa	2325
Db	2160	TGCTGTATGAGAGAGGACGCGCTGAAGAAGACCATCGGATCATGCGCTTGACAAACA	2219
QY	2326	gatactctggtttagctgtgttcatatgaatcattccctctctctgtgtgagcctggcc	2385
Db	2220	GCATCCTCTGGTTTAAGCTGGTTTCATTAGCTCATTTCTCTTCTTGAGCCCTGGCC	2279
QY	2386	tgtcagtgatcactcctgaagttaagaaactgtgcctcacaatgataccagcgtgtgt	2445
Db	2280	TGCTATGTGTCATCTCGTAAGTTAGGAACCTGCTCCCTACAGATGCCGCGTGGTGT	2339
QY	2446	ttgtctcctgtccgltgttctgtgtgtgtgaaatctcgtcagtgctctctgtattgacac	2505
Db	2340	TGTCTTCTGTCCGCTGTTGTGCTGTGGTACATCTCAAGTGTCTTCTGTATTGACAC	2399
QY	2506	tcttctccagaagccaacttggcagcagcctgtgggggatcatctacttcaacgtctaac	2565
Db	2400	TCTTCTCCAGAGCAACCTGGCAGCAGCCTGTTGGGGCATCATCTACTTCACTGCTGATCC	2459
QY	2566	tgcctcagtcctctgtgtgtgcaatgcaagcactgagtggtcttcaactcaagatctcgt	2625
Db	2460	TGCTCTACCTCTCGTGTGTGGCATGGCAGGACTACGTGGGCTTCACTCAAGATCTTCCG	2519
QY	2626	ctagccctgtctcctcctgtgagcttcttggatgttggctgtgagtaacttgccttltgag	2685
Db	2520	CTAGCCTGCTGTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTCCTTTTGAAG	2579
QY	2686	agcagggcatctgagtgcaagtgagacaacclgttltgaagatcctgttggagaagaatgct	2745
Db	2580	AGCAGGGCATTTGAGTGGCAGTGGGCAACCTGTTGAAAGTCTGTGAGAGAAATGGCT	2639
QY	2746	taaatctcaaccttgcatactcatalgactgcttggaaacttctcctaibtgagtgatga	2805
Db	2640	TGATCTTCACTTCTTGCTGTCTCATGATGCTGTGTAACACTTCTCTATGGGTATGA	2699
QY	2806	cctgtatcatctgagcgtgtcttctccaagccagtaagaaatcccaagccctgtatcttc	2865
Db	2700	CCGTGATCAATGAGGTGCTTCTTCCAGGCCAATGAGAAATTCAGAGCCCTGATTTTTC	2759
QY	2866	cttggaccaagctctactgctgttggccaaggaagtgaatgaagaagccaactgtttcca	2925
Db	2760	CTTGCACCAAGTCTTACTGTGTGGCGAGAAAGATGAGAAAGCACCTCGATGTTCA	2819
QY	2926	accagaagaagaatgttcaagaatctcataltggagggagaaacccaacacttgaagcttggcg	2985
Db	2820	ACCAGAAGAAATATCAGAAATCTGCATGGAGAGAAACCCACCTTGAAGCTGGGGC	2879
QY	2986	tgtcattcaagaacctggttaaaagtctaccagagatgggaatgaaggtgtgtctgatatgcc	3045
Db	2880	TGTCATTTGAGAACCTGTGTAAGGTCCTACCGAGATGGGATGAAGGTGCTGTGATGGCC	2939
QY	3046	tggcaatgaaatttatatggagccagatcaacctctctccttgcggacaacat	

QY	3346	ttggtttgcataagcaagcttgaaaagcaaaacagccagctgttcaggttgaaatgcaga	3405
Db	3240	tttggtttggccatcamaaccaagctgaaaagcaaaaacaaagccactgtccagtggaattgcaga	3299
QY	3406	gaaagcatctctgagccttgagcctttgttcgggggatactcaagttgtcattcttgatgaac	3465
Db	3300	gaanagctatctgtggcctttggcctttgttcgggggattctaaagttgtctattcttgatgaac	3359
QY	3466	ccaagctgtgtgtgaccccttaacctcccgcaagggataatggagctgtcgtctgnaatacc	3525
Db	3360	ccaagctgtgtgtgaccccttaacctcccgcaagggaaatmgagactgtcgtctgnaatacc	3419
QY	3526	gacaagcgcaacattatctctcttaacacacaaatgatagaagcgaagctctctgggg	3585
Db	3420	gacaagcgcccaacattattttctcttaacacacaaatgatgaagcgaagctctctgggg	3479
QY	3586	acaagatctgcacatctcccatggaagctgtgtctgtgtgagctccctccgtttctga	3645
Db	3480	acaagattggtgcattcattctccanngsaacctgtgtgtgtggcctccctctgtttctga	3539
QY	3646	agaacagcttggaagagctactactgtgacttggtcaagaagaatgtgnaatctccc	3705
Db	3540	agaacacagctgggaagaaagctactactgtgacttggtcaagaagaatgtgnaatctccc	3599
QY	3706	tcagttcttcbaaaaaagtaagagacgtgtctaaacttaaaaaaggaagacgtttt	3765
Db	3600	tcactttcttcbaaaaaagtaagagacgtgtctaaacttgaaaaaaggaagacagtgttt	3659
QY	3766	ctcagagcaattctcgtatgtctgcgcttgtagagacacatgagatgtaacagcttgacatcg	3825
Db	3660	ctcagagcaattctcgtatgtctgcgcttgtagagacacatgagatgtaacagcttgacatcg	3719
QY	3826	atgtctctgtatctccaacctcaatcaaggaagcaatgtgtctgaagcccgcttgltbgaag	3885
Db	3720	atgtctctgtatctccaacctcaatcaaggaagcaatgtgtctgaagcccgcttgltbgaag	3779
QY	3886	acataaggaatgagctgacactatgtctctccatagaagctgtcttagaaggagaacctttg	3945
Db	3780	acataaggacatgacactatgtctctccatagaacctgtcttagaaggagaacctttg	3839
QY	3946	tggacctcttcatagagatgatactgataccgagctctcagaaccttggaacttctagttatgga	4005
Db	3840	tggaaacttttcatagagattgataagccgagctctcagaaccttggaacttctagttatgga	3899
QY	4006	tctcaagagacgaaccttggaaagaatatctccaaagttgtagaagagatgggtgtgatatg	4065
Db	3900	tctcagagacgaaccttggaaagaattttctccaaagttgtagaagagatgggtgtgatatg	3959
QY	4066	cttgagacctcaagatgtgtaactgtgcagcaagacgaagcaagcggtgtcttgaggacaagc	4125
Db	3960	cttgagacctcaagatgtgtaactgtgcagcaagacgaagcaagcggtgtcttgaggacaagc	4019
QY	4126	agagctgtcttcggccgttcaactgaagaatgatatctctataccaatatgtcttgacatag	4185
Db	4020	agagctgtcttcggccgttcaactgaagaatgatatctctataccaatatgtcttgacatag	4079
QY	4186	accagaatctcagaagagacagacttgtctcaatgtgggaatggaatgggttctctaccag	4245
Db	4080	accagaatctcagaagagacagacttgtctcaatgtgggaatggaatgggttctctaccag	4139
QY	4246	tgaagagcttgaaacttaacacgaacaagtttgttgcccttttgtgaaagagactgctaa	4305
Db	4140	tgaagagcttgaaacttaacacgaacaagtttgttgcccttttgtgaaagagactgctaa	4199
QY	4306	ttgcaagacggaatctcgaagaagatattttgtctcaaatgtctcttgcaagctgtgtgtct	4365
Db	4200	ttgcaagacggaatctcgaagaagatattttgtctcaaatgtctcttgcaagctgtgtgtct	4259
QY	4366	gcaatgcacctgtgttcaagctgtatgtgcaaccttttgcaagtaaccaacacacctgagac	4425
Db	4260	gcattgtgcccttgtgttcaagctgtatgtgtgcacaccttttgcaagaatnccccacacctgagac	4319
QY	4426	ttcaagcccttgatgtaaacgaacagataacatttgtcaagcaatgatactgtcctgagaca	4485

[illegible]

Dh 5400 CCCTTACTTTTGGTGTATGGGTGATCAATACACACTCTCATATGCCAGCCCTCTTG 5459
Qy 5566 tgtcaaatcccccaagcagcagctatgttggtccaccagcgtlgaacctcttcattgca 5625
Dh 5460 TGTTCAGATGCCAGACAGCCATATGTGNGCTCACACAGGTGAACCTCTTCATTGGCA 5519
Qy 5526 ttaatggcagcgtgcccactttgtgtgagcgtgtccaccgacaataagctgaataa 5685
Dh 5520 TTAATGGCAGCGTGGCCACTTGTGTGGAGCTGTTCACCGCAATAAATCAATATAT 5579
Qy 5586 tcaatgatccctgaagtcgtgtcttgatcctccacattttgtccggagcagagc 5745
Dh 5580 TCAATGATATCCGTAAGTCGGTGTGTGATCTTCCACATTTTGGCTGGAGCAGAGGC 5639
Qy 5746 tcatcgacatggtgaaaaaaccagcnaatggtcgtatgccttggaaggtttgggagaatc 5805
Dh 5540 TCAATGCAATGTGTAAAAACAGCAGCAATGCTATGCCCTGGAAGAGTTGGGAGATTC 5699
Qy 5806 gcttgtgacacatctatcttggaactgtgtgagcgaagaaacctctgcagctgagcgtg 5865
Dh 5700 GCTTGTGTACCATTTATCTTGGACTGTGGAGCAAAACCTTCCGATGCGCTGG 5759
Qy 5866 aaggggtgtgtcttccctcattactgtgttgatccagtaagatcttcattcagccca 5925
Dh 5760 AAGGGGTGTCTCTCTCTCATTTACTGTGTGATCCAGTACAGATTTCTTCATCAGGCCCA 5819
Qy 5926 gactgtgaatgcaagaactatctcctctgaaatgaatgaatgaatgaatgaatgaatga 5985
Dh 5820 GACCTGTAATATGCAAAACCTATCTCTGTGATGATGAAGTGAAGTGAAGCGGGGAAA 5879
Qy 5986 gacagaagaatcttgatgtgtgagcgaagatgacalcttaagaatcaagaagttgaag 6045
Dh 5880 GACAGAAATTTCTGATGTGTGAGGCGCAAGATACATCTTGAATATCAAGATTTACCA 5939
Qy 6046 agatataagaagaagcgaagcgtgtgtgtgacaggaattgtgtggaactcctcctg 6105
Dh 5940 AGATATATTAAGAAAGGAGCGGAAAGCTGTGTGATGATGATGATGATGATGATGATG 5999
Qy 6106 gtatgtccttggcctcctgtgaggttaatgaggtctggaatcaatacatttcaaat 6165
Dh 6000 GTAGTGTCTTGGGCTCTGTGGAGTTAATGGGCTGGAAATCATTAACCTTTCATATAT 6059
Qy 6166 taacaggaagatcacactgttaccagaaggaatgtcttcttaacaaaaatagatctat 6225
Dh 6060 TAAACAGAGATACACACTGTGTACAGAGAGATGCTTCTTAAACAGAAATAGATCTTAT 6119
Qy 6226 caaacatcagatgagatcagaacatgagcagcagcagcagcagcagcagcagcagc 6285
Dh 6120 CAATATCCATGATGATACATCAACATGAGGCTACCTGCTCAATGATGATGATGATG 6179
Qy 6286 agctgtgacgtgagagagacagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6345
Dh 6180 AGCTGTGACTGTGGAGAGAAACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6239
Qy 6346 aagaatgtgcaaggt 6405
Dh 6240 AAATAATGTGGCAAGT 6299
Qy 6406 aaaaatgt 6465
Dh 6300 AAAAATATGT 6359
Qy 6466 tgaatggcagcgtcctgt 6525
Dh 6360 TGAATGGCAGCGGCTCTGT 6419
Qy 6526 cccggcgt 6585
Dh 6420 CCCGGGCTTCTTGT 6479
Qy 6586 ttacatctcatagtagaagaatgtgaagcctctgtcactagatgtgcaatcatgtgtca 6645
Dh 6480 TTACATCTCATATGTATGAAAGATGTGAAGTCTTTTGCACGTAGATGTGAATCATATGTCA 6539
Qy 6645 atggaagttcaggtgtcctgtgcaatgtccagcacttaaaaaataggtttgagaatgt 6705
Dh 6540 ATGGAAGTTTCAAGTGTGCTGTGGCACTGTCCACATCTTAAAAATATGTTTGAATGTGT 6599
Qy 6706 atacaatgtgtacgaatagcaggtgtccaaacccgagcctgaagcgtgtcagaatctt 6765
Dh 6600 ATACATATGTTTACGAATATGAGGAGGTCCAAACCCGAGCTCAAGGCTGTCCAGATTTCT 6659
Qy 6766 ttggaatcattctcctgaaggt 6825
Dh 6660 TTGGACTTCATTTCTCTGGAAGTGTTCAAAAGAAAGAACCGGAGATGTGTACAAATACC 6719
Qy 6826 agcttccatctcatatcttctcgtgcagagatataagatcctctccagagcaaaa 6885
Dh 6720 ACTTCATCTTCATTTATCTTCTGTGGCAGGATTTTCAGATCCTCTCCAGAGCAAAA 6779
Qy 6886 agcgaatccacatagaagaactcctgttctcagacaacacttgaccaagtattgtga 6945
Dh 6780 AGCGACTCCCATGTAGAAAGTACTCTGTCTCAGACAAACCTTGACCAAGTATTTGTGA 6839
Qy 6946 acttgcgaaggaaccaaagtgtatgaatgaacacttaaaagcctctcatatacaaaaac 7005
Dh 6840 ACTTGGCAAGGACCAAGTATGATGACCACTTAAAGACCTCTCATTTACACAAAAAC 6899
Qy 7006 agacagtagtgaaggtgtcagttctcacaacttctcagagatgagaagtgagaagaa 7065
Dh 6900 AGACAGTGTGTGACGCTTGT 6959
Qy 7066 gctatgtatgaagaatctcgtgtcagaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7125
Dh 6960 GCTATGTATGAAGATCTGT 7019
Qy 7126 ccttgcacacatgtgaaggt 7185
Dh 7020 CTTTGCACCAATGTGAAGT 7079
Qy 7186 aactgtgactgt 7245
Dh 7080 AACTGTGATGT 7139
Qy 7246 tccattcaagagcagtgagccttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7305
Dh 7140 TCCATTTACAGGGAGGAGT 7299
Qy 7306 tgaattgagtttttactataactatgtgaactctatataatggaaccaaagtaacat 7365
Dh 7200 TGAATTTAGTTTTTACCTATATCTATGTGAACCTATATATGAAACCAATGTGACATAT 7259
Qy 7366 ggttgtgacacacacttt 7425
Dh 7260 GGGTTTGAACACACACTT 7319
Qy 7426 caataatcatcaaglaatcatgagcagcagattatgatalcaaaaatcaaaagtaatgac 7485
Dh 7320 CAATATATTCATCAAGTATATCATGTGCCAGCGATTATGATCAAAATCAAAAGTAAATGCAC 7379
Qy 7486 atccatctcaatcaagcagatgagcagcagcagcagcagcagcagcagcagcagcagcagc 7545
Dh 7380 ATCTCATTTCACTAAGCAGTGTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7439
Qy 7546 gcttgcgaatgt 7605
Dh 7440 GCTGGCAATGAGTGTGCGAGAGTATATAGGCCAAGTTTTTCAAGAAAGTTTGAAGCACCA 7499
Qy 7606 tgggt 7665
Dh 7500 TGGT 7559
Qy 7666 tcaatgtacagaatgt 7725
Dh 7560 TCAATGTACAGAAATGT 7619

Oy	7726	tgctctggtgagcgtataacgtgcaacaaaaatgtaggtgtcctctcgtgcaagggaacctg	7785
Db	7620	tggtctgctgtgcagctatgacatgcacacaaaaatgggtctctctgagcaacggaaacctgg	7679
Oy	7786	ttccatggtatactctccatgctctcgagccatggtgctcacaaggtcatccctatgaga	7845
Db	7680	ttccattggtatattgtgtcctatgcttcgcagccatggggtctcagaggggtcatccttatgaga	7739
Oy	7846	ctcttaataatactatgataccctggttaagagggcaagaatcaacagccaactctgtgggc	7905
Db	7740	ctcttaataatattactgtatgatactctggttaagggcaagaatcaacagccaactctgtgggc	7799
Oy	7906	tgcaagctgctggaagccaaggcatggaagttaaagatctgctgtcaaacctgaagaa	7965
Db	7800	tgcaagctgctggaagccaaggcatggaagttaaagatattggtgcgttaaacctgaagaa	7859
Oy	7366	ccgtgtgcccaattgtctcctgaactgtcgtcttaacaatggtacacatctcaagaatggttat	8025
Db	7860	ccctgtgcccaattgtgtcctgaactgtcgtcttaacatggtatggtacatctcaagaatggttat	7919
Oy	8026	ctgcacacaagtgtatctattcttcgagccttttgatatacctcgaagaatgaagaatgagt	8085
Db	7920	ctgcacacaagtgtatatttttgcgctttttgaaattatctgaaaaatgaaatgtagact	7979
Oy	8086	tgatctttgcaaaaaatgctgtactctttaaigtatcttggaattaaigtctatcaag	8145
Db	7980	tgatattttgcaaaaaatggtgtgacttttttaattgattttggaatttaattgactctatcag	8039
Oy	8146	tgactcttgatcctcttagaatggccctcttgaagaacctgtgtatagagaatgtagc	8205
Db	8040	tgactcttgatcctcttagaatggccctcttgaagaacctgtgtgatagagaatgtagc	8099
Oy	8206	cactgcccacatcttctatctcttaigttaaigtgcatalcaqtcatgactgactgtcct	8265
Db	8100	cactgcccacatcttctatctcttaigttaaigtgcatalcaqtcatgactgactgtcct	8159
Oy	8266	agaaagaacatgtgatgtgcaggaatcctcatgaacatatattgagttctcttcagataat	8325
Db	8160	agaaagaacatgtgatgtgcaggaatcctcatgaacatatattgagttctcttcagataat	8219
Oy	8326	taagaatacctcttaacatccatctcatcaatcaaatcttcttgagtgtatgctgtacgtga	8385
Db	8220	tagagtaactcttaacatccatctcatcaatcaaatcttcttgagtgtatgctgtacgtga	8279
Oy	8386	aagsgatgtaactgataagaactagagagatatlaagtcacgaactcttcgtgyc	8445
Db	8280	aagsgatgtgtaactgataagaactagagagatatlaagtcacgaactcttcgtgyc	8339
Oy	8446	catcttaataagcctcactgtgttaaagaataatgagttgctcttggtttagaagcccaat	8505
Db	8340	catgtttatcagctcactggtgttaacaaatrtatagttgtcttggtttagaagcccaat	8399
Oy	8506	gtacaacatattggtgcagcct	8565
Db	8400	gtacaacatattggtgcagcct	8458
Oy	8566	aagatataaggttccaaagtttaacaatgaatctcttcaacagggaaaaacagctagcttga	8625
Db	8459	aagatataaggttccaaagtttaacaatgaatctcttcaacagggaaaaacagctagcttga	8518
Oy	8626	aaactgtctgaaaaaacaacactctgtcttatagtcatlltagtcaactcacaataatgtgct	8685
Db	8519	aaactgtctgaaaaaacaacactctgtcttatagtcatlltagtcaactcacaataatgtgct	8578
Oy	8686	tgcaagatatgtgataccccaataatcctgaacagttcctcaaatlltcaactcttcaatcac	8745
Db	8579	tgcaagatatgtgataccccaataatcctgaacagttcctcaaatlltcaactcttcaatcac	8638
Oy	8746	tagtcaagaanaataataaaaaacaacaaatctccaaatgtagagcatllttcagaagtcttc	8805
Db	8639	tagtcaagaanaataataaaaaacaacaaatctccaaatgtagagcatllttcagaagtcttc	8698
Oy	8806	taaccagctctatcttctctagtcagtaaacatcttgtaaaaaactggttcaactaataact	8865

Dh	8639	TAACCACTCTATTTTTTCAGCATATAACATTTGTAAATAACTGTTCACATAACT	8758
Qy	8866	tactgttaactgctcttgagagaaagaataatgagagaactatgcttgggggaagttc	8925
Dh	8759	TACTGTTAACTGCTTCGAGGAAAMAAAATATGAGAACTATGTGGGCAATTC	8818
Qy	8926	aagtgactttcaatacatcaatacttaactactcttccaaacttttccaaatttgaacatcaac	8985
Dh	8819	AAGGATCTTTCATATACATTACTACTAATCTTCACATTTTCGAAAATATGAATATTAAC	8878
Qy	8986	gctaaagtgtaagaactcagatltccaalaaacttccatatlattttaaatttcaga	9045
Dh	8879	GCTAAAGGTGTAAAGCTTCAGATTTCCAAATATCTCTTATATTTTAAATTTACGA	8938
Qy	9046	atattataiaaccacgcgcgtgaaagaasaaatgagtgttttgaagaatgaagtcacat	9105
Dh	8939	ATATTATATACCCACGCTGGAAGAAAAGAAAATGATTTGTGAAAGTTAAAGTCAT	8998
Qy	9106	atgattttaataataagtaaegaagcatalttccaatactagtagatgcaatcgtt	9165
Dh	8999	ATTGATTTTAAATATATAGTAAATGAAGCATATTTCCAAATACATGATGATGGATGCTT	9058
Qy	9166	gcaatttaagatcttccaasaaatacagaattatagaataatttccatccaatttaaat	9225
Dh	9059	GCATTTTACATATCTTCAAAATAACAGATTTTATGATATATTTCTCTCATTTAAAT	9118
Qy	9226	ttttcaaaatccaagaatgtagtcttccatcttactaaatcgatattcatttccaat	9285
Dh	9119	TTTTCAAAATCAAAAGTTATGTTTCCTCATTTACTAAATGCTATTCATTCCTCATY	9178
Qy	9286	atagttaactctatgagaactccttacttccgttccctcgtgatttaaggccatatttaa	9345
Dh	9179	ATAGTAATTCATATAGGACACTCTTACTCTGGTCTCTCGATTTCAAGGCCATATTTTAA	9238
Qy	9346	aaatccaagaagcacttgaaactatttgaagaagaacagacattttaaacaagattgaa	9405
Dh	9239	AAAATCAAAAGCAGCTGTAACATATTTTGAAAGAAAACACACATTTTAAACAGATTGAA	9298
Qy	9406	aggaccctcttgaagctagaacaacatctatgattataacttcaatcaactgctgta	9465
Dh	9299	AGGACCTCTTGAGAGCTAGAAACAAATCTATAGTATTCATCTTATTAATACGTGTGA	9358
Qy	9466	ccctttaaactagtaatttttcaactttccctgftaaaccatatttggtagaactttt	9525
Dh	9359	CCTTTTAAATATAGTAATTTTTCATTTTCGTGTGTAACCTAATTTGGTATGAATTTT	9418
Qy	9526	taccaactctatactcaatcaagcaaaattctgtatattccctgtggaatgtactatg	9585
Dh	9419	TACCAACTCTATACCAATCAATCAAGAAAATTTCTGTATTTCCCTGTGAAATGTACATG	9478
Qy	9586	tgaacttcaagaattctccaataatcggttcaasaaattctgcttttgatcttggagac	9645
Dh	9479	TGAGTTTGAAGAAATTCCTCAAAATATCGTGTTCAAAAATTTCTGCTTTTGATCTTTGGGAC	9538
Qy	9646	acctagaagaactatttaacaactgtaalatagagaatatcagaagaataataaagccc	9705
Dh	9539	ACCTCAGAAAACCTTATTAACAACTGTAATATGAGAAATACAGAGAAATATATTAAGCCC	9598
Qy	9706	tctatacaataatgcccagagcaatctatgtgttaasaaacaacaaactcacaactatg	9765
Dh	9599	TCTATACATAAATGCCCAGCAATTCATTTGTATTAATAACACCAAACTCTCACACTACTG	9658
Qy	9766	tatttcatatctgtactgaagaagaaatgcttgtgactatitaaatgtygcacatcttc	9825
Dh	9659	TATTTCAATATCTGTACTGAAGCAATGCTTTGTGACTATTAATATGTGCACATCATTC	9718
Qy	9826	attca 9830	
Dh	9719	ATTCA 9723	

RESULT 12

Db 1740 TCATCAACAAGTCATGAGAGCTGCTGATGAGAGAAATTCTGGGCTGGTATTCTTCA 1799
QY 1906 CTGGAATtactccagagcaagcatltagcttccccatcatlgtcaaglaacaagatccgaatlg 1965
Db 1800 CTGGAATtactccagagcaagcatltagcttccccatcatlgtcaaglaacaagatccgaatlg 1859
QY 1966 acatltgacaatltgtgagaggaacaataaatacaaggaatgggtactgtgagacccgttcc 2025
Db 1860 ACATTTGACATGTGAGAGAGACAAATAATCAAGATGGGTACTGGAGCCCGTGTCTTC 1919
QY 2026 gaactaaccccttggagacatgcgtltagcttgggggggcttcgcctacttgcagatg 2085
Db 1920 GAGCTGAGCCCTTGGAGAGATCGGTACTCTGGGGGGGCTTCGGCTACTTGCAGGATG 1979
QY 2086 tgggtgagagcaatcatcaatcaaggtlgtgagagcaacgagaaagaacatgtgtctata 2145
Db 1980 TGGTGGAGAGGAGCATATCATAGAGGTGCTGACGGGACCCGAGAAAGAAACGTGCTCAT 2039
QY 2146 tgcacaagatgacctatccctgttaeqtltgataacatcttctgcggtgtgataagccgt 2205
Db 2040 TGCAACAGATGCCCTATCCCTGTACCTGTGATGACATCTTTCGCGGGTGTATAGCCGT 2099
QY 2206 caatggcccttcatbagctgtgagcgtggttactcaatggtgtgtgtatcatcaaggga 2265
Db 2100 CAATGCCCTCTTCATACGCTGGCTGGATTTACTCAGTGGCTGTGATATCAAGGCA 2159
QY 2266 tctgtata tgcagaagagcaagcaagcgtgaaagaacatltgcagatcatltaggcttgcaca 2325
Db 2160 TCGGTATGAG 2219
QY 2326 gcaatactctgtttagctgtltagttagttagttagttagttagttagttagttagttag 2385
Db 2220 GCAATCCCTGTGATGAGTGTATGTAGCTCATCTCTCTCTGTGAGAGAGAGAGAGAG 2279
QY 2386 tgcagtgtgtatcatcaatltgaagaacatltgcacctacgttgcagatccagcgtgtgt 2445
Db 2280 TGTAGTGTGTATCTTAAGTTAGAGAACTGCTGCTTACAGTGTATCCAGCTGTGTGT 2339
QY 2446 ttgtcttctgttccgtgtlgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2505
Db 2340 TTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2399
QY 2506 tcttctcagaagcaacatgtgagcaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2565
Db 2400 TCTTCTCCAGAGCAACCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2459
QY 2566 tgcacctacgttctgt 2625
Db 2460 TGCCCTACGTCTGT 2519
QY 2626 ctgacctgtgtctgt 2685
Db 2520 CTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2579
QY 2686 agcagggagatgtgag 2745
Db 2580 AGCAGGGAGATGTGAG 2639
QY 2746 tcaatctcaacatctgatactcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2805
Db 2640 TCAATCTCAACCACTTGGT 2699
QY 2806 cctgttacctgt 2865
Db 2700 CCTGTACATTTGAGGCTGTCTTTCAGGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2759
QY 2866 ctgtgacaagcttctactgt 2925
Db 2760 CTGTGACCAAGTCTACTGT 2819
QY 2926 accagaagaagaatgtcaagaatctgtcatgtgagagagagagagagagagagagagag 2985
Db 2820 ACCAGAAGAAGAATATCAGAAATCTGCATGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2879

QY 2986 tgtccatccagaacctgtgttaaagtctacagagatgtgagatgaaggtgtgtgtgtgtgtgt 3045
Db 2880 TGTTCATTTACAGAACTGTGTAAAGTGTACAGAGATGGAGATAGAGTGTGTGTGTGTGTGT 2939
QY 3046 tggcactgaatttataagagccagatcacctcttctgtgtgtgtgtgtgtgtgtgtgtgtgt 3105
Db 2940 TGGCAGTGAATTTTATAGAGGGCCAGATCACCTCTTCTGTGGCCACAAATGAGAGCGGGA 2999
QY 3106 agacagaccacatgtcaatctctgacaggtgtgttccccagactcgtgtgtgtgtgtgtgt 3165
Db 3000 AGACAGCACCATGTGTCAATCTGTACCGGGTGTTCCTCCCGACCTCGGGCACCCCTACA 3059
QY 3166 tctctggagaagaacttgcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3225
Db 3060 TCTCTGGAAAGAACATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3119
QY 3226 cccagacataagctgt 3285
Db 3120 CCCAGCATATAGCTGT 3179
QY 3286 gcttgaagagcttctgt 3345
Db 3180 GCTTGAAGAGGCTCTCTGT 3239
QY 3346 ttgt 3405
Db 3240 TTGTTGTGCATTCAGCAAGAGT 3299
QY 3406 gaaagctatctgt 3465
Db 3300 GAAAGCTATCTGT 3359
QY 3466 ccagaagctgt 3525
Db 3360 CCACAGCTGT 3419
QY 3526 gcaagaagcagacatcttct 3585
Db 3420 GACAAAGGCGCACATTTATTTCTCTACACACCATGTGATGAAGAGAGAGAGAGAGAGAG 3479
QY 3586 acagagatgtcatalctctccatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3645
Db 3480 ACAGATTTGCAATCTCTCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3539
QY 3646 agaaagagctgt 3705
Db 3540 AGAACAGCTGT 3599
QY 3706 tcaagttctgtcagaagaacagtagtagacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3765
Db 3600 TCGATTCTCTGACAAACAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 3659
QY 3766 ctcaagagagctgt 3825
Db 3660 CTCAGAGAGATTTGT 3719
QY 3826 atgtctctgtctatctcaacctcatcaagaagaatgtgtgtgtgtgtgtgtgtgtgtgtgt 3885
Db 3720 ATGTCTCTGTATCTCAACCTTATCAAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3779
QY 3886 acataagagcatgtgacatgt 3945
Db 3780 ACATAGGGCATGTAGGT 3839
QY 3946 tggaaactcttcatgtgatgt 4005
Db 3840 TGGAACTCTTTCATGTAGATTTGATGACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3899
QY 4006 tctcaag 4065
Db 3900 TCTCAG 3959


```

QY 8446 catgltatcagctacgtggtttacaataatagtgctgtgtgttagagccact 8505
DB 8340 CATGTATTCAGCTCAGCTGGTTTACAAATATAGTTTCTCTGTGGTTTGAGAGCCACT 8399
QY 8506 gtaacaatattggcagccttttttttttttlaattgcaacaatgcaaaagcaaga 8565
DB 8400 GTAACAATACCTGGGCAACC-TTTTTTTTTTTTTTAAATTCACAAATATGCAAAAGCCACA 8458
QY 8566 aagataaggtgtcaagtttaacaatagatcttccaagaaggaaagcagctgttga 8625
DB 8459 AAGATATAGGGTCCAGCAAGTCTTAACAAATGATTCATCAAGGGAAGAACAGTACGTGA 8518
QY 8626 aaactgtcgaanaaacaactgtgtttagtggcaattagacctcaataatgtgctt 8685
DB 8519 AAACCTGTGAAAAACACACTGTGTATGGCATTTAGTACCTTCAATATATGTGCTT 8578
QY 8686 tgcagatattggtacccttaactgtgcacgtcccaatttcaatcttcaatcac 8745
DB 8579 TGCAGATATTGGATACCCCAATTAATCTGACAGTCTCAAAATTTTCATCTTCATATCAC 8638
QY 8746 tagtcaagaanaataataaacaacaatactccatagagacatlttccagatcttc 8805
DB 8639 TAGTCAGAGAAATATATAAACAACAATCTTCATATGAGACATTTTTCAGAGTTTTC 8698
QY 8806 taaccagcttatttctttagtcaaglaaacattgtlaaanaactgtttccactaact 8865
DB 8699 TAACCCAGTCTATTTTCTAGTCAGTAAACATTTGTAATAATCTGTTCATATATCT 8758
QY 8866 tactgttaactgtctggaagaaagaaataatgagagacatgtttggggaagctc 8925
DB 8759 TACTGTTAACTGTCTGAGGAGAAAGAAATATGAGAGAACTATTTGGGGAAGTTTC 8818
QY 8926 aagtgatcttcaatatactactacttcttccacttlttccaanaattggaatatac 8985
DB 8819 AAGGATCTTTCATATATCATATCTACTACTTCTTCCAAATTTGAAATATTAAC 8878
QY 8986 gctaaagtgtaagacttcaagattcaaatatccttctataatttttaattacaga 9045
DB 8879 GCTAAAGGTGTAGACTTTCAGATTTCAAAATTAATCTTATATTTTAAATTTACAGA 8938
QY 9046 atattataaaccactgtcgaanaaagaaagaaatgattgttttaagtttaagtcact 9105
DB 8939 ATATATATATACCCACTGCTGGAAGAAAGAAATATATGTTTGTAGAAATTAAGTCAAT 8998
QY 9106 attgattttaaataatgaatgaagacatatttccaataactagatgatatgcatcgt 9165
DB 8999 ATATGATTTTAAATATATAGTAATGAAGCATATTTCCAAATAGTATGATGACATCGTT 9058
QY 9166 gcaatttacaatcttccaanaatacagaattatagaataatttctcctcaatataat 9225
DB 9059 GCATTTTACAGTATCTTCAAAAATACAGAAATTAATAGAAATATTCCTCCATTTAAATAT 9118
QY 9226 tttccaanaatacagaatgatttctcctcaatatttcaataactgatttcaattcact 9285
DB 9119 TTTTCAAAATCAAAAGTTATATGTTTCTCTCATTTTACTTAAATGTAATTCATTTCTTCANT 9178
QY 9286 atagaataactgtggaactccttactcgttctcctgatttcaaggaatatttaa 9345
DB 9179 ATATGTAATATCTATGAGCAACTCTTCACTTCGTTCCCTGATTTCAAGGCCATATTTTAA 9238
QY 9346 aaatacaaaagcactgttgaactatttgaagaanaacagacatatttaataagaattaa 9405
DB 9239 AAAATCAAAAGGCACGTGTAATCTATTTGAGAAAACACMACATTTTATATACAGATTTGA 9298
QY 9406 aggaactcttctgaagctagaacaacataagtatatacatccttcaataactgttga 9465
DB 9299 AGGACCTCTTCTGAGAGCTAGAAACAATCATATAGTATATACATCTTCAATTAATCTGTGTTA 9358
QY 9466 ccttttaaaatagtaatttttaccatttccgtgtttaaactaatgtgtgtagaacttt 9525
DB 9359 CTTTTTAAATATGTAATTTTATACATTTTCCGTGTAACCTAATTTGAGGAATTTT 9418
QY 9526 taaccaacttatactcaatcaagaacaaatttctgtatatactccctgtgaagtgtaactatg 9585

```

```

DB 9419 TACCAACTTATACCTCAATCAAGCAAAATTTCTGTATATTTCCCTGGTAATGCTATG 9478
QY 9586 tgaatttcagaatacttccaataatglttcaaaaatttgccttltgcatcttggagc 9645
DB 9479 TGAGTTTTCAGAAATTCACAAATATACGTCTTCACAAATTTTGTGCTTTCATCTTTGGGAC 9538
QY 9646 accatgaanaaacttatacaactgttgaataatggaataacagaagaataataagccc 9705
DB 9539 ACCTCAGAAAACCTTATATTAACAACCTGTGAATATGAGAAATTAAGAAATTAATAGCCC 9598
QY 9706 tctatataatgccccagcaacttcaattgttlaaaaaacaacaacactcaactatg 9765
DB 9599 TCTATACATTAATATGCCAGCAACATTCATTTGTTAAAAACAACCAACCTACACTACTG 9658
QY 9766 tatttcattatctgactggaagcaaatgcttgtgactatlaaagtltgacatcatc 9825
DB 9659 TATTTTCATTATCTGTACGAAAGCAAAATGCTTGTGATATTAATGTTGACATCATTC 9718
QY 9826 attca 9830
DB 9719 ATTCA 9723

```

RESULT 13
AX059973 9497 bp DNA linear PART 22-JAN-2001

LOCUS
DEFINITION Sequence 91 from Patent W0078970.
ACCESSION AX059973
VERSION AX059973.1 GI:12405631
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 9497)
Denefle, P., Rosler-Montus, M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Assmann, G., Rust, S., Funke, H., and Brewer, H.B.
Nucleic and proteinic acids corresponding to human gene abcl
JOURNAL Patent: WO 0078970-A 91 28-DEC-2000.
Aventis Pharma S.A. (FR)
Location/Qualifiers
FEATURES
source 1..9497
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2600 a 2115 c 2217 g 2564 t 1 others
ORIGIN

Query Match 90.4%; Score 9444.6; DB 6; Length 9497;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 9464; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

```

QY 351 caacaatgtaagctgttaactggaagtgtgcctgtatcttctcgtatcgtatc 410
DB 1 CAACATGTGACGCTGTACGGAAGTGCCGCGCTCTATTATTTCTCCGATCTGATC 60
QY 411 tcttgcggtgagctacccaccctatgatacaaatgaatgcatlttccaataagaacc 470
DB 61 TCTTTGGGCTGAGCTACCCACTTATGAAACAACATGATGCCATTTTCCAAATTAAGCC 120
QY 471 atgcctctgaggaacacttcttgggttcaaggagattactgtlaatgccaaacacc 530
DB 121 ATGCCCTGTGACGAGAACATTTCTTGGGTTGAGGGGATATCTGTATATGCAACAAACCC 180
QY 531 tgttccgttaccgactcctctgtgggaggtcccgaggtgtgtggaactttaaactc 590
DB 181 TGTTCCTGTTACCCGACTCTGTGGGAGGCTCCGGAAGTTGTGGAACCTTTAAACAATCC 240
QY 591 atgtgctgcgctgttctcagatgctcggaggtccttatacagccagaagaagacc 650
DB 241 ATGTGCTGCTGCGCTGTTCTCAGATGCTCGAGGCTCTTTTATACAGCCAGAAAGACACC 300

```

OY	651	agatgaggaacatgtgcaagaattcttggaacaattacagagatcaagaatccagctca	710
Db	301	AGCATGGAAGACATGGCGAAAGTCTGAGAACATTACAGCAGATCAAGAAATCCAGTCA	360
OY	711	aacttgaagcttcaaaatttctctgtgtggaacaatgaacctctctctgtgttctatatac	770
Db	361	AACTTGAAGCTTCAGATTCTCTGGTGGACATGAACCTTCTGGGTCTTGATTAC	420
OY	771	aacctctctcccaagtctactgtgacaagaatgctcgaaggtctgatttcttccac	830
Db	421	AACTCTCTCTCCCAAGTCTACTGTGGACAAGATGCTGAGGGGTGATGTATTCTCCAC	480
OY	831	aaggtattcttgcgaagctcacagattacaattgacaagtctgtgcaatgatacaaatca	890
Db	481	AAGTATTCTTTCGAAAGGTACACGTTACTATTGACAATCTGTGCATTTGATCAAAATCA	540
OY	891	gaagaatgatactaacctgtgtgacaagaagttcttgagctttgtgtcctacaagaag	950
Db	541	GAAAGATGTGATTAACATTGGTGACCAAGAAAGTTCTTGAGCTTTGTGGCTTACCAAGGAC	600
OY	951	aaactgtctcgaacagcagagactgtgttccacaatgagacacccgaagccaatctgt	1010
Db	601	AAACTGCTCTGACAGACGAGACTCTGTCTCCAACTATGACATCTGTAAACCAATCTCG	660
OY	1011	agaacactaaactatatactccctcccgagcaagagctgtgctgaagccaaaaa	1070
Db	661	AGAACACTTAAACTCTACATCTCCCTTCCGACCAAGAGAGCTGGCGAAGCCACAAAACA	720
OY	1071	tgtgtgataatgctcttggaactcttgcccaagagcgtgttcacaagaagaagtgaagtgac	1130
Db	721	TTCGCTGATATCTTGTGGAGACTCTGCGCCAGAGAGCTTTCAGATGAGAAAGTGGAGTGAC	780
OY	1131	atgagcaaggaagtgtatgtttctgtaccaaigtgaacagctccagctcctccaccaaatc	1190
Db	781	ATGCGACAGAGGAGTGAATGTTCTTGACCAATGTGAACAGCTCAGTCTCTCCACCCCAATC	840
OY	1191	taccaggtctgtctgattgtctgtcgcggactcccgaggagagggggtctaaataag	1250
Db	841	TACACGCTGTGTCTGATTTGTCTCGGGCAATCCGAGGGGGGGGCTCAAAATCAAG	900
OY	1251	tctctcaactgtgatatgagagcaacaactacaagccctcttggagagaaatggaactgag	1310
Db	901	TCTCTCAACTGATGATGAGGACAACTACAAAAGCCCTCTTGGAGGCAATGGCACTGAG	960
OY	1311	gaagatgtcgaacctctatgacaactctacaactccttactgcaatgtattgataag	1370
Db	961	GAAAGTGTGTGAACCTTCTGTGACAACCTGTACAACTCTTACTGTCAATGATTTATGATAG	1020
OY	1371	aatttggagcttagtctctcttcccgatatacttgaaagctctgaagcgcgtcgtglt	1430
Db	1021	AATTTGGAGTCTAATCTCTTCTTCCCGATTATCTGAAAAGCTCTAAGCCGCTGCTGTT	1080
OY	1431	gggaagaactctgtatacaacttgaaactcgaagccacaaggaagtlcagcttgatgagac	1490
Db	1081	GGGAAGATCTGTATACACCTGACACTCCAGCCACAAAGSCAAGTATGGCTAGAGGTGAAC	1140
OY	1491	aagaccttccgaagcagctgctgtgttccatgatacttggaaagcagatgttgggaggaactcagc	1550
Db	1141	AAGACTCTTCCAGGAACATGGGTGTGTTCAGATCTTGAAGGATGTGGAGAGAACTCAGC	1200
OY	1551	ccaagaatctgaaactcttcaatggagaacagccaagaatgaaactgtctccgaatgctgtg	1610
Db	1201	CCCAAGATCTGGACCTTCAATGGAACAGCAAGAAATGAGACTTGTCCGATGCTGTGG	1260
OY	1611	gacagcaaggagaacatgacaacttttgggaacagcagttgagatgcttagatgtgacagcc	1670
Db	1261	GACACACAGGACAAATGACACTTTTGGGAACACAGACTTGGATGGCTGTGATGTGGACACC	1320
OY	1671	caagagctcgtgagggttttttggccaagcaccgagagatgctcagatccaagtaatgattct	1730
Db	1321	CAAGACATCTGTGGGCTTTTGTGGCCAAACACCAAGAGATGTCCAGTCCAGTAATGTGTTCT	1380

QY	1731	gttcaacccctggagagaagacttccaacgagactaaacggaaatccggacacatactcgg	1790
Db	1381	gtgtacacccctggagagaagacttccaacgagactaaacggaaatccggacacatactcgg	1440
QY	1791	tctcatgagtggttcaaccctgaaccaagcttagaacaccttagacaagaagttctgctcatc	1850
Db	1441	tttcattgagtggttcaaccctgaaccaagcttagaacaccttagacaagaagttctgctcatc	1500
QY	1851	aacaagctcaatgagactgctgctgagatggaagaaattctcggctgblatgtgtcaatgga	1910
Db	1501	aacaagctcaatgagactgctgctgagatggaagaaattctcggctgblatgtgtcaatgga	1560
QY	1911	attactccaggcagcatctgagctgcccccaactgtfcaagtgtaagaatccgaatggaact	1970
Db	1561	attactccaggcagcatctgagctgcccccaactgtfcaagtgtaagaatccgaatggaact	1620
QY	1971	gacaatgtggaaggaacaaataaactcaagagatggtagactggaacctgctcccgagct	2030
Db	1621	gacaatgtggaaggaacaaataaactcaagagatggtagactggaacctgctcccgagct	1680
QY	2031	gaacctcttgaagacatgctgcgtacgtctcggggggcttcgcctacttgcaagatgtgtg	2090
Db	1681	gaacctcttgaagacatgctgcgtacgtctcggggggcttcgcctacttgcaagatgtgtg	1740
QY	2091	gagcaggaacatcatcaagtggtgctgacgggacacggaaagaacacgtggtctataatgcaa	2150
Db	1741	gagcaggaacatcatcaagtggtgctgacgggacacggaaagaacacgtggtctataatgcaa	1800
QY	2151	cagatgcccctatcccctgttatcgttgaatgaactttctcgggtgataagtcggttcaatg	2210
Db	1801	cagatgcccctatcccctgttatcgttgaatgaactttctcgggtgataagtcggttcaatg	1860
QY	2211	ccccctctcatgacgctgctgcctggatcttactcaatgagtgctgtgataccaagggcatgtg	2270
Db	1861	ccccctctcatgacgctgctgcctggatcttactcaatgagtgctgtgataccaagggcatgtg	1920
QY	2271	tatggaagagggagacagggctggaagaaacatatccggaatcaatggctcggagaacagata	2330
Db	1921	tatggaagagggagacagggctggaagaaacatatccggaatcaatggctcggagaacagata	1980
QY	2331	cctcgttgtaactgctgtcatatagtagcctatctccctctcttctgttagcgctgacgtcta	2390
Db	1981	cctcgttgtaactgctgtcatatagtagcctatctccctctcttctgttagcgctgacgtcta	2040
QY	2391	gttgatcatccctgaagattagaagaaactgctgcctctacagtatccaagcgtgtgtgttgc	2450
Db	2041	gttgatcatccctgaagattagaagaaactgctgcctctacagtatccaagcgtgtgtgttgc	2100
QY	2451	tcccgtgtccgtgttgcctgtgtgtgagaaatctctcgtcagtgcttcctgattagaacactctc	2510
Db	2101	tcccgtgtccgtgttgcctgtgtgtgagaaatctctcgtcagtgcttcctgattagaacactctc	2160
QY	2511	tccagagccaacccggcagcagcagctgtgvggggagcatcatctactcaagcgttacctgcc	2570
Db	2161	tccagagccaacccggcagcagcagctgtgvggggagcatcatctactcaagcgttacctgcc	2220
QY	2571	tacgtccctgtgtgtgcatctgagcagagactacgtgtggcttcacactcaagaatctctgtagc	2630
Db	2221	tacgtccctgtgtgtgcatctgagcagagactacgtgtggcttcacactcaagaatctctgtagc	2280
QY	2631	ctgctgtctcctgtgtgcttlttggtctgtgctgtgagtaacttgcccttlttgaaagagag	2690
Db	2281	ctgctgtctcctgtgtgcttlttggtctgtgctgtgagtaacttgcccttlttgaaagagag	2340
QY	2691	ggcatttgagtgagttggaagaaactgttggaagtcctgttgaaagaaagatgagctcaat	2750
Db	2341	ggcatttgagtgagttggaagaaactgttggaagtcctgttgaaagaaagatgagctcaat	2400
QY	2751	ctcacacactgcatctccatgatgtctgttggacaactctccctatagtgggtgtgtagcctg	2810
Db	2401	ctcacacactgcatctccatgatgtctgttggacaactctccctatagtgggtgtgtagcctg	2460
QY	2811	tacatttgagtgctcttctccagccagtlacaggaattcccaagccctgtlatlttccctgc	2870

|||||
Db 2461 TACATTGAGGCTGCTTTCCAGGCCAGTACGGAATTCGCCAGGCCCTGTATTTCCTTCC 2520
QY 2871 accaagtcctactggttttggcaggaagatgatgaagaagccaccccttgcttccaaacag 2930
Db 2521 ACCAAGTCTTACTGggttggcaggaagatgatgaagaagccaccccttgcttccaaacag 2580
QY 2931 aagaagaatgcagaatctcgaatgaagaagaagccacccacttgaagcttgagcgttcc 2990
Db 2581 AAGGAATATCAGAAATCTCATGAGAGGAGAACCCACCACCTTGAAGCTGGGCGTCTCC 2640
QY 2991 attcagaacctggttaaaagctacccagatggaatgaagtggtctgtcatgtgctgca 3050
Db 2641 ATTTCAGAACTGGTAAAGCTTACCCAGATGGGATGAAGTGGCTTCATGGCTGGCA 2700
QY 3051 ctgaattttatagaggccagatcacctcctcttgaggcacaatggaacgaggaagacg 3110
Db 2701 CTGAATTTTATAGGGCCAGATCACCTCTTCTGGCCACATGTGAGCGGGGAAGAG 2760
QY 3111 accacatgtcaatcctctgaccggtgttcccccgaacctgggagccgactacatctg 3170
Db 2761 ACCACATGTCAATCCTGACCGGGGTGTTCGCCGACCTCGGGCACCCCTACATCTCG 2820
QY 3171 ggaaaagacatcgcctctgagatgagacacatccgacagaaaccttgagggtctgtccca 3230
Db 2821 GGAAGAAGACTTGGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGTCTGTCCCGAG 2880
QY 3231 catacgtgctgtttgacatgctgactgtctgaaacacatcgtgtctatagccgctg 3290
Db 2881 CATAAGTGTGCTTTTACATGTGTGATGTGCAAGAACACATCTGGTTCATGCCCTTGG 2940
QY 3291 aaagggtcctctgagaagacgctggaaggcgagatggaacagatgagcccttgatgtgt 3350
Db 2941 AAAGGGCTCTCTAGAGAGCGTGGAAGGCGGAGATGAGACAGATGGCCCTGTGATGTGT 3000
QY 3351 ttgcacatcaagcaagcttgaagaaacaaacaaagccagctgttcaggttgaaatgcagaag 3410
Db 3001 TTGCCATCAAGCAAGCTGAAACAAACAAAGCCACCTGTCAAGTGTGATGCAAGAAAG 3060
QY 3411 ctatcgtgaccttgacctgtctgaggagatcgaaggtgtatcttgaatgaaccaca 3470
Db 3061 CTATCTGTGGCTTTGGCTTTGTGGGGGATCTAAGGTGTATCTTGATGAACCCACA 3120
QY 3471 gctgtgttggaaccttactcccgcaagggaatataggagctgctctgaataaccgaca 3530
Db 3121 GCTGTGTGTGAGCCCTTACTCCCGCAGGGAATATGAGACTGCTGTAATAACGACAA 3180
QY 3531 ggcgcgacattatctctctacacacacatgatatgaagcggaagcgtctctggggagag 3590
Db 3181 GGCGCACCATTTTCTCTCTACACACACATGATGATGAAGCGAGCTCTGGGGGACAGG 3240
QY 3591 attgcatcatctcccatlbggaagctgtgtgtgtgagcttccctgttctgaagaac 3650
Db 3241 ATTGCCATCATCTCCCATGGGAAGCTGTGTGTGTGTGTCTCCCTGTTCTGAAGAAC 3300
QY 3651 cagcttggaagacggtactactactgacctgtgtcagaagaatagtgtgaatccctccat 3710
Db 3301 CAGCTGGGAACAGGCTTACTTACCTGACCTTGCTGAAGAAAGATGTGAATCCCTCCAT 3360
QY 3711 tccctgagaacacgtatgtagcactgtgtcataccctgaanaaagagagacagtttctca 3770
Db 3361 TCTCGAGAAACAGTATGACACTGTGTCTATACCTCAAAAAGAGAGACAGCTGTCTCAG 3420
QY 3771 agcagttctgtagtctgacctgggagcagacacatgagatgacacgctgacacatcgtc 3830
Db 3421 AGCAGTTCTGATGCTGGCTGGGACGACCATGAGAGTGAACACCTGACCTCATGTGTC 3480
QY 3831 tctgcatctccaacctacatcaggaagcatgtgtctgaagcccgctgttgaaacacata 3890
Db 3481 TCTGCTATCTCAACCTCTATCAAGAAACATGTGTGTGAAGCCCGCTGTGGAACACATA 3540
QY 3891 gggcatalgagctgacctatgtgtctgcacatacgaagctgctaaggagagaccttctgaa 3950
|||||

Db 3541 GGGCATGAGCTGACCTATGTGCTGOCATATGAAGCTGCTAAGAGAGAGCCTTGTGAA 3600
QY 3951 cctcttcagatgtatgagacgggtctccaaacctgggacatlttaattatgacatca 4010
Db 3601 CTCTTCTATGAGATTGATGACCGGCTCTCAAGCTCGGACATTTCTATGATGACATCTCA 3660
QY 4011 ggaagacccttggaagaatatctcccaaggctggccgaagaagctgggttgatgtctgag 4070
Db 3661 GAGAGACCCCTGGAAGAAATTTCTCTCAAGTGGCCCAAGAGATGGGGTGGATGCTGAG 3720
QY 4071 acctagaatgtacctgtgccagcaagacgaacagcgggctctcgaggacagacagc 4130
Db 3721 ACCCTGATGTGTACTCTTCCAGCAAGACGAACAGGGGGGCTTCCGGGACCAACAGAGC 3780
QY 4131 tgtctgcgcccttcaactgaagatgtagtctgtatccaaatgatatctgcatagacca 4190
Db 3781 TGTCTGCCCGCTTCACTGAAGATGATGCTGCTGATCCAAATGATTTGTGACATGACCCA 3840
QY 4191 gaatccagaagacagactgtctcagtggatggaatgacaaaggctcctaccagtgaaa 4250
Db 3841 GAATCCAGAGAGACAGACTTGTCTCAGTGGATGGATGGCAAAAGGCTCTACAGGTGAAA 3900
QY 4251 ggcctggaacttacacagcaacagcttggtggcccttctgtggaagagactgctaattg 4310
Db 3901 GCTTGAACCTTACACAGCAACAGTTGTGSCCTTTTGTGGAAGAACTGTATTTGCC 3960
QY 4311 agaaggagctggaagaaagatttttgcacagatgtcttgccagctgtgtctgcat 4370
Db 3961 AGAGGAGTCCGAAAGGATTTTGTGTCAAGTGTCTTGCACAGTGTGTGTGTGTGTGAT 4020
QY 4371 ggcctgtgtcagcctgagatgtgtccaccccttggcaagatccccacccctggaaatcag 4430
Db 4021 GCCCTGTGTACCCCTGATGTGTCCACCCCTTGTGCAAGTATCCCAAGCTGTGAACCTT 4080
QY 4431 cccctgagtlacacagacagtlacacatltgttcagcaatgagctccttgagacacgga 4490
Db 4081 CCTTGATGTACCAAGCAAGTATGATCATATTTGTGCAATGATGTCTCTGAGGACAGGGA 4140
QY 4491 accctggaactctaaagccctccacaaagacccctgtgtctggagaccgctgatggaa 4550
Db 4141 ACCCTGGAATCTTAAAGCCCTCACCAAGACCTGTGCGGACCCCTGTATGGAA 4200
QY 4551 ggaaccccaatcccaagacagcccttgccagcagggaggaagaaagtlgaaacactgcccc 4610
Db 4201 GGAACCCCAATCCCAAGACAGCCCTGCCAGGAGGAGGAAGTGTGACACTGTGCCCA 4260
QY 4611 gttcccaagacatcagagacctcttccagaatggaacgtgcaatgacgaacctca 4670
Db 4261 GTTCCCAAGACATCATGAGACTTCTCCAGATGGGAATGTGAACATGTCAAGAACCTTCA 4320
QY 4671 cctgcatgacctgttaagcagagcaaaatcaagaagatgtctgctgtgttccccaagg 4730
Db 4321 CCTGATGCCAGTGTAGACAGCAACAAATCAAGAAAGATGTGCTGCTGTGCCCAAGG 4380
QY 4731 gcaagggggtgctgctctcccaagaagaacaaacacctgcagatatccttcagacctg 4790
Db 4381 GCAGGGGGGCTGCTCTCTCCCAAAAGAAACAAACCTCAATATCTTCAGGACTG 4440
QY 4791 acaggaagaacatctcgatattatctgtgaagacgtatgtgaatcatatagccaaagc 4850
Db 4441 ACAGGAAGAAATTTTGGATATCTGTGTAAGACGATGTGACATCATAGCCAAAAGC 4500
QY 4851 ttaagaacaagatctgggtgaatgagtttaagtatggcggttccctgggtgtcagtt 4910
Db 4501 TTAAGAACAAGATCTGGGTAATGATTTAGATATGAGCGGCTTTTCCCTGGGTGTACAG 4560
QY 4911 aatatcaagacactctccgagtcagaagatgaatgaatgacatcaaaacaaatgaaagaa 4970
Db 4561 AATACTCAAGCACTTCTCCGAGTCAAGAAAGTTAATGATCCACCAACAAATGAAGAAA 4620
QY 4971 caactaaagcttgccaaagacagcttctgcagatcgaatlttccaaacagcttggaaagatt 5030
Db 4621 CACCTAAAGCTGGCAAGGACAGTTCGAGATGCAATTTCTCAACAGCTTGGGAATTT 4680
|||||

QY 5031 atgacagacgtgagaccagaaataatgcaagtggtgttcaataacaaaggtctgagat 5090
|||||
Db 4681 ATGACAGAGACTGACACACAGAAATATGTCAGAGTGTTGGTTCATTAACAAAGGGCTGGCAT 4740
QY 5091 gcaatcagctcttctctgaatgcatcaaatgcaatctccgggccaactgtcaaaag 5150
|||||
Db 4741 GCATATGAGCTTTCTTGAAATGTCATCAACAAATGCGCATTTCCGGGCCAACTGGAAAAAG 4800
QY 5151 ggaagaacacctagccatattgaaatctactgtcttcaatcatccctgaatctcaacag 5210
|||||
Db 4801 GGAGAGAACCCCTTAGCCATTATGGAATTAAGTTTCAATCAATCCCTGAAATTCACCAAG 4860
QY 5211 cagcagctctcagaggtgtgctgtgcaacacatcagtgagctgtctgtgtcactgt 5270
|||||
Db 4861 CAGCAGACTCTCAGAGGTGGCTCCGATGACACATCATGATGATGTCCTTGTCATCTGT 4920
QY 5271 gtaactcttgcaatgtctctgtctccagcagcttgtctgtatctctgatacagaagcg 5330
|||||
Db 4921 GTCATCTTTGCAATGTCTTGTCCAGCACCTTTGTGTATTCCTGATTCAGAGAGCGG 4980
QY 5331 gtcaagaagaacaaacctgtcagttcatcagtgagtgagtgaaactgttcaactgtctc 5390
|||||
Db 4981 GTGACGAAAGCAAAACACTGCGATTCATCAAGTGAAGTAAAGCTGTCTACTAGGCTC 5040
QY 5391 tctcaattgtcttgagatatgtcaaatctacgtgtctccctgcacacactgtgtcaatc 5450
|||||
Db 5041 TCTAATTTTGTGTGGATATGTGCAATTAAGTTTGTCCCGACCACTGGTCTATTATCATC 5100
QY 5451 ttcaatctgtccagcagaagatctctgtctccctcccaaatctgtctgtctagccctt 5510
|||||
Db 5101 TTCAATCTGTCTCCAGCAGAAAGTCTATGTCTCTCCACCAATCTGTCTGTAGCCCTT 5160
QY 5511 ctacttctgtatgagtgatcaacacactctcaatgtaccagcccttgtgttc 5570
|||||
Db 5161 CTACTTTGTGTATGAGTGATGTAATCAACCTCTCATGTACCAAGCTCTTGTGTTTC 5220
QY 5571 aagatcccaagcagacactatgtgtgtctcacaagcgttgaactcttcaatgtgcatat 5630
|||||
Db 5221 AAGATCCCAAGCAGACACTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5280
QY 5631 ggcagcgtgtgcaactgt 5690
|||||
Db 5281 GGCAGCGTGTGCGACCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5340
QY 5691 gatactctgaagtcgt 5750
|||||
Db 5341 GATATCTCTGAAGTCCGT 5400
QY 5751 gacatgtgtaaaaacacagcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5810
|||||
Db 5401 GACATGTGTAATAAACAGCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5460
QY 5811 gtgtcaacatctctgtggaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5870
|||||
Db 5461 GTGTACACATTATCTGT 5520
QY 5871 gt 5930
|||||
Db 5521 GT 5580
QY 5931 gtaaatgtcaaatctctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5990
|||||
Db 5581 GTAAATGTCAAAAGCTATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5640
QY 5991 agaatctctgtatgt 6050
|||||
Db 5641 AGAATCTCTGTATGT 5700
QY 6051 tatagaagaagcaggaagcgt 6110
|||||
Db 5701 TATAGAAGGAAGGGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5760
QY 6111 tgccttggtcctctggaagtaatctggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6170
|||||
Db 5761 TGCCTTGGGCTCTCGGGAGTTAATGGGGCTGGAAAAATCATCACTTTCAAGATGTTAAACA 5820
QY 6171 ggaataccactgtttacagaaggagatgtcttctcttaaaaaatgatatcttataaac 6230
|||||
Db 5821 GGAGATACCACTGTGTACAGAGAGATGCTTCTTCAACAAATATATCTTATCAAC 5880
QY 6231 atccatgaagtaacatcaagaatgtgactgtccctcagttctgtatgtgtgtgtgtgtgt 6290
|||||
Db 5881 ATCCATGAAGATACATCAAGAACATGGGCTACTGCTCTCAGTTGTATGTGCATACAGACTG 5940
QY 6291 ttgactgtgagaagaacacgt 6350
|||||
Db 5941 TTGACTGTGGAGAGAACACGT 6000
QY 6351 gtgtgcaaggt 6410
|||||
Db 6001 GTTGGCAAGGTTGT 6060
QY 6411 tatgtgttaactatagtgaggaacaaacgaagcctctcaagcattgtgtgtgtgtgtgt 6470
|||||
Db 6061 TATGTGTGTATCTATAGT 6120
QY 6471 ggcgggctctgt 6530
|||||
Db 6121 GCGGGGCTCTCTGT 6180
QY 6531 cgtgtctgt 6590
|||||
Db 6181 CGGTCTGT 6240
QY 6591 tctcaatgtatgagaagatgt 6650
|||||
Db 6241 TCTCATGTATGTGAAGATGTGAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6300
QY 6651 aggtcaggt 6710
|||||
Db 6301 AGGTTCAGGTGCTGT 6360
QY 6711 atagttgtgaagaatagcaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6770
|||||
Db 6361 ATAGTTGTGACAAATAGCAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6420
QY 6771 ctgtgactctgtgaaggt 6830
|||||
Db 6421 CTGTGATTTCTGT 6480
QY 6831 ccatcttcatlactctctgt 6890
|||||
Db 6481 CCATCTTCAATATCTTCTGT 6540
QY 6891 ctcaacatagaagactactgt 6950
|||||
Db 6541 CTCCACATAGAAAGACTACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6600
QY 6951 gccaaaggaacaaatgt 7010
|||||
Db 6601 GCCAAAGGACCAAGT 6660
QY 7011 gtagtgaagctgt 7070
|||||
Db 6661 GTAGTGTGAGCTGT 6720
QY 7071 gtaagaagaatccgt 7130
|||||
Db 6721 GTATGAAGAAATCTGT 6780
QY 7131 gcaacatgtgaaggt 7190
|||||
Db 6781 GCACCATGTGAAGT 6840
QY 7191 gatactgtactgtactatctcaatgtcaatgtcaatgtcaatgtcaatgtcaatgtcaat 7250
|||||

RESULT 14
AF165281

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 9497)	Rust,S., Rosier,M., Funke,H., Real,J., Amoura,Z., Piette,J.C., Delencq,J.F., Brewer,H.B., Duvenger,N., Denefle,P. and Assmann,G.	Tangier disease is caused by mutations in the gene encoding	
		ATP-binding cassette transporter 1	
		Nat. Genet. 22 (4), 352-355 (1999)	

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source
2 (bases 1 to 9497)	Rust, S., Rostler, M., Funke, H., Real, J., Amorra, Z., Piette, J. C., Deleuze, J. F., Brewer, H. B., Duvergier, N., Denelle, P. and Assmann, G.	Direct Submission	Submitted (01-JUL-1999)	Genomics, Rhone-Poulenc Rorer	2 rue Gaston Crémieux, Evry 91006, France
					Location/Qualifiers
					I..9497

```

/note="ABC transporter; ABC1 protein"
/codon_start=1

```

```
/translation="MPSAGTLPWVGIIICNANNPCFRYPPTGEPGVGNFNKSIVAR
LESDARLLLYSQKDTSMKDMRKVLPRTLQIKSSSNLKLQDFLVDNETFSGLYHNL
```

SLKPSYVDMKLRADYLIHKFVLOGOYLOLHSLCNGSKSEEMJLQGOVESELOJGLPRE
KLAABEYVJNSMMDIKTLILRTLSNHSPPRSKLEATKTLHSLSTLQAOELFSPMSM
SDMRQEMVLTWNSSSSSTOITQVSRVLYCGPBEGGLKIKSLMYEDNNYKALPFG
NGTEAELETFTYDNSTPYCDIMKBLNLSKSPLSIIMAKLVLGKILITPDTPATRO
VVAEYVKTFOELAVFHDLMBEKBLNLTWTEFNESOMELVMLLDZNRONHPWEOQ
LDGIDTADODIAVAFKAKHPEDVSSNSVYTAWEAEANETQAOARTISREMECVANLKL
EPLATEWELINKSMELLDERKPMWAGIYFTPTGSEILTEPHVYKTIIMDIDVERTNK
IKGYNCDPGRADPPEDMRVYMGFADLOVBOAIIIRVLTGKTKTGVMOOMPYC
YVDIDILRWKSRMPLMTLWATYSAVITIKGIVYKEANLKEKTRMGLDNLWFS
WFSLIPLVBSAGLVLITGLCNLPEYSDPVAFPLFAVVTIIOQLISTLSR
ANLAAOCGITFTPLYLPLYLVCAAMDYGFPTLIFASLSPVAFGQCEYALFEQ
GIGVOMDNLPESEPEEDGFMILTTSVMKLLDPTLGYMTWYIAVPPGOYGIDPWYF
PKKSWMEGSEDEKSHSGSNOKRISITGCEEPHTLKLVSIONLYVXRDCKAVY
DGLALNTYBQGITFTSLGNKAGNSKNTITGLPPEPSTGATITMGLDIREMSTIRON
LGYCPHONHVLDMLTVEHMTFARLKGSLSEKHYKAKBEMALDVLPSKLSKTSO
LSGMORKLISALAVFGSGRVVILDEPTACVDYSRGLWELLKTRQGTITLSTHH
LDEMDVLDGRILAIISHGKLCCVGSLELKNQLOSTGYLILVKVDYESSLSCHNSST
VSYLKEDEVSSOSDGLSDHSDPTLIDYVAISNLIKRHSVALVSDVADTIELHY
VLEPEAKEGAFVPELFEHIDRLDGLDTSYGETLLEELPLKFAEESVADTOSNG
TLARRRRRAFGKOSCLRPETBEDDAPNDSDIPEPSREGLDLSGMDGSGYOKVM
KITOOOFVALLMKLILARRSKCFEQAQIYLVAVYCYLALFSLIYPRCKYSLELO
PMMNEOYFTLVKNDLPEDTGTLELNLITLDPGEGTOMCSGNLPDTPCOAGEBETT
APAYQOITMDLFONGMNTMONPSPACQOSSDKIKMLPECPGAGGAPPOPKRONTAI
LODITGRNISDYLVKTYVQIILAKLKNIVANREYSGEFLGSGNTOALPSEVDNA
TKOMKRLKLAHOSADRPGLDREPMFTGQDTRNNYVWNNKGMHAISEFLVAINNA
TLRANLDKNGENSHYGTATFANHPLNLTIKOOLSEVAPMTYSDVLYISCVIFAMSEVA
SEFVELLOERYSKAKHLOFTISGKAPUTYMLNSNPMDCNKNVVPATVITIIIFCPOOKS
VYESSTNLPVALLLILGLYGSITPLMTYASVEKLPSTPAVYVVLVSNLEITGINSVATF
VLEETFTNKLNNINDILKSVELPHFCLCEGLIDPDAVNOAMALAEFEENRVSPL
SMDVGNLFMAVEGVYFPLITVLOJREFIRIRPANAISPLDNDEDEVRRRQOIT
LMDGGONDILTEKELTLPGRKKRPAYDRIQVGLPEPCGFLGNGAGKSGFTKMLT
GDTYLVGDAFENRNSLISNHEHVMGKQOPDADITELLGZEHNEFPAIAGVE
KEVKGEBMAIRKLGVLGKRYKAGNYSGNKRRKLSTMAALIGSPRVYFIDEPPTGMD
PKARFPLMNCALSVYKKGSRVYLTSHSMEDEEALCTMAITANVNERFCLDSVOHLAR
FGDGYTIVRIRAGSNPDLKQDPFFGLAPSVYSEKHRNMLDQIPLSPSLASTARF
ILSOSKRRKLIHEDYSQOTILDQYFVFNFAKDQSDDHKLKDLSTHKNOTVYDAVLTSEF
LODKREVSERY"

Query Match	Score	DB	Length
90.4%	944.6	9	9497
Best Local Similarity	99.8%	Pred. No. 0	
Matches 9464	Conservative	0	Mismatches 15; Indels 1; Gaps 1;
QY	351	caaaatgltcaagctgttactggaaglygacctgagctattatcttcctgactgac	410
Db	1	CAAACTGTCACCTGTACTGGAAGTGCGCTGACCTATTTATTTCTGTATTCCTGATTCCTGATTC	60
QY	411	tctgttcgctgagcttaccaccacctatgaacaaactlgaatgscattctccaaataaac	470
Db	61	TCGTGTGGCTGAGTACCACCCCTATGAAACAATGAAATGCAATTTCCAAATTAAGCC	120
QY	471	atgcacctcgcaggaacaccttccttgggtlctcaggggagtatctgtlaatgccaaacccc	530
Db	121	ATGCCCTCTGCAGGAACAACATCTCTGGGTTCAGGGGATATCTGTAATGCCAACAACCCC	180
QY	531	tglttcgcgttaccgacacctctcggggaagctcccgagttglttggaacctttaaacaatcc	590
Db	181	TCGTTCGGTATACCACCACTCTCTGGGGAGCTCCCGAGTGTGGAAACCTTTAAACAAATCC	240
QY	591	atctgagctcgcgcttcttcagatctcggagagcttcttlaaagccagaagaacacc	650
Db	241	ATTGTGGCTCGGCTGTCTCAGATGCTCGGAAGCTTCTTTATACGCCGAGAAAGCACCC	300
QY	651	agcatlgaagagacatgcgcaaaagtlctgagaaattacagcagatcaagaataatccagctca	710
Db	301	AGCATGAAGACATGCGCAAAAGTTCTGAAACAAATTACACAGCAATCAAGAAATCCAGACTCA	360
QY	711	aactlgaacctcaagaattctctgtgtagcaatlgaaaccttctcgggttctcatatacc	770
Db	361	AACCTGAACCTTCACATTTCTCGGGGCAATGAACCTTCTCTGGTTCCTGTATCAC	420

QY	771	aacccctctccccaagaatctactgctgagcaaatctgtagggctgatatctctccac	830
Db	421	AAACCTCTCTCCAAATCTACTGtTGAAAGATGCTGAGGCTGATATCTATCTCCAC	480
QY	831	aaggtatctttgccaagcgtacacgtttacatttgcacaagtcgtgcgaattgacaaatca	890
Db	481	AAGGTATTTTGGCAAGGCTACCAATTCATTTCACAAAGTGTGCAATGATCAAAATCA	540
QY	891	gaagagatgattcaacttggtggtaccagaagttcttgagcttggcttaccagaagag	950
Db	541	GAAAGATGATTCAACTTGGTgACCAAGAAAGTTCTGAGCTTGTGCTTACCAGGGAG	600
QY	951	aaactggtctgacaagagcgaagtacttcgttccaacatlgaaacatccatgaaccaatc	1010
Db	601	AAACGTGCTCAGCAGACGACGAGTACTTTCGTTCCAAATGAGACATCCTGAAGCCAT	660
QY	1011	agaacataaaccttacctctccctctccgagcaagagctgtgctaagccaataaca	1070
Db	661	AGAACTAAATCTTACTACTCTCCCTTCCAGAGAAAGAGCTGGCCCAACCCAAAAACA	720
QY	1071	ttgcgtcaatctttggaactctgcccagaagctgttcaagcatgaagctcgtgagttac	1130
Db	721	TTGCTGCAATATCTTTGGAGCTGTGGCCAGAGACTGTTCAGCATGAGAACTGGAGTGC	780
QY	1131	atgcgacaagagatgatagtttctgacaaatgtaaacagctccaagctctccaccaaatc	1190
Db	781	ATGCACACAGGAGGATGATGTTCTCACCAAATGTAACAGCTCCACGCTCCACCCAAATC	840
QY	1191	taccagagctgtgtctcgatattgtcttgtaggcatacccgagggagggagctgaagaatcaag	1250
Db	841	TACCAAGCTGTGTCTCGATTTGTCTGTGGGGCATCCGAGAGAGGGGGCTGAATGTCAAG	900
QY	1251	tctctcaactggtatlgaggaacaacatlaaagccctctttgagagcaattgcactgag	1310
Db	901	TCTCTCAACTGTGATGTAGAGCAACAATCAAAAGCCCTTTGGAGGCAATGTGCCTGAG	960
QY	1311	gaagatgttgaaacctctcttgaaactacagacccctacttgaaatgattgtglaag	1370
Db	961	GAAATGCTGAAACCTTCTATGACAACTTACAACTCTTACTGCAATGATTTGTGTAAG	1020
QY	1371	aattggaagctagtcctctctctcccgatlatcttgaaagctctgaagccgtctgctgt	1430
Db	1021	AATTGGAGTGTATGCTCTCTTCCCGGATATGTGAAAGCTGTGAAGCCGCTGCTGTT	1080
QY	1431	gggaagatccctgataaccttgacactccagccacaagagcaagtcatgctgtagagtgaaac	1490
Db	1081	GGGAAGATCCTGTATPACCTGACACTCCACCAAGGACAGGTATGGCTGAGGTGAAC	1140
QY	1491	aagaccttccaggaagcagctgtgttccatgactctggaagagcatgtggaagaaactagc	1550
Db	1141	AAGACCTTCCAGSAACTGGCTGTGTTCATGATCTGGAAGGATGTGGAGAGAACTCAGC	1200
QY	1551	cccaagatctggaaccttcatatgtaggaagcaagccaagaatggaaccttgcggatgctgttg	1610
Db	1201	CCCAAGATCTGGACCTTTCATGAGGAACAGCAAGAATGAGACTTGTCCGATGCTGTGG	1260
QY	1611	gacagcagaggaacaatgacacatttttggaacagcaattgattggtttgatttggaagcc	1670
Db	1261	GACAGCAGGACAAATGACCACTTTTGGGAAACACCAATTTGATGGCTTGAATTTGGACAGCC	1320
QY	1671	caagacatcgttgcgttlltlygccaagcaccagagagatgtccagtccaagttaattgcttct	1730
Db	1321	CAAGACATCTGTGGGCTTTTGGCCAAAGCAACCCAGAGAGATGTCCACTCCAGTAAATGCTTCT	1380
QY	1731	gttgaacctctggagagaagtttccaacgagactaaacaggaatccggaaacatatctgcg	1790
Db	1381	GTGTACACCTGTGAGAGAAAGCTTTCACGAGACTAAACACAGCATCTCCGACCATATCTGC	1440
QY	1791	tctcatgagatgttccaacctgaaacaagcttagaacatcatagcaagaagctctgctcatc	1850
Db	1441	TTCTATGAGATGTGTCAACCTGAACCAAGCTAGAAACCATATGCAACAGAAAGTCTGGCTCATC	1500
QY	1851	aacacagtccatlgagagctgtcgtgattgagagaagttcttggctgtgattgtgttcaatgga	1910

Db	1501	AACAAAGTCACATGAGACTGCTGGATGAGAGAAAGTTCGGCTCGATATGTTGTTCACTGGA	1566
Qy	1911	attactccaagcagaattgaactctgcccacatcaltcaagfacaaagatccgaatlygacat	1970
Db	1561	ATTACTCCAGGAGACATTGAGCTGCCCATCATGTCAAGTACAAAGATCCGAATGGACATT	1622
Qy	1971	gacaaatgtygagagagacaataaataaagatfygagtaactyggaaacccctgctctgaagct	2033
Db	1621	GACAAATGTGAGAGACAAATAAATCAAGATGAGTACGTGGGACCCCTGCTCGAGCT	1680
Qy	2031	gacccctctlgaggaatcgcgttaacgtctgggggggctgcgaactctgagaatlygctg	2096
Db	1681	GACCCCTTTGAGGACATGCGGTACGTGGGGGGGCTTCCCTACTTTCAGAGATGTGCTG	1744
Qy	2091	gagcagagcaatcaatcaaggyctctgaagggcaacgagaagaanaactygtctatatcgaa	2155
Db	1741	GAGCAGGGAATCATCAGGGTCTCACGGGACCGAGAAAGMAAACCTGGTCTCATATGCA	1800
Qy	2151	gagatggccctaccctgttaacgttgaatgaacatctttctggggtygaatggacggatgaatg	2211
Db	1801	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGGGGGTGATGAGCCGGTCAATG	1866
Qy	2211	ccctctctcaatgaagctgagcctgagattactcagtygactgtygtalcatcaagggacatg	2270
Db	1861	CCCTCTTCATGAGCGCTGGCCCTGGATTTACTCATGAGCTGTGATCATCAAGGCAATCGT	1920
Qy	2271	tatgtaagagagagacagctctbaaagaacatcgcgatcatggacgttgagacaaagcata	2333
Db	1921	TATGGAAGAGAGACACAGGCTTAAGAACACATGGGATCTGAGGACCAACAGCATC	1986
Qy	2331	ctctggtttaagctggttcaatagtaagctatctctctcttcttcttctgagcgtgagctgta	2390
Db	1981	CTCTGTTTACTGTTGATTCATTAGTAGAGCCCTATTCCTCTTCTGTGAGCCCTGGCCCTGA	2044
Qy	2391	gtggtacatccctgaagttaggaanaactctgctcctacaaglygatcccaagctggtgtttctc	2455
Db	2041	GGGTGTCATCTGAAGTTTAGGAACCTCTCCCTACAGTATCCACGCGGTGGTGTGTGTC	2100
Qy	2451	tctcgtctcgtttctgctgtygtatcaatcctgcaatgctgtcttctctgtaatgacaactctc	2510
Db	2101	TTCCGTGCGGTGTTGCTGTGTGATGACAAATCTGCAGAGTGCCTGTGATAGCACACTTTC	2166
Qy	2511	tccagagccaactcctggaagcagcctgtygggggcaatacttaactcaagctgtactgccc	2570
Db	2161	TCCAAAGCCAACCTGGAGAGAGCGCTGGGGGATCATCTACTTCAACGCTGTACCTGGCC	2220
Qy	2571	tacgacctgctgtgagcatggaagatlaagtyggtctcaactcaagaatctctgctagc	2630
Db	2221	TACGCTCGGTGTGTGGCATGAGCAAGATACGTGGGCTTCAACTCAAGATCTTCCGTACG	2288
Qy	2631	ctgctgtctcctgtgaccttlyggtlytgctgtgagtaactlygccccttlyagaagcag	2690
Db	2281	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGATACTTTGGCCTTTTGAAGAGCAG	2340
Qy	2691	ggaacttggaagcagtygggaacaacttlytgaagfcccgtlygagaagaatgactcaat	2750
Db	2341	GGCATTGGAGTGCAGTGGGAAACCTGTTTGAAGATCTGTGTGAGAAAGATGCTTCAT	2400
Qy	2751	ctcaacaacttgaactcaatgaatgactgttlytgaacaacttccatlatagggtygaatccg	2810
Db	2401	CTCAACAACCTTGGTCTCATGATGTGTGTGACACTTCTCTATGGGGTGATGACGTGG	2460
Qy	2811	tacatgaagctgtcttccagaccagtaacgaatcccaagccctgatatcttccctgc	2870
Db	2461	TACATTGAGGCTGTCTTTCCAGGCGAGTACGGAATTTCCAGGCCCTGGATATTTCTTTC	2520
Qy	2871	acaaagctccactgcttctggcgaagaaatgtaatgaagaagcacaacctggtttccaaacag	2930
Db	2521	ACCAAGTCTACTAGTTGTTGGCGAGAAAGTGAAGAAACCCACCTGTGTTCCAAACAG	2580
Qy	2931	aaggaatgctcgaatctgcatlygaaggaagaaacccaacctlygaactyggcgtgtcc	2990

Db 2581 AAGAGATATCAGAAATTCGATGAGAGAGAAACCCACCTTGAAGCTGGCGGTGCC 2640
QY 2991 attcaaaacctgtaaaatctacacgagatggatgaaggtgctgctgcatgctgca 3050
Db 2641 ATTCAACACCTGGTAAATCTACCGAGATGGATGAAAGGTGGCTGTCATGGCTGGCA 2700
QY 3051 ctgaattcttaagagccagatacaacctctccctgggacacatggagcggggaagac 3110
Db 2701 CTGAATTTTATGAGGGCCAGATCACTCTCTCTGGGCCACAATGAGAGGGGAAAGAC 2760
QY 3111 accaccaatgcaatccctgaacgggtgtgtcccccgcacctgggacgcgcctacatctg 3170
Db 2761 ACCACCATGTCAATCCTGACCGGGTGTTCCTCCCGACCTCGGGACACCCCTACATCTCG 2820
QY 3171 ggaagaagacattcgctctgagatggacacaccccgcaaaccttgggggtctgtccacg 3230
Db 2821 GGAAGAAAGATTCGCTCTGATGATGAGCACCATCCGGCAACCTGGGGGTGTCTCCCGC 2880
QY 3231 cataacgtgctgtttgacatgctgacgtgctgcaagaacacatctgttctatgcccagctg 3290
Db 2881 CATAAAGTGTCTGTTTACATGCTGACTGCTGAGAAACACATCTGGTCTATGCCCCGTTG 2940
QY 3291 aaaaaggctctgagaagaacgltgaaggcgagatggagcagatggccctggatgtgtgt 3350
Db 2941 AAAGGGCTCTTGAGAGACACGTGAAGCGGAGATGAGACAGATGGCCCTGGATGTGTGT 3000
QY 3351 ttggcatcaagcaagctgaaagaacaaacaaagccagctgtcaagggtggaatgcaagaaga 3410
Db 3001 TTGCCATCAAGCAAGCTGAAAGCAAAACACACCTGTCTAGGTGGAATGAGAGAAAG 3060
QY 3411 ctactgtgaccttgacctgttgcggggatctaaaggtgtcatcttggatgaaaccaca 3470
Db 3061 CTATCTGTGGCTTGTGGCTTGTTCGGGGGATCTAAAGTTGTATCTGATGATACCCACA 3120
QY 3471 gctgtgtggaaccttactcccgcaagggaataatggagcgtgctgcaataacacgaca 3530
Db 3121 GCTGTGTGGACCTTACTCTCCGCAAGGGAATATGGAGCTGCTGTAATACCCACA 3180
QY 3531 gggcgacacattatctctctacacacacatgatatgaagcggaagctctgggggaacag 3590
Db 3181 GGGCGACCATTTATCTCTACACACACATGATGAAAGCGGACCTCTGGGGGACAG 3240
QY 3591 attgcatcatctcccatgggaagctgtgtgtgagctccctccgttcttcaagaac 3650
Db 3241 ATTGCCATCATCTCCATGGGAAGCTGTGCTGTGTGGCTCTCCCTGTTTCTGAAGAAC 3300
QY 3651 cagctgtggaacagctactactactgacctgtgtcaagaagaatgtggaatccctccagt 3710
Db 3301 CAGCTGGGAACAGGCTACTACCTGACCTTGTGCAAGAAAGATGTGAAATCCCTCCAGT 3360
QY 3711 tccctgagaacacagtagtagcactgtgtcataccctgaaaaaggaagacagtttctcag 3770
Db 3361 TCTCGAGAAACAGTAGTACACTGTGTCTATACCTGAAAAAGGAGGACAGTGTCTCAG 3420
QY 3771 agcagttctgaatgctgagcgtggcagcagacacatgaagatggaacgcctgacatcgaatgc 3830
Db 3421 AGCAGTTCTGATGCTGGCCCTGGGACGACGACCATGAGAGTGAACGCTGACATCGATGTC 3480
QY 3831 tctgcatatctcaacctcatcagaagaatgtgtctgaaagcccgctgtgtgaaacata 3890
Db 3481 TCTGCTATCTCCAACTCATCAAGGAAGCATGTGTGAAAGCCCGGTGTGGAAGCATTA 3540
QY 3891 gggcagagctgaacctatgtctgcatatgaagctgctcaagagaggaacgtttgtggaa 3950
Db 3541 GGGCATGAGCTGACTATGTGTGCTGCTATGAAGCTGTCTTAAGAGGAGGACCTTTGTGGAA 3600
QY 3951 ctcttcaatgaatgtaagacggctctcaagacctgagcattctagttaatgcatctca 4010
Db 3601 CTCTTCATGAGATGATGACCGGCTCTCAGACCTGGGCAATTTCTAGTTATGGCATCTCA 3660
QY 4011 gaagacgaacctggaagaataatctctcaaggtgtgcggaagagaggtgggtgtgactgag 4070
Db 3661 GAGACGACCTCTGGAAAGAAATATTCCTCAAGGTGGCCGAAGAGAGTGGGTGTGCTGAG 3720
QY 4071 aacctgaatggttaccttgcgcaagaagaacagcgccgttccgggggaacagcagac 4130
Db 3721 ACCCTGATGTGTACCTTGGCCAGCAAGAGGAACAGGGGGCTTCCGGGACACAGCAGAC 3780
QY 4131 tgtctgcgcccgttcaactgaatgtaatgctgcatcacaatgatactgcatatgaccca 4190
Db 3781 TGTCTGCGCCGTTCACTGAAGATGATGCTGTGATCCAAATGATCTGACATGAGACCA 3840
QY 4191 gaatccagaagaacagactgtctcaatgtggaatggaatggcaaaaggttctaccagtgaaa 4250
Db 3841 GAATCCAGAGAGACAGACTTCTCAGTGGATGGCAAGGGTCTCTACAGAGTGA 3900
QY 4251 ggcctggaacttacaagcaacagtttggcccttctgtggaagagacgtcaatctgac 4310
Db 3901 GGCTGGAACTTTACACAGCAACAGTTTGTGGCTTTGTGGAAGAACTGTAAATGGC 3960
QY 4311 agacgagctcggaagaagatttctgctcaatgtgtctgcaagctgtgtgtctgcat 4370
Db 3961 AGACGAGATCGGAAGATTTTGTGCTCAGATGTGTGACAGCTGTGTGTGAT 4020
QY 4371 gacctgtgttcaagcctgatactgtgcaaccttggcaagtaeccacgcctggaaacctcag 4430
Db 4021 GCCCTTGTGTTCAGCTGATGCTGACCTTGTGGCAAGTACCCACCTGGAACTTCA 4080
QY 4431 ccttgatgttacaagcaagctacacattgttcaagaaatgtgtctctggaagacagga 4490
Db 4081 CCTGTGATGTACACAGACATACATTTTTCACATGATGCTCTCTGAGGACACGGGA 4140
QY 4491 aacctggaactcttaaaagccctcaccaaaagccctgctcgagacgcctgtatgaa 4550
Db 4141 ACCCTGGAACCTTTAAACGCCCTCACCAAGAACCTTGCGGACCCGCTGTATGAA 4200
QY 4551 ggaaaacccaatcccaagacagccttgcagcgagggaggaaggtggaacactgcccaca 4610
Db 4201 GGAACCCCAATCCACAGACACCCCTGCGAGGAGGAGAGTGGACACCTGCCCCA 4260
QY 4611 gtccccaacacatcatgacactcttccagaatggaaatggaacatgcaagaacacctca 4670
Db 4261 GTTCCCAACACATCATGAGACTCTCTCCAGATGGAAGCTGGAATGCAACACCTTCA 4320
QY 4671 cctgcatgcccagtgtagcagcgaacaaatcaagaagatgtcgtgtgtgtgtcccaagg 4730
Db 4321 CCTGCATCCCATGTGAGCAGCAGCAAAATCAAGAAAGATGCTGTGTGTGTGTGTGTGT 4380
QY 4731 gcaagggtggtcgtccctcccaaaagaacaaacactgtaagatcttccctcaagactg 4790
Db 4381 GCAAGGGGGCTGCTCCCTCCACAAAGAAACAAACACTGCAAGATATCTTCAGGACCTG 4440
QY 4791 acaaggaagaacattctgcatctatctgttgaagacgtatgtgcatatcatatgcaaaaagc 4850
Db 4441 ACAGGAAGAAACATTTGGGATTTATCTGTAAGACGTAATGTGACATGATGATGCAAAAGC 4500
QY 4851 ttaagaagaacatctgggtgaatgaatgtagtataggcggttccctgtgtgtcagt 4910
Db 4501 TTAAGGAACCAAGATGTGGGTGAATGAGTGTAGATGAGCGGCTTTTCCCTGGGTGTAGT 4560
QY 4911 aatctcaagacattccctccaggttcaagaagttlaatgaatgcatcaaaaatgaagaa 4970
Db 4561 AATFACTCAAGCACTTCTCCCGAGTCAAGAGCTTAATGTATGTCACCAACAAATGAAGAA 4620
QY 4971 caacctaaagctggcgaagaagcttctgacagatcgatttcccaagcttggagaatt 5030
Db 4621 CACCTTAAGAGCTGGCAAGAGAGCTTCTCAGATGATGATTTTCAACAGGTGTGGAAAGATT 4680
QY 5031 atgacagacatgagacacagaataatgttcaaggtgtgtgttcaataacaaggtcgcac 5090
Db 4681 ATGACAGAGACTGGAACACCAAGAAATATGTCAAGGTGTGTGTCAATTAACAAAGGCTGCAT 4740
QY 5091 gaaatcagcttcttcttaagttaatgaatgaatgcatgcatctccggggccaacctgcaaaag 5150
Db 4741 GCAATCACCCTTTCTTAATGTATCAATCAACATGACATTTCTCGGGCCAACTCCCAAAAG 4800

QY 5151 ggagagaaacctagccattatgaattactgcttcaatcaatccctggaatcacaag 5210
|||||
Db 4801 GGAGGAAACCTAGCCATTATGGAATTAAGTCTTTCAATCAATCCCGAACTCCACCAAG 4860
QY 5211 cagcagcctcagaagtgagcctatgacacacalcagtgagtgctccttgctcatctgt 5270
|||||
Db 4861 CAGCAGCTCTCAGAGTGGCTCCGATGACCAATCAGTGGATGCTTGTGTCTATCTGT 4920
QY 5271 gtcactcttgcaatgctcctgctccagccagcttctgctatctccgatccagagcgy 5330
|||||
Db 4921 GTCAATCTTGGCAATGCTCTGTGCTCCAGCCAGCTTTGTGATTCGATCCAGAGGACGG 4980
QY 5331 gtcagcaaaagcaaacctctgcaatcagtgagtgagtgaaagcctgcaatcctgctc 5390
|||||
Db 4981 GTCAGCAAAAGCAAAACACTGCACTGATCATGAGAGGAAAGCCTGTATCTACCTGCTC 5040
QY 5391 tcaattctgctggagatgcaatgcaatgcaatgctcctgctcagacagtgctatcctc 5450
|||||
Db 5041 TCTAATTTTGTCTGGGATATGCAATTTAGCTTTCCCTGCGACACAGTGTATATCATC 5100
QY 5451 ttcactgctccagcagaagtcctatgctgctccacccaatctgctgtgtagccct 5510
|||||
Db 5101 TTCAATCTGCTTCCAGCAAGAACTCTATGCTCTCCACCAATCTGCTGTGCTAGCCCTT 5160
QY 5511 ctacttctgctgtagtggtgcaatcacaacctctcatgtaaccaagcctcttgctgtc 5570
|||||
Db 5161 CTACTTTTGTCTGTAGGCTGTCAATACACTCTCATGTACCAAGCCTCTTGTGTCTC 5220
QY 5571 aaagtcaccaagcagacatgctgctgctcagcagcgtgaaacctctcatcttgccatcaat 5630
|||||
Db 5221 AAGATCCCGACACAGCAGCTATGTGTGCTCCACAGCGTGAACCTCTCATTTGGCATTAAT 5280
QY 5631 ggagagcctggccaccttgctgctgagcctgttcaaccaataagcctgcaataatcaat 5690
|||||
Db 5281 GGAGGCGGGCCACCTTTGTGCTGAGCTGTTCACCAATTAAGTGAATTAATCAAT 5340
QY 5691 gatactcctgaagtcgctgcttctgctcctccacatttgcctggagcagagcgtcatc 5750
|||||
Db 5341 GATATCCGTAAGAGTCCGTGTCTGTATCTTCCCATTTTGGCTGGGACAGAGGCTCATC 5400
QY 5751 gacatggtgaaaaaacagcgaatgctgctgagcctggaaggttggggaagatcgctt 5810
|||||
Db 5401 GACATGGTGAAGAAACAGGCGCAATGGCTGATGCCCTGGAAGGTTGGGGAATTCGCTTT 5460
QY 5811 gctgcacattatcttggaacttgctggaagcaaaccttctgcacagcgcctgggaaggg 5870
|||||
Db 5461 GTGACACCATATCTTGGGAGCTTGTGGGAGGAACCTTTCGCCATGAGCCGTGGAAGGG 5520
QY 5871 gtggtctctcctcattactgcttctgacacagtacagattctcatalcagccagacct 5930
|||||
Db 5521 GTGGTGTCTTCCCTCATTTACTGTTCTGATCCAGTACAGATTCCTTCATCAGGCCACACT 5580
QY 5931 gtaaatcaaaagctatctcctctgaatgagatgaaatgtgaaagcggaagagcag 5990
|||||
Db 5581 GTAAATGCAAAAGCTATCTCCTCTGAATGAAATGAATGAATGAATGAATGAATGAATGAAT 5640
QY 5991 aagaattctgagtgaggaagccagaatgacatcttgaataatcaagagtgagcaagata 6050
|||||
Db 5641 AGAATTCCTGATGAGTGAGGAGGCAAGATGACATCTTAGAATCAAGAGTTGAGAGAGATA 5700
QY 6051 tataagaaggaagcgaagcctgctgctgtagacagattgctgtaggcatctcctctgtgag 6110
|||||
Db 5701 TATAGAAGGAAGGCGGAAGCCTGCTGTGACAGATTTGCTGGGCAATTCCTCTGTGGAG 5760
QY 6111 tgccttgagctcccgagtgatlaaatgggctggaataatcacaacttcaagatgitaaca 6170
|||||
Db 5761 TGCTTTGGGCTCCTGGAGATTAATGGGCTGGAAATATCATCAACTTTCAAGATGTTTAA 5820
QY 6171 ggagataccactgcttaccagaagagatgcttctccttaacaaaatagatctatcaaac 6230
|||||
Db 5821 GGAATATCCACTGTTTACCAAGAGGAGATGTTCTTAAACGAAATAGTATCTTATCAAA 5880
QY 6231 atccatgaagtaactcaagaacatgagtgctactgcccctcagttgtagccatcaagagctg 6290
|||||
Db 5881 ATCCATGAAGTATCATGAAACATGGGCTACTGCCCTCATTTTGAATGCCATCAAGAGCTG 5940
QY 6291 ttgactggagagaacacatggaatcttctgccccttttagagagatcccaagaagaa 6350
|||||
Db 5941 TTGACTGGGAGAAACACCTGGAGTTCTTGGCCCTTTTGAAGAGATCCAGAGAAAGAA 6000
QY 6351 gttgcaaggttggtgagtgagtgagatcgaaactgggctcgtgaagtatgagaaaaa 6410
|||||
Db 6001 GTTGGCAAGTTGTTGAGTGGGCGATTCGAAACACTGGGCTGTGAAGTATGAGAAAAA 6060
QY 6411 tatgctgtaactatagtgaggaagcaaaagcaagctctctcaagccatggtctgtc 6470
|||||
Db 6061 TATGCTGTATATATATGAGGCAACAAACCAAGCTCTTACAGCCATGGCTTTGATC 6120
QY 6471 ggcggccctcctgtgtgtcttctgtagaacccacacagagcatgattcccaagcccg 6530
|||||
Db 6121 GCGGGGCTCCTGTGTGTCTTCTGATGTAACCCACACAGGCGATGATCCCAAGCCGCG 6180
QY 6531 cgttctcttggaatgagccctaaagtgctcaaggaagggagatcagtagtctaca 6590
|||||
Db 6181 CGGTTCTTGTGAATGTGCTCCCTAAGTGTTCGAAGAGGGGAGATCAGTATGCTTACA 6240
QY 6591 tctcatagatggaagaatgtagaagcctcttgcaatgaatgagcaatagtgtaatgga 6650
|||||
Db 6241 TCTCATATGATGGAAGAAATGTAAAGCTTTTGCATAGGATGCAATATGATGTCATATGA 6300
QY 6651 aagttcaagtgcttgagcagtgctccagcaatcaaaaaataggtttgagatggtatata 6710
|||||
Db 6301 AGGTTAGGCTCTTGGCGAGTGTCCAGCATCTAAAAAAATAGTTGGAGATGTTATACA 6360
QY 6711 atagttgtagaatagcagaggtccaaacccgagccggaagcctgccaagattcttga 6770
|||||
Db 6361 ATAGTTGTAGAAATGACAGAGGTCACACCCGAGCTGAAGCCTGTCCAGGATTTCTTGA 6420
QY 6771 ctgcaatctcctggaagtgcttctaaagaagaaacacggaatgctaaatcacaagctt 6830
|||||
Db 6421 CTTGCAATTTCTGGAAGTGTTCACAAAGAGAAACCCGGAATATGCTCAATATACAGCTT 6480
QY 6831 ccatcttcaatctctctctgcccagagatatcagcatcctctcccaagacaaaaagcga 6890
|||||
Db 6481 CCATCTTCAATTTATCTTCTGTGCGCAGAGATTTTCACCATCTCTCCACAGCAAAAAAGCGA 6540
QY 6891 ctccacataagaagactcctgttctcagacaacacttgaccagaatgttctgaactt 6950
|||||
Db 6541 CTCACATATGAAGACTACTCTGTCTTCAGACAAACATTTGACCAAGTATTTGTGAACTTT 6600
QY 6951 gccaaagcaaaagtatgataagcaacttaaaagcctctcatalcacaacaaacagaca 7010
|||||
Db 6601 GCCAAGAGACCAAAAGTATGATGATGACCACTTAAGAGACCTCTATTACACAAAAACAGACA 6660
QY 7011 gtagtggaagtgcaagtgctcctcatalcttctcagagtgaggaagtgaaagaaagctat 7070
|||||
Db 6661 GTAGTGGAGGTTGCAAGTTCTTCAATCTTTTCTACAGATGAGAAAGTGAAGAAAGGCTAT 6720
QY 7071 gtagtaagaatcctgtcatalcaggggtgctgtaaaagtaaaaggaacacagactcctt 7130
|||||
Db 6721 GTATGAGAAATCTCTGTATACGGGGTGGCTGAAGTAAAGAGGNACTAGACTTCTCTT 6780
QY 7131 gtaacatgtgaaagtgcttgaggaagaaagccagaagtgtagtgaggaagaaagtaactg 7190
|||||
Db 6781 GCAACATGTGAAGTGTGTGGAAGAAAGAGCCAGAAAGTGAATGTGGAAGAAAGTAACTG 6840
QY 7191 gatactgataactatcatalcagtaagtaagtaagtaagtaagtaagtaagtaagtaagta 7250
|||||
Db 6841 GATACTGCTATATCTATTTCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 6900
QY 7251 taacagggcagtgcttgtagcctatgctgtgataagcctcagtgcaagtgaaagactgaa 7310
|||||
Db 6901 TACAGGGGAGAGCTTGTGTAGCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6960
QY 7311 ttagtttttactataactatgtaaaactatattgaaacccaatgagactggtt 7370
|||||

[illegible][illegible]

QY 9531 acctatactcaatcaagcaaaattctgtatatctccctgtggaatgtactatgtgagt 9590
Db 9180 ACTGTATACCTCAATCAAGCAAAATTTCTGTATATTCCTGTGAATGTACTTGTGAGT 9239
QY 9591 ttcaagaattctcaaaatagtggttcaaaaattcttgcttttgcatctttggagacccctc 9650
Db 9240 TTCGAAATTCCTCAAAATAGCTGTTCAAAATTTCTGCTTTTGCAATCTTTGGACACCTC 9299
QY 9651 agaaacttatacaactgtgaaatagaaataacagaagaataaataagccctctat 9710
Db 9300 AGAAATCTATTAACAACCTGTGAATATGAGAAATACGAGAAATATATAGCCCTCTAT 9359
QY 9711 acataaatggcccgcaaatctatctgttaaaaaaaccaaccactcaactgtatctt 9770
Db 9360 ACATTAATGGCCACCAATTCATGTATAAAAAACAACCAACCTCACACTACTGTATTT 9419
QY 9771 catatctgtactgaagcaaatgtctgtgaactatgaatgttgcacatctatctatc 9830
Db 9420 CATATCTGTACTGAAGCAAAATCTTTGTGACTATTAATGTGTGACATCTATCTCA 9479

RESULT 15
AX059978 9495 bp DNA linear PAT 22-JAN-2001
LOCUS Sequence 96 from Patent WO0078970.
DEFINITION AX059978
ACCESSION AX059978
VERSION AX059978.1 GI:12405636
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 9495)
AUTHORS Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,U., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.
and Brewer,H.B.
TITLE Nucleic acid and proteinic acids corresponding to human gene abcl
JOURNAL Patent: WO 0078970-A 96 28-DEC-2000;
Aventis Pharma S.A. (FR)
FEATURES
source location/Qualifiers
1..9495
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2599 a 2115 c 2216 g 2564 t 1 others
ORIGIN

Query Match 90.3%; Score 9430.6; DB 6; Length 9495;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 9462; Conservative 0; Mismatches 15; Indels 3; Gaps 2;

QY 351 caacatgtcagctgtactgtgaagtgagctgtgacctatattcttcctgactccgagtc 410
Db 1 CAAACATGTAGCTGTACTGGAAGTGCGCTGGCCTCTATTATTCCTTCGATCCTGATC 60
QY 411 tctgtctgctgagctacccacccatgaaacaacatgaaatgacatllcccaataaagcc 470
Db 61 TCTGTTCTGCTGAGCTACCCACCTTGAACAACATGAAATGCGCATTTTCCAAATAAAGCC 120
QY 471 atgccccttcaggaacactctctgtgttcaggagatattcgtatgccaacacccc 530
Db 121 ATGCCCTCTCAGGAACACTTCTTG6GTTCAGGGATATCTGTATGCAACCAACCC 180
QY 531 tgttcctgtacccgactcctctgggagagctcccgagctgttggaaactllaaacaatcc 590
Db 181 TGTTCGCTTACCCGACTCTCTGGGAGGCTCCCGGAGTTGTGGAATCTTAAACAATCC 240
QY 591 atgtgtgctgctgttctcagaatgctcggagagctcttttatacagccagaagaacacc 650
Db 241 ATTGTGCTGCTGCTGTCTCAGATGCTCGAGGCTTCTTTATACGCGCAAGAAAGACACC 300
QY 651 agcatgaagacatgccaagctctggaacattacaagatccaagaatcccaactca 710

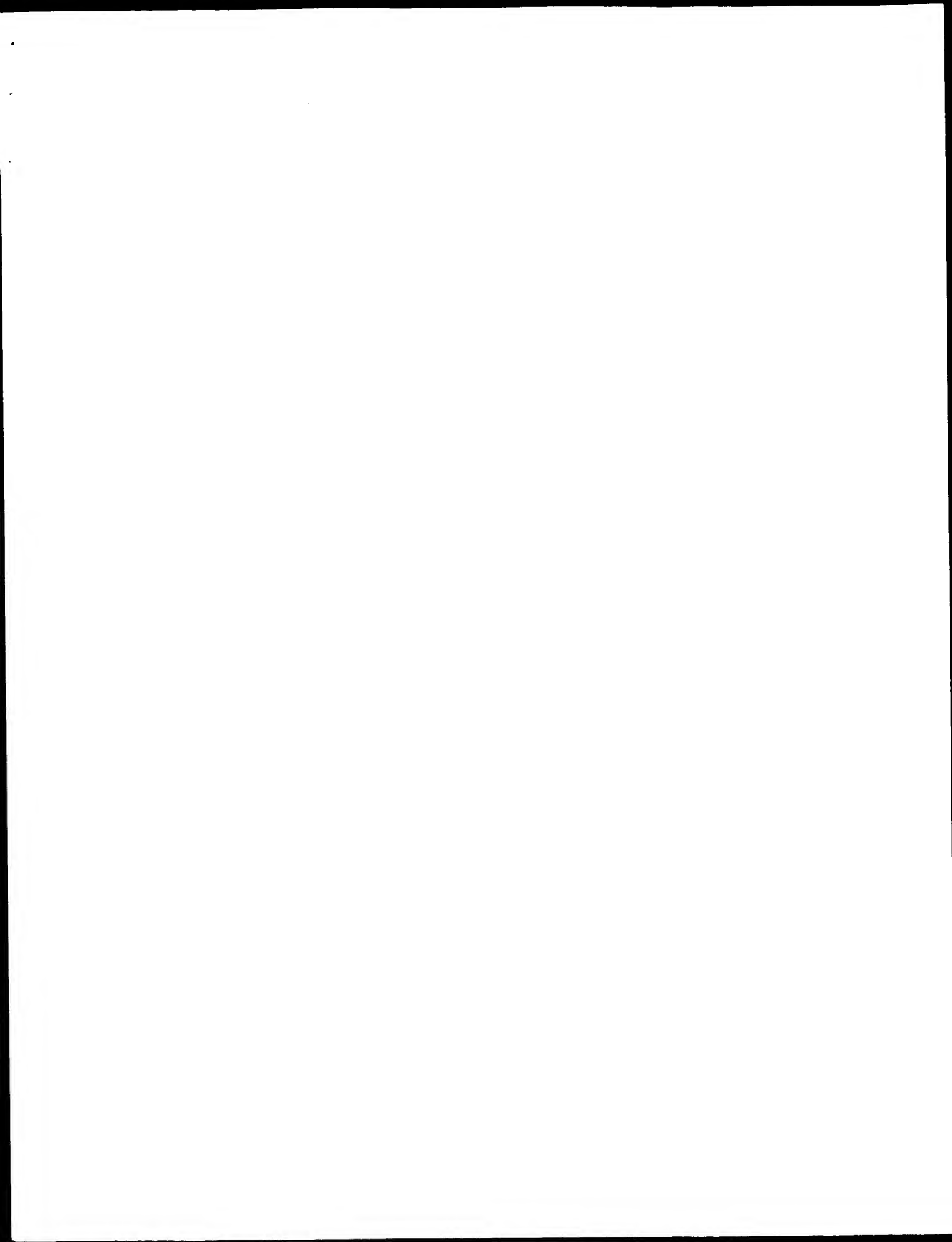
Db 301 AGCATGAAGGACATGCGCAAAAGTTCTGAGAACATTACAGAGATCAAGAAATCCAGCTCA 360
QY 711 aacttgaagcttcaagattctcctgtgtgacaatgaaacctctcgtggttccatatacc 770
Db 361 AACTTGAAGCTTCAAGATTCTCTGCTGACAAATGAACACTCTCTGCTGCTGATACAC 420
QY 771 aacctctctcccaagctactgtgtgacaagaatgctgagggctgatatctctccac 830
Db 421 AACCTCTCTCTCCAAAGCTTACTGTGCAAGATGCTGAGAGGCTGATGTATCTCTCCAC 480
QY 831 aaggtatcttgcagaggtaccagttacattgacaatgctcgtgcaatgataaataca 890
Db 481 AAGGTATTTTTCACAGGCTACCACTTACATTTGACAACTCTGTGCATGTCAATCA 540
QY 891 gaagagatgattcaacttgtgtgaccaaagaatttctgaacttltgtgcttaccaaagag 950
Db 541 GAAGAGATGATTCACACTTGTGTGACCAAGATTTCTGAGCTTTGTGGCTTACCAAGGAG 600
QY 951 aaactgtgtcagcagcagcagagtaactctgttccacaatgacatccctgaaagcaactc 1010
Db 601 AAACGTGGCTGACGACGACCGAGTACTTGTTCACACATGACATCTGAAACCAATCTCG 660
QY 1011 aagaactaaactacatctcccttcccgagcaagagctggtctgaaagccacaataa 1070
Db 661 AGAACACTTAACCTGTACATCTCTCTTCCGAGCAAGAGCTGGCGGAAGCCACAAAACA 720
QY 1071 ttgtgtcatagctcttggagactctgcccagagagctgttcaagcatgagaagctgtgag 1130
Db 721 TTGCTGCAATAGCTTGGGACCTGTGCCCCAGGAGCTGTTCACACATGAGAGTGAAGTGA 780
QY 1131 atgagcagagagtgatgttcttctgacaaatgtgacagctcagctccctccacccaatc 1190
Db 781 ATGCAACAGAGAGATATTTTCTGACCAATGTGAACAGCTCAGCTCTCCACCCAAATC 840
QY 1191 taccagagctgtctcgtatgtctgtcgtggacatcccgagagggagggctgtgaatacag 1250
Db 841 TACCAGGCTGTCTGCTGATTTGTCTGCGGATCCCGAGGAGGGGCTGAATATCAAG 900
QY 1251 tctctcaactgtatgagaacaacactacaaagccctcttggaggaatgagactgag 1310
Db 901 TCTCTCAACTGCTATGAGACACACACATACAAAGCCCTTGTGAGCGCAAGGACAGTGA 960
QY 1311 gaagatgttgaacactctatagacaactctaaactccttacttgaatgatttgaag 1370
Db 961 GAAGATGCTGAACCTCTGTATGACAACTTACAACTCTTACTGCAATGATTGATGAG 1020
QY 1371 aatttgaagctagctccctcttcccgcatctcgtgaagactctggaagccgtctgct 1430
Db 1021 AATTTGAGAGCTAGTCCCTCTTCCGCAATCTGTGAAGGCTGTGAAGCCGCTCTGCTT 1080
QY 1431 ggaagagctcctgtatatacctcgacactcagccacaagagcaggtcagctgaagtgaac 1490
Db 1081 GGAAGATCTCTGTATACACTGACACTCCAGCCACCAAGGAGGATCATGTGCTGAGGTGAAC 1140
QY 1491 aagacttccagaaactgtgtgttccatgactgtgaaagcatgtgtggaagaaactcagc 1550
Db 1141 AAGACTTCCAGGAAGACTGCTGTGTCATGATCTGGAAGGCAATGTGGAGAACTCAGC 1200
QY 1551 cccaagatctgacactatagagaacagcaagaatgagacctgttccggatgtctgt 1610
Db 1201 CCCAAGATCTGAGCTTATGAGAACAGCCCAAGAAATGACCTTGTCCGATCTCTGTG 1260
QY 1611 gacagcagaggaacaatgacaacttlttggaaacagagatgtgagctttagatltgagaccc 1670
Db 1261 GACAGCAGGAGCAATGACCACTTTTGGAAACAGAGTGTGATGTGAGATTTGACAGCC 1320
QY 1671 caagacatcgtgtgttlttggccaagcaccagaagatgttccagttcaagttaagtctc 1730
Db 1321 CAAGCATCTGTGTGCTTTTGGCCAAAGCACCAAGAGATGTCCAGTCAAGTAAGTCTT 1380
QY 1731 gtgtacactgtgagaagacttcaacagagactcaacaggaatccggagacatatctcgc 1790
Db 1381 GTGTACCTCTGAGAGAAAGCTTTCAACGAGACTTAACCAAGGCAATCCGACATATCTCGC 1440

QY	1791	ltcatgagtggtgtcaaccctggaacagctagaaccccatagaacagaaagtcgtgctatc	1850
Db	1441	TTTCATGAGGTGTCAACCTGAAACAAGCTAGAACCCATAGCAACAAGACTGGCTCATC	1500
QY	1851	aaagaatcctatgagctgctgctgagatgagagaattctctgctgtgtattgttcatctga	1910
Db	1501	AACAAATCCATGGAGTGGCTGAGATGAGAGAAAGTTCGGGCTGGATGTGTTGTTCACTGGAA	1560
QY	1911	attactccaggcagcalttgctgctggcccaalcaltcaaglacaaagatccgaatgagcalt	1970
Db	1561	ATTACTCCAGGACACATTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATTT	1620
QY	1971	gacaaatgtgagaggaacaaataaaatcaagaaatggttactgggaacccctggtctctgaact	2030
Db	1621	GACAAATGTGAGAGACAAATTAATAATCAAGATGGGTACTGGAGACCCGTGCTCCAGACT	1680
QY	2031	gaaccccttgagagacatgctgctacgtctgtgagggagcttcgacacttgacagaaatgctggt	2090
Db	1681	GACCCCTTTGAGGACATGGCGGTACGTGTGGGGGGCTTCCGCTCACTTGGCAGATGGTGGTG	1740
QY	2091	gagcaggaacatcatcaaggtgtgtctgaacgggacacgagaagaanaacatggtgtctatgcaaa	2150
Db	1741	GAGCAGGCAAAATCAACAGAGTGCT--CGGGACCCAGAGAAACCTGGTGTCTATATGCAA	1798
QY	2151	cagatggccataccctcttctgctgagatcatcttctgagggtgagtgaacgggtcaatg	2210
Db	1799	CAGATGCCCTATCCCTCTTACGTGTGATGACATCTTCTGCGGGTGATGAGCCGGTCAATG	1858
QY	2211	cccccttcatgaaacgctgagcctgattactcatcagttgctgtgcatcaaggacatcgtg	2270
Db	1859	CCCCCTTCATGAGACGTGGCGCTGGATTACATCAGTGGCTGTGATCATCAAGGGCATATGTTG	1918
QY	2271	tatagaagaaggagcaacggctcgaaagagaacatgcggaatcatggtgctgtgacaacagcata	2330
Db	1919	TATAGAAGAGGAGGACCGGCTGTAAAGACACATGGGATCATGTGGCCCTGGACAACAGATTC	1978
QY	2331	ctcgtgattagctgtgtcatagtagcctcatctctctctctgtgacgctgtgacctgtcta	2390
Db	1979	CTCTGGTTTACCTGTTTCATTAGTAGCCTCATTCCTCTTCTTGAGACGGCTGGGCTTCCTA	2038
QY	2391	gttgtcatcctgtaaattaganaaacctgctgcctcacagtgatcccaagcgtgtgttctgttc	2450
Db	2039	GTGGTCATCCCTGAAATTAGGAAACCTGCTGCCCTACAGTATCCCAACGCTGGTGGTTTGTCTC	2098
QY	2451	ttctctgtccggtgtgtctgtgtgtatcaaatcttgaaatgcttccctgatttaacaactcttc	2510
Db	2099	TTTCCGTCCGTTTGTGCTGTGTGACAAATCCTGCAATGCTTCCGATTTCGATTACACACTCTTTC	2158
QY	2511	tcacagaagcaaacctggagcagcagcctgtgtgagggacatcatctactcaacgcgtcatccgtgc	2570
Db	2159	TCCAAGGCCAACCTGTGGACGAGCGCTGTGGGGGCATCATTACTTACAGCGTGTACCTGCC	2218
QY	2571	taagtcctgtgtgtgtgaatgagcaggaactaagtgttgcttacaactcaagaatctctcgtagc	2630
Db	2219	TACGCTCGTGTGTGGCATGTGGACAGACTACGTTGGCTTTCACACATCAAGATCTTTCGCTAGC	2278
QY	2631	ctgctgtctctgtgtgacctgttggtgtgtgtgctgtgaatfactttgcccccttttgaggaacag	2690
Db	2279	CTGCGTCTCCTGTGGGCTTTTGGGTTTGGCTGTGAGTACTTTCGCCCTTTTGAAGAGACAG	2338
QY	2691	ggcattgtgagtgcagltvggagacaactglttgaagatccctgttgaagaaagtgtcttcaat	2750
Db	2339	GGCATTGTGAGTGCAGTGGGACAACTGTTTGAAGTCTCTGTGGAGGAATGTGGCTTCCAT	2398
QY	2751	ctcaccaacttgatctcacaatgactgtttgaacacttccctctatagggagtgaiaacgttg	2810
Db	2399	CTCACCACTTGTGGTCTCATATGCTGTTTACACCTTTCCTATGGGGGTGATGACTGG	2458
QY	2811	taacattgagctgtcttccagcgcagtaacgaaatccccaagccctgtgatatcttccctgtc	2870
Db	2459	TACATTGAGGCTGTCTTCCAGGCCAGTACGAATTCACAGGCCCTGTGTATTTTCTTCTTGC	2518
QY	2871	accaagtctctactgttctgtgaggaagaagtgtatagaagaagccacccctgtgttccaacag	2930
Db	2519	ACCAAGTCTCTACTGGTTTGGGAGAGAAATGATATGAAAGCCACTCGTGTCCATCAACAG	2578
QY	2931	aagaaatcctcagaatctgtcatgtgaggaagaacccacacttgaaactgagcctgtgtcc	2990
Db	2579	AAGAAATATCAGAAATGTGATGAGAGGAACCAACCCACTTGAAGCTGTGGGCTGTCC	2638
QY	2991	attcagaacctggtataaagttcatcccgagatgagatggaagtgtgctgtcgatgacctggca	3050
Db	2639	ATTCAGAACCTGTGAAAAAGTCTTACCGAANTGGATGAAGGTGCTGTGTATGGCTGTGGCA	2698
QY	3051	ctgaattttttagagggccagatcaacccctctctctggccaacatgtagagcggaagaagc	3110
Db	2699	CTGAATTTTATGAGGGCCAAATACCTCTCTCTGGGCCAATGGAACGGGGAAACAGC	2758
QY	3111	accacacatgcaatctcgtaccggyatgtgtcccccgaactcggcagccgtcatatccctg	3170
Db	2759	ACCACCATGTCAATCTGACCGGGGTTGTCCTCCCGACCTGCGGCACCGGCTCATATCTTG	2818
QY	3171	ggaagaagacattcgtctctggaatgagacacatcccggaagaacctgagggtgtctgtccccaag	3230
Db	2819	GGAAAAGACATTGCTGTGAGATGAGCAACCATCCGGCAAGACCTGGGGGTGTGCCACAG	2878
QY	3231	cataaagctgtgtttgacatctgactctcgaagaacaacatctgtgtctatgtgccctgtg	3290
Db	2879	CATTAAGTGTCTTGTGACATGCTGACTGTGCAAGAACACATCTGTTCTATGCCCCGCTTG	2938
QY	3291	aaaaggctctctctgaaagcagltgaaggcgaatggaacagatgagctgtgccctgagatgtgtc	3350
Db	2939	AAAGGGCTCTCTGAGAAACACGTGAAGGCGGAGATGTGAGCAATGGCCCTGTGATGTTGGT	2998
QY	3351	ttgcacataagaaagcttgaagaagcaaaacaaagccagcgtgtcaagttggaatgcaagaaga	3410
Db	2999	TTGCCATCAAGCAACTGAAAAAGCAAAACAGCAGCTGTAGGTGGAATGCCAAGAAG	3058
QY	3411	ctatctgtgacctgtgacctgtgtcgagggaatcaaggtgtgtcatctctgaltgaatgaaccaca	3470
Db	3059	CTATCTGTGGCTTGGCTTGTTCGGGGGATCTTAAGTTGTTCATTCTGATGAACCCACA	3118
QY	3471	gctgtgtgtggaaccttactcccgcaagggaatatgaggagcgtcgtctgtgaatlaaccgaa	3530
Db	3119	GCTGTGTGTGACCTTTACTTCCCGAGGGGAATATGTGGAGCTGCTGTGAATATCCGACAA	3178
QY	3531	ggcgcgaacatlatctctctacaacacacatgtaatgaagagacgyltctcttgagggaacag	3590
Db	3179	GGCCGACCATTAATTCCTCTACACACCAATGATGAAGGAGCGTCTGTGGGACAGG	3238
QY	3591	attgccaatcatcccatgaggaaagctgtgtgtgtgtgtgtgtgtccctccctgttctgaagaac	3650
Db	3239	ATTGGCATATCTCCCATGTGGAGAGCTGTGCTGTGTGGGCTCTCCCTGTTCTAAGAAC	3298
QY	3651	cagcttgggaagagcgtctactaaccttgacctgtgtgcaagaagaatgttgaatatctctccatgt	3710

Db 3599 CTCTTTCAATGAGATTGATGACGGCTCTCAGACCTGGGCACTTTCAGTTATGATGCA 3658
QY 4011 gagacaccccttggaaataatctccaaagg tggccgaagagtggtgtgacgtcga 4070
Db 3659 GAGACGACCTTGAGAGAAATATCTCTCAAGGTGGCCGAGAGAGAGTGGGCTGATGCTGAG 3718
QY 4071 acctagatgttaccttgcagcaagagaagaacaggggacctccgggagacaagagagc 4130
Db 3719 ACCTGATGATGATCTTCCACGCAAGAGCAAGAGGCGGCTTCGGGAGCAACAGAC 3778
QY 4131 tgcctgcaccttcaactgaatgatgtctgatcccaatgattctgcacatagacc 4190
Db 3779 TGTCTTCGCCGCTTCACGAGATGATGCTGCTGATCCAAATGATTCGACATAGACCA 3838
QY 4191 gaatccagaagaagacacttgcctcagtgagtgagtgagcaagggctccacagtgaa 4250
Db 3839 GAATCCAGAGAGACAGACTTCTCAGTGGATGGCAAGGGCTCTACAGCTGAAA 3898
QY 4251 ggtcgaacttacacagcaacagtttggtgacctttgtggaagagactcattggcc 4310
Db 3899 GGCTGGAATCTTACACAGCAACAGTTTGCGCTTTGTGTGAGAGAGACTTAATTGCC 3958
QY 4311 agaagagtcggaagagatltttgtcagaatgtcttgcagactgtgtgtgtcgt 4370
Db 3959 AGACGAGACTCGAAAGGATTTTGTCTCAGATGCTGTGACAGCTGTGTGTGAT 4018
QY 4371 gcccttgttccagccttgatgtgtgcaccttggcaagtaaccacacgtgaactcag 4430
Db 4019 GCCCTTGCTTCAAGCTGATGCTGACACCTTTGGCAAGTACCCACGCTTGGAACCTTACG 4078
QY 4431 ccttgatgtacacagcaacagtlacacatltgtcagcaatgatgtctcttgagcaagga 4490
Db 4079 CCTGTGATGTACAAAGCAACAGTACATTTGTGACATGATGCTCTGAGAGAGAGGA 4138
QY 4491 accttgaactcttaaaagccctacacaaagacccctgtgctcggagccgtatgaa 4550
Db 4139 ACCCTGGAATCTTAAAGGCCCTTACCAAAACACCTGCTGGGACCGCTGTATGAA 4198
QY 4551 ggaacccaatcccaagacagccttgcagcagggaggaagagtgagcaactgccc 4610
Db 4199 GGAACCCCAATCCGAGACACGCCCTGCGAGGAGGAGAGAGTGGACCACTGCCCA 4258
QY 4611 gtccccaagacatcatgagaccttccagaatggagacttgcacatgcaaaccttca 4670
Db 4259 GTTCCCAAGACATCATGAGACTCTTCCAGATGGAACTGAGCAATGCAAGAACCTTCA 4318
QY 4671 ccttcagtcagtttagcagcagcaaaatcaagaagatgtgtgtgtgtgtgtgtgtgt 4730
Db 4319 CCTGCTATGCCAGTGTAGCAGGACAAATCAAGAGATGCTGCTGTGTGTGTGTGTGTGT 4378
QY 4731 gcaaggggggtgtcctctccacaagaagaacaaacactgcagatctccttcagacctg 4790
Db 4379 GCAGGGGGGCTGCTCTCCCAAAAGAAACAAACACTGCAGATATCTTTCAGAGACTG 4438
QY 4791 acaggaagaacatttgcgattatctgtgtgaagacgtatgtgcagatcatgccaaagc 4850
Db 4439 ACAGGAAGAAACATTTGGATTATCTGTGTGAAGACGTATGTGAGATCATGACCAAAAGC 4498
QY 4851 ttaagaagaagaatcgtgtgtgaatgattagttatgtgagggctttccctgggtgtcagt 4910
Db 4499 TTTAAAGAACAGATCTGGGTGAATGACTTAAAGTATGGCGGCTTTTCCGTGGGTGTGAGT 4558
QY 4911 aatactcaagacttctccagatcaagaagttatgatgccaaccaaaatgaagaag 4970
Db 4559 AATACTCAAGCAGCTTCTCCGAGTCAAGAGTTAATGATGCCAACAAATGAAGAAA 4618
QY 4971 caactaaagtcgcaagaagatgtcagatcgatlttccaacagcttgggaagatt 5030
Db 4619 CACCTAAAGCTGGCAAGGAGCTGTGAGATCGATTCTCAACAGCTTGGGAGATTT 4678
QY 5031 atgacagactgtgacaccaaataatgtcaaggtgtgtgttataacagggctgcat 5090
|||||

Db 4679 ATGACAGGACTGGACACAGAAATTAATGTCAGAGTGTGTTCAATTAACAGGCTGGCAT 4738
QY 5091 gcaatcagctcttcttgatgtcatcaacaatgtccattccgggccaactgcgaag 5150
Db 4739 GCAATCAGCTCTTCTCGTAATGTCAATCAACAAATGCCATTCTCGGCCCACTGCAAAAG 4798
QY 5151 ggaagaacaccttagccattatggaattactgtcttcaatcccttgatltccaag 5210
Db 4799 GGAGAGAACCCATAGCCATTATGGAATTAAGTCTTCAATCAATCCCTGATCTCACAG 4858
QY 5211 cagcagctcgaaggtgtgtcctgatgacacataagtgagtgctctgtgtcactgt 5270
Db 4859 CAGCAGCTCTCAGAGTGGCTCGATGACCAATCATAGTGAATGCTCTGTGTGTGTGTGTGT 4918
QY 5271 gtaacttggaaatgtccttgcgtccagcagacttgcgtatctccatccaagagcg 5330
Db 4919 GTCATCTTGGCAATGTCTTCGTCAGCAGCAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 4978
QY 5331 gtcagaagaagaacacactgtcagttcagtgagtgagtgagtgagtgagtgagtgagtgag 5390
Db 4979 GTACGAAAGCAAAACACTGCAATTCATCAGTGGAGTGAAGCTGTCTATCTAGTGTGCTC 5038
QY 5391 tctaatttgcctggagatagtgaatlaactgtgtccctgcagacactgtcatlatac 5450
Db 5039 TCTAATTTGTCTGGGATATGTCATTAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5098
QY 5451 ttaacttgcctcagaagaagttcctatgtgtcctcaacacactgtcgtgtcagcctt 5510
Db 5099 TTTATCTGTCTCCAGAGAAAGTCTATGTCCTTCCACCAATCTGCTGTGTGTGTGTGTGTGT 5158
QY 5511 ctacttctgtatagtggtgtcaatcaacactcctcaatgtacacagcctctgtgtc 5570
Db 5159 CTACTTTGCTGTATGAGGT 5218
QY 5571 aagatcccaagcaacagcctatgtgtgtcacaagcgtgaacctcattatggaat 5630
Db 5219 AAGATCCCAAGCAACGCTATGT 5278
QY 5631 ggcagcgttgcaacacttgtgtgtgagctgtgtcagcagcaatgaactgaataatcaat 5690
Db 5279 GGCAGGCTGGCACTTTGT 5338
QY 5691 galatcctgaatccgtgtgtccttgaatctccacatlttgccttggagcagggctatc 5750
Db 5339 GATATCTGAATGCTGT 5398
QY 5751 gacatgtgtgaaaacacagcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5810
Db 5399 GACATGTGAATAAACCCAGCAATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5458
QY 5811 gftcacacatltcttgagactgtgtgagacgaaccccttcgcatagtgcgtggaagg 5870
Db 5459 GTGTACCATTTATCTTGGGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5518
QY 5871 gtgtgtgttcttccatcaactgt 5930
Db 5519 GT 5578
QY 5931 gftaatgtcaaaactatcctccttgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 5990
Db 5579 GTTAATGTCAAAAGCTATCTCTCTGTAATGATGAATGAATGAATGAATGAATGAATGAATGA 5638
QY 5991 aqaattccttgatgtgtgagggccagaatgacatcttagaactcaaggaagtgtgaagaata 6050
Db 5639 ACAATTTTGATGAGTGGAGGCCAGATATACATCTTAGAATATCAAGAGACTTACCAAGATA 5688
QY 6051 tatagaagaagcgggaagcctgt 6110
Db 5699 TATAGAAGGAAGCGGAACCTGT 5758
QY 6111 tgccttggcctcctcgggagttatgtgggctgtgaaatcaacttccaagatgttaca 6170
Db 5759 TGTCTTGGCTCTGAGGATTAATGGGCTGTGAAATCATCACTTCAAGATGTTAACA 5818
|||||

QY	6171	ggagataccactggtaccagagagatgcttccctaaacaaatagltactataaac	6230
QY	6172		
Db	5819	GGAGATACCACTGTTACCAGAGAGATGCTTCCCTTAACGAAATAGTATCTATCAAC	5878
QY	6231	atccataaagtaacatacgaacatgagctgacccctcaagtttgaatgcatcacagaatg	6290
Db	5879	ATCCATGAAGTACATCAAGACATGGGCTACTGCCCTAGTTTGATGCCATCACAGAGCTG	5938
QY	6291	ctgaactgggaagagacacagtggaattctcttgcccttttgagagagagtcaccaagaaagaa	6350
Db	5939	TTGACTGGGAGAGAACAGTGGAGTCTTGTCCTTTTGAGAGAGATGCCAGAGAAAGAA	5998
QY	6351	gttgagcaaggtctggtgagtgaggcatccgaaactgggctcgtgaagtctgagaaaaa	6410
Db	5999	GTTGGCAAGGTTGGTGGATGGGGCATTCGGAACTGGGCCCTCGGAAGTATGAGGAAAAA	6058
QY	6411	tatgtgttaactaatagtgagagcaacaacgcaagctctctatacagcaatggctttatc	6470
Db	6059	TATGCTGGTAACTATAGTGGAGGGCCACAAAGCAAGCTCTCTACAGCATAGGCTTTGATC	6118
QY	6471	ggcgagccctcgtggtgttcttgatgaacccaaccaagcatbgaatcccaagcccg	6530
Db	6119	GGCGGGCCCTCGTGGTGTTCTGGATGAACCCACAGGCAATGATCCCAAAAGCCCGG	6178
QY	6531	cggttctgtggaatttgagccctaagtgtgttcaagagaggagataagtaagtgttaca	6590
Db	6179	CGGTTCTTGGAATGTGGCCCTTAAGTGTGTCAAGAGGGGAGATAGTATGCTTTACA	6238
QY	6591	tctcaatgaatgaagaatgaatgaagctctctgacatagatgagcaatcagttaatga	6650
Db	6239	TCTCATATATGAAGAAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGTGCAATGGA	6298
QY	6651	aggttcaggtgctcttgtagagtgctccagcatctataaaatagtttgtagatggttataca	6710
Db	6299	AGGTTCAAGTCCCTTGGAGTGTCCAGCATCTTAAAAATAGTGTGAGATGGTTATACA	6358
QY	6711	atagttgcaagaatagcaggtgtccaacccggagctgaagctcgtgccaggaattcttggga	6770
Db	6359	ATAGTTGTAGCAATTAGAGGGTCCAAACCCGGACCTGAAGGCTGTCCAGGATTTCTTGA	6418
QY	6771	cttgcatctccgtgaagtgtcttaaaagagaacacggaaatgctatacatlacagctt	6830
Db	6419	CTTGATTTCTCGGAAGTGTCCAAAAGAGAAACCGGAAACAATGCTATACATACCACTT	6478
QY	6831	ccatctcaatatctctctcgtgcagagatattagcatctcctctccagagaaanaagcga	6890
Db	6479	CCATTTATTAATCTCTCTGCGAGGATATTTCAGCATCCTCTCCAGAGCAAAAAACGA	6538
QY	6891	ctccacatagaagaactactcctgttcttcaagaacaacacttgaccagaatttgaactt	6950
Db	6539	CTCCCATAGGAAGACTACTCTGTTTCTGACAAACACTTGACCAAGTATTGTGAACTTT	6598
QY	6951	ggcaagagccaaagtatgatgatgacacttaaaagactcttataacaaaaaaccaaca	7010
Db	6599	GCCAAAGGCAAAAGTAGATGACCACTTAAAGAACCCTCTATTACCAAAAACCAACACA	6658
QY	7011	gtagtgagacgttgcaagttctcacatcttcttcaagagatgaaagatgaaagaaaglat	7070
Db	6659	GTAGTGGACGTTGACGTTCTCACATCTTTCTACAGAGTGAAGAAAGGAAAGAAAGCTAT	6728
QY	7071	gtataagaataatccgttctatacaggggtggcctgaaagtataaagaaactagaacttccctt	7130
Db	6719	GTATGAATAAATCTGTTGTATACGGGGGTGGTGAAGAGTAAAGAGNACTATGACTTTCCTTT	6778
QY	7131	gaaccaatgtgaagtctgtgagaaaaagacagaagtttgatgtgggaaagatlaaatctg	7190
Db	6779	GCACCATGTGAAGTGTGTGAGAAANAAGCCAGAGTGTGATGTGGGAGAGAAAGTAAACTG	6838
QY	7191	gatactgtactgtatactatccaatgcaatgcaattcaatgcaatgaaacaaatcccat	7250
Db	6839	GATACTGTACTGATACTATTCATATGCAATGCAATTCGAATTCGAATGAAGAAACAAATTCAT	6898
QY	7251	taccagggagagcgttggtagccatgctctgtatagctctccaaagtgaaagacttgaa	7310
Db	6899	TACAGGGGAGTGGCTTTGTATGCCCTATGTCTTGTATGGCTCTCAAGTAAAGACTTGAA	6958
QY	7311	ttagtttcttaacctatacctatgtaaacactatataatggaacccaatgtaacataatggtt	7370
Db	6959	TTAGTTTTTACCTATACCTATGTAACACTATATATGGAACCAATGAGCATATGCGTT	7018
QY	7371	tgaactacaacttcttcttcttcttctgtctgtatctcatttccattgggttgcaacata	7430
Db	7019	TGAACACACACTTTTTTTTTTTTTTTTTTTTGTTCGGTGTATTCATGTGGGGTTGCAACATA	7078
QY	7431	attctcaagtaataatgagccagatattgatataaataaanaagtaatgcaatcct	7490
Db	7079	ATTTCATCAAGTATATATGCGCAGCAATTAATGATCAATAAAGTAATGCATCTCT	7138
QY	7491	catctcaatagccatgcccctgcagagagactggttcccggttgacacatccatctgtcg	7550
Db	7139	CATTCACTAAGGCATGCGCATGCGCCAGAGAGCTGTTCCGGTGACATCATGCTTGG	7198
QY	7551	caatgagtggtccagaagtataatggtccaaagtttccaagaaagttgaagcacaatggtg	7610
Db	7199	CAATGAGTGTGCGAGGTTATTAAGGCCAAAGTTTTCAAGAAAGTTTGAAAGCACAATGGTG	7258
QY	7611	tctcaatgctcaccttctgttaaaagcgcctctgtctcaagctctatacaatgtaatacaat	7670
Db	7259	TGTCATGCTCACTTTTGTATAAAGCTGCTCTGCTCAAGACTCTATCAACTTGAATATCAGT	7318
QY	7671	tgaacagaatggtgccaatgctgtgctataacatccctgttctccctctgataaagctgtc	7730
Db	7319	TGACAAATAGTGGCCATGCGTGGTAAACATCCTGCTTGATTCCTCTGATAAAGCTGTTC	7378
QY	7731	tgtgtgcagtaaacatgcaacaaanaatgtgtgggtgtctctcaagcagcaggaacttggttcca	7790
Db	7379	TGTTGGACGTAACATGCAACAAAAATGTGGGTCTCTTAAGCAGCGGGAACCTGGTTCCA	7438
QY	7791	ttgttatalgttccctatgcttctgagccatggtgtctacagggatccatctatgagaactct	7850
Db	7439	TTGTATATTGTCATGCTTGTGACCCATGGGTCTTAACAGGGCATCTTATAGACTCTYT	7498
QY	7851	aaataactaataatcctgtglaagaggaanaagatacaagaaccaaatctgtgggttgaa	7910
Db	7499	AAATATATCTTAACCTCTGTATGAAGGCCAAAGATCAACAGCCAAACTCTGGGCTGTGAA	7558
QY	7911	gtctcgtgaagccaaggtgcatlaaagagaatgtgtcttcaaacccaggagaaagcctgt	7970
Db	7559	GTGCTGAAGCCAGGCAATGGGATTTAAAGAGATTTGGCTTCAAACTAGGGAAGCCGT	7618
QY	7971	ggccattgttccctgacgtctgtcacaatgltgaacatgcatcccaagaatglttaltcgtac	8030
Db	7619	GCCCATTTGCTGATGCTGCTCTTAACATGATGACCTGCATCTCAAGATGTTTATCTATC	7678
QY	8031	acaaagtataatcttctgcttcttggaataatctagaanaatgaaagatgagatgtgat	8090
Db	7679	ACAAAGTATTAATTTCTGCTTTTGATTAATCTTAGAAATAAGAAACATGAGAGTTGAT	7738
QY			



PA (CVTH-) CV THERAPEUTICS INC.

PI Lawn RM, Made D, Garvin M;

XX WPI; 2001-137812/14.

DR Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
XX useful for the development of agents for the treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -

PS Disclosure; Page 122-128; 215pp; English.

XX The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC membranes and utilizes ATP hydrolysis to transport a wide variety of
CC substrates across the plasma membrane. ABC1 is a pivotal protein in
CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC stores. ABC1 is defective in Tangier disease, a genetic disorder
CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC useful for developing pharmaceutical agents for the treatment of heart
CC disease and other disorders associated with hypercholesterolemia and
CC atherosclerosis. The genes are useful for developing screening assays to
CC screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC other disorders associated with hypercholesterolemia.

SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 100.0%; Score 10438; DB 22; Length 10442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggcggggccgcaagcgcagccctctccgggctgcgcaaggcaggcg 60
DB 1 ggcggggccgcaagcgcagccctctccgggctgcgcaaggcaggcg 60
QY 61 ggaagtcgcgcacacacagagccgctctcagggcgcttgcctctgttttcccg 120
DB 61 ggaagtcgcgcacacacagagccgctctcagggcgcttgcctctgttttcccg 120
QY 121 gttcgttttccctctccggaagcttcaagggttagaagaagaagcaaac 180
DB 121 gttcgttttccctctccggaagcttcaagggttagaagaagaagcaaac 180
QY 181 acaaaagtcgaacaaaglaattgacacagccagcgccgctctgttgaagtcggcgc 240
DB 181 acaaaagtcgaacaaaglaattgacacagccagcgccgctctgttgaagtcggcgc 240
QY 241 tgccttccagggctccgagccacagctggcgctgctgctgaggggaacatgctgtt 300
DB 241 tgccttccagggctccgagccacagctggcgctgctgctgaggggaacatgctgtt 300
QY 301 ggcctcagctaggctgtgctgttggagaagcctcacttccagaagaagaacaatgctc 360
DB 301 ggcctcagctaggctgtgctgttggagaagcctcacttccagaagaagaacaatgctc 360
QY 361 agctgttacttggagctgctgctcctatattatcttcctgcatctgcttctgcgc 420
DB 361 agctgttacttggagctgctgctcctatattatcttcctgcatctgcttctgcgc 420
QY 421 tgaatccccccatgaaacaatgaatgaatatttccaaataaagcactgctcctc 480
DB 421 tgaatccccccatgaaacaatgaatgaatatttccaaataaagcactgctcctc 480
QY 481 caggaaacttcccttgggttcagggaattatctgttaatgccaacacccctgttccggt 540
DB 481 caggaaacttcccttgggttcagggaattatctgttaatgccaacacccctgttccggt 540
QY 541 accggaactcttggggagcctccggagctgttggaaactttaaacaatcatgtgtc 600

DB 541 accggaactcttggggagcctccggagctgttggaaactttaaacaatcatgtgtc 600
QY 601 gctgttctcagatgctcgaagctctcttatacagccagaagaacacagcatgaag 660
DB 601 gctgttctcagatgctcgaagctctcttatacagccagaagaacacagcatgaag 660
QY 661 acatgcaagaagcttctggaacattacagagcatcaagaatccagctcaacttgaagc 720
DB 661 acatgcaagaagcttctggaacattacagagcatcaagaatccagctcaacttgaagc 720
QY 721 ttcaagattctctgttgacaaatgaacactctctctgttccctatatacaacactctc 780
DB 721 ttcaagattctctgttgacaaatgaacactctctctgttccctatatacaacactctc 780
QY 781 tcccaagttcactgcttgacaaatgaacactctctctgttccctatatacaacactctc 840
DB 781 tcccaagttcactgcttgacaaatgaacactctctctgttccctatatacaacactctc 840
QY 841 tgaaggtctacaaattacattgacaaatgcttgacaaatgcttgacaaatgcttgacaa 900
DB 841 tgaaggtctacaaattacattgacaaatgcttgacaaatgcttgacaaatgcttgacaa 900
QY 901 ttcaacttgtgacaaagagttcttgaagcttctgagcttctgacaaagagagagctgctg 960
DB 901 ttcaacttgtgacaaagagttcttgaagcttctgagcttctgacaaagagagagctgctg 960
QY 961 cagcagagcagatcctctcttccacacatgacacatccctgaagccatccctgagacata 1020
DB 961 cagcagagcagatcctctcttccacacatgacacatccctgaagccatccctgagacata 1020
QY 1021 acttcaatctcccttcccgagcagagagctgctgaagccacacaaatctgtgcata 1080
DB 1021 acttcaatctcccttcccgagcagagagctgctgaagccacacaaatctgtgcata 1080
QY 1081 gcttggagactctgcccagagccttgaagcattgagagcttgaagcattgagagcattg 1140
DB 1081 gcttggagactctgcccagagccttgaagcattgagagcttgaagcattgagagcattg 1140
QY 1141 aggtgatgcttctcgaacaaatgacacagctcagctcctccacacaaatctcagagctg 1200
DB 1141 aggtgatgcttctcgaacaaatgacacagctcagctcctccacacaaatctcagagctg 1200
QY 1201 tgcctcgtatctgctcgggacatcccgagagaggggcttgaagatccatctccaaat 1260
DB 1201 tgcctcgtatctgctcgggacatcccgagagaggggcttgaagatccatctccaaat 1260
QY 1261 ggtatgaggaacaaactacaaagccctcttggaggaatgagcactgagagaatgctg 1320
DB 1261 ggtatgaggaacaaactacaaagccctcttggaggaatgagcactgagagaatgctg 1320
QY 1321 aaacctctatgacaaactacaaactccttactgcaatgatttgaagaatttggagt 1380
DB 1321 aaacctctatgacaaactacaaactccttactgcaatgatttgaagaatttggagt 1380
QY 1381 ctatgctcttcccgacattatcttgaagccttgaagcctgctgtcttggagaatcc 1440
DB 1381 ctatgctcttcccgacattatcttgaagccttgaagcctgctgtcttggagaatcc 1440
QY 1441 tctatacacttgaacactccagccacaaagcagtgatagcttgaagtgaaagactctcc 1500
DB 1441 tctatacacttgaacactccagccacaaagcagtgatagcttgaagtgaaagactctcc 1500
QY 1501 aggaactgctgttctcctatgacacacacacacacacacacacacacacacacacacac 1560
DB 1501 aggaactgctgttctcctatgacacacacacacacacacacacacacacacacacacac 1560
QY 1561 ggaacttcaatgagacagccaaagaaatgagacactgttccggaatgctgttgaacagcag 1620
DB 1561 ggaacttcaatgagacagccaaagaaatgagacactgttccggaatgctgttgaacagcag 1620
QY 1621 acaatgacacacttgggaagcagctgagctgagcttgaagcccaagaacatcg 1680

Dh	1631	acaaatgaccacttlttvgaaacagcttvgatggtctagatcttgaaacagcccaagaacatcag	1680
Qy	1681	tgagcttlttvgccaaagcaacccagagatgctccagctccagtaatggtctctgttcaacct	1740
Dh	1681	tgagcttlttvgccaaagcaacccagagatgctccagctccagtaatggtctctgttcaacct	1740
Qy	1741	ggagagaagcttccaacgagactaaccaaggaatcccgagcaatctcgtcttcatatgaggt	1800
Dh	1741	ggagagaagcttccaacgagactaaccaaggaatcccgagcaatctcgtcttcatatgaggt	1800
Qy	1801	gtttccaaccttgaaagaactctgaagcccatatgccaagaanaatctcgtctcatcaagaattcca	1860
Dh	1801	gtttccaaccttgaaagaactctgaagcccatatgccaagaanaatctcgtctcatcaagaattcca	1860
Qy	1861	tgagagctctgtagatgtaagaagaaatctctggagctgtgatacttgcttcaactgtaattactccag	1920
Dh	1861	tgagagctctgtagatgtaagaagaaatctctggagctgtgatacttgcttcaactgtaattactccag	1920
Qy	1921	gcaagcatctgagcttgcccatcatatgtcgaagtacaaagatacccgaaatgagacatgtgacaatgttg	1980
Dh	1921	gcaagcatctgagcttgcccatcatatgtcgaagtacaaagatacccgaaatgagacatgtgacaatgttg	1980
Qy	1981	agagagacaataaataataaagatgaggttactgggaagccctgtctctcagatgaccccttgg	2040
Dh	1981	agagagacaataaataataaagatgaggttactgggaagccctgtctctcagatgaccccttgg	2040
Qy	2041	agagacaatgagcttactgtctggggagctctcgccactctgcaagatcttggtgtagagagcaaa	2100
Dh	2041	agagacaatgagcttactgtctggggagctctcgccactctgcaagatcttggtgtagagagcaaa	2100
Qy	2101	tcatcagaggtgctgacgagcgagccgagaagaanaactgtgtctataatgcaacagatgacct	2160
Dh	2101	tcatcagaggtgctgacgagcgagccgagaagaanaactgtgtctataatgcaacagatgacct	2160
Qy	2161	atccctgttaagatgttagatgacaatcttctctcgggtgtgataggccggttcaatgcccccttcca	2220
Dh	2161	atccctgtgttaagatgttagatgacaatcttctctcgggtgtgataggccggttcaatgcccccttcca	2220
Qy	2221	tgaagctgagcccttgatattactcagctgagctgtgtgtatctcaaggagcatctgttatgtgaagaag	2280
Dh	2221	tgaagctgagcccttgatattactcagctgagctgtgtgtatctcaaggagcatctgttatgtgaagaag	2280
Qy	2281	aggcaacggtctgaaagaagacaatctgcgatactatgagccatgtagacaacaagcaatactctgtttaa	2340
Dh	2281	aggcaacggtctgaaagaagacaatctgcgatactatgagccatgtagacaacaagcaatactctgtttaa	2340
Qy	2341	gctgtgttcaatagatgacccaatctcctctctctgtgtgagcgtcgtcgtctagtgtgtcatcc	2400
Dh	2341	gctgtgttcaatagatgacccaatctcctctctctgtgtgagcgtcgtcgtctagtgtgtcatcc	2400
Qy	2401	tgaagtttagaagaactctgcgcctcaacagtgatattcccaagctgtgtttgtgtcttcgcgttcg	2460
Dh	2401	tgaagtttagaagaactctgcgcctcaacagtgatattcccaagctgtgtttgtgtcttcgcgttcg	2460
Qy	2461	tgattgctgtgtgtatgacaatctctgcagtgatcttccctgtgattagacaacactctctccagaagcca	2520
Dh	2461	tgattgctgtgtgtatgacaatctctgcagtgatcttccctgtgattagacaacactctctccagaagcca	2520
Qy	2521	acctgtgcaagcagcctgtgggggtgacatactacttcaacgcgtgtgaacctgcctacgtctgt	2580
Dh	2521	acctgtgcaagcagcctgtgggggtgacatactacttcaacgcgtgtgaacctgcctacgtctgt	2580
Qy	2581	gtgtgtgcaatgtagaagactatgagctcttcaacataaagaatcttgccttagcctgtcttc	2640
Dh	2581	gtgtgtgcaatgtagaagactatgagctcttcaacataaagaatcttgccttagcctgtcttc	2640
Qy	2641	ctgtgtgcttctgggttctgtgctgtgtgagtaacttgccttlttgtagagagcagggcatgtgag	2700
Dh	2641	ctgtgtgcttctgggttctgtgctgtgtgagtaacttgccttlttgtagagagcagggcatgtgag	2700
Qy	2701	tgcagttgagacaacctgttttagagatctctctgtgtgagaagaatggtctcaatctcaccact	2760
Dh	2701	tgcagttgagacaacctgttttagagatctctctgtgtgagaagaatggtctcaatctcaccact	2760

QY	2761	cgatcccaatgagtcgttttgacaccttcctctabtgagtgatgacccgtgtacatvtgag	2820
Db	2761	cgatcccaatgagtcgttttgacaccttcctctabtgagtgatgacccgtgtacatvtgag	2820
QY	2821	ctgtcttccagggccagtaagaaatccagggccctgagtttctctgaccaaagtcct	2880
Db	2821	ctgtcttccagggccagtaagaaatccagggccctgagtttctctgaccaaagtcct	2880
QY	2881	actggtttcgaggaagaagtgatgagaagaagccacccctgtgtccacaagaagaagatgt	2940
Db	2881	actggtttcgaggaagaagtgatgagaagaagccacccctgtgtccacaagaagaagatgt	2940
QY	2941	cagaaatctgcagtgagagaggaacccacccactttgaagctggtgtccatgaagac	3000
Db	2941	cagaaatctgcagtgagagaggaacccacccactttgaagctggtgtccatgaagac	3000
QY	3001	tggttaaaaggtctaccagagatggagatgaaggtgctgtcatgtgacctgtgaattttt	3060
Db	3001	tggttaaaaggtctaccagagatggagatgaaggtgctgtcatgtgacctgtgaattttt	3060
QY	3061	atgaagggccaatatcaactccttcctcgagccacatbtgaagccgggagaaagcaccaatgt	3120
Db	3061	atgaagggccaatatcaactccttcctcgagccacatbtgaagccgggagaaagcaccaatgt	3120
QY	3121	caatctcgaccgggtgtgtcccccgcgaactcggtgcacgcgtacactctgtggaaaaagaca	3180
Db	3121	caatctcgaccgggtgtgtcccccgcgaactcggtgcacgcgtacactctgtggaaaaagaca	3180
QY	3181	ttcgctctgaaatgaagacacatcccgagagaaccttgaggctgtctccagacataacgtgc	3240
Db	3181	ttcgctctgaaatgaagacacatcccgagagaaccttgaggctgtctccagacataacgtgc	3240
QY	3241	tgtttgacatctctacgctctgaaagaaacacatctcgtgtcatgtcccgcttgaagggtcct	3300
Db	3241	tgtttgacatctctacgctctgaaagaaacacatctcgtgtcatgtcccgcttgaagggtcct	3300
QY	3301	ctgagaagcacgtgaaagcggagatgtagacagatgtagccctgtgagtgtgtgtgccatcaa	3360
Db	3301	ctgagaagcacgtgaaagcggagatgtagacagatgtagccctgtgagtgtgtgtgccatcaa	3360
QY	3361	ggaagctgaaaaaagaaaaaacagccagctgttcagatgtagatgaagaagaagctatctgag	3420
Db	3361	ggaagctgaaaaaagaaaaaacagccagctgttcagatgtagatgaagaagaagctatctgag	3420
QY	3421	cccttgacctgtctcgaggagatcctaaggtgtcatctctgatatcaaccacagctgtgtgag	3480
Db	3421	cccttgacctgtctcgaggagatcctaaggtgtcatctctgatatcaaccacagctgtgtgag	3480
QY	3481	acccttactccgcagagggaatatgtagagctgtgtctgataataccgaacaaagccgcacca	3540
Db	3481	acccttactccgcagagggaatatgtagagctgtgtctgataataccgaacaaagccgcacca	3540
QY	3541	ttattctctcaacacacaaatgtagatgaacggagactcttgagggaacagagtgtgcacca	3600
Db	3541	ttattctctcaacacacaaatgtagatgaacggagactcttgagggaacagagtgtgcacca	3600
QY	3601	tctccacatgggaagctgtgctgtgtggtgcctccctgttcttgaaagaaacgaagctgggaa	3660
Db	3601	tctccacatgggaagctgtgctgtgtggtgcctccctgttcttgaaagaaacgaagctgggaa	3660
QY	3661	caaggtactacacttgatgtgtcaagaagaatgtagaatctctccctcaagtctctgcagaa	3720
Db	3661	caaggtactacacttgatgtgtcaagaagaatgtagaatctctccctcaagtctctgcagaa	3720
QY	3721	acaagtaagacagctgtcatcaacttgaaaaaggaagaagctgttctcaagaacatttctg	3780
Db	3721	acaagtaagacagctgtgtgtcaaaccttgaaaaaggaagaagctgttctcaagaacatttctg	3780
QY	3781	atcgctgaccttgagcagacacatgagaatgaaacgctgtgacacatcgatgtctctgatatct	3840
Db	3781	atcgctgaccttgagcagacacatgagaatgaaacgctgtgacacatcgatgtctctgatatct	3840

QY 3841 ccaacctcatcaggaaagatgtgtctgaagcccggtcgtgtggaagacatatggcgctagac 3300
|||||
Db 3841 ccaacctcatcaggaaagatgtgtctgaagcccggtcgtgtggaagacatatggcgctagac 3300
QY 3901 tgaacctatgtctgcctcatalgaagaactcgaagagagagcctctgtlbgaaactcttcata 3360
|||||
Db 3901 tgaacctatgtctgcctcatalgaagaactcgaagagagagcctctgtlbgaaactcttcata 3360
QY 3961 agatttgatgacggcgctctcagaactcgtggaattctcattatgcatctcagaagaccc 4020
|||||
Db 3961 agatttgatgacggcgctctcagaactcgtggaattctcattatgcatctcagaagaccc 4020
QY 4021 tggagaagaataatctcctaaggttgccgaagaagatggtgtgtgagtgtcgtgagacctcagat 4080
|||||
Db 4021 tggagaagaataatctcctaaggttgccgaagaagatggtgtgtgagtgtcgtgagacctcagat 4080
QY 4081 gtacacctgacagcaagacagagcggtcctcgtggaagcaagcagagctgtctctgc 4140
|||||
Db 4081 gtacacctgacagcaagacagagcggtcctcgtggaagcaagcagagctgtctctgc 4140
QY 4141 cgttcactggaagatgagtctgtctgatalccaaatgattcttgacatagaccgaatccagag 4200
|||||
Db 4141 cgttcactggaagatgagtctgtctgatalccaaatgattcttgacatagaccgaatccagag 4200
QY 4201 agacagaactgtctcagtgtggaatggaatggcaaggtctcaccaggtgaaagagcttgaaac 4260
|||||
Db 4201 agacagaactgtctcagtgtggaatggaatggcaaggtctcaccaggtgaaagagcttgaaac 4260
QY 4261 ttacacagcaacagtttctgtgaccttctgtggaagagagactgtaatttgccagacgagatc 4320
|||||
Db 4261 ttacacagcaacagtttctgtgaccttctgtggaagagagactgtaatttgccagacgagatc 4320
QY 4321 ggaagaagattttctgcataatgtctctgcagactgctgtgtctgtcgtacgacctgtgt 4380
|||||
Db 4321 ggaagaagattttctgcataatgtctctgcagactgctgtgtctgtcgtacgacctgtgt 4380
QY 4381 tcagccgcatcgtgtgcacaccttctgtgcagatgacccacgacctggaactcagacctgtatc 4440
|||||
Db 4381 tcagccgcatcgtgtgcacaccttctgtgcagatgacccacgacctggaactcagacctgtatc 4440
QY 4441 acaacggaacgatacactgtctcagcaatgactctcctgaggaacacggaacctgtgaac 4500
|||||
Db 4441 acaacggaacgatacactgtctcagcaatgactctcctgaggaacacggaacctgtgaac 4500
QY 4501 tcttaaacgacctcacaacaaagacctgtctcgtgagaccgctgtatggaaggaacccaa 4560
|||||
Db 4501 tcttaaacgacctcacaacaaagacctgtctcgtgagaccgctgtatggaaggaacccaa 4560
QY 4561 tcccaagacagccctgtgcagagcgaggaagaaagtgaaccactgccccagatcccccaga 4620
|||||
Db 4561 tcccaagacagccctgtgcagagcgaggaagaaagtgaaccactgccccagatcccccaga 4620
QY 4621 ccatcatalggaactcttcacaagaatggaactggaacaaatgacgaacctctcactgcatgc 4680
|||||
Db 4621 ccatcatalggaactcttcacaagaatggaactggaacaaatgacgaacctctcactgcatgc 4680
QY 4681 agtgtatgacagcgaacaaatcaagaagatgtcctgtgtgtccccaaggggaagggggc 4740
|||||
Db 4681 agtgtatgacagcgaacaaatcaagaagatgtcctgtgtgtccccaaggggaagggggc 4740
QY 4741 tgcctcctcacaagaagaacaaacactgcatatctccttcagagacccgtgaacggagaaga 4800
|||||
Db 4741 tgcctcctcacaagaagaacaaacactgcatatctccttcagagacccgtgaacggagaaga 4800
QY 4801 acatttgcgattatctgtgtgaagacgtatgttgagatcatagcaaaagcttaagaaga 4860
|||||
Db 4801 acatttgcgattatctgtgtgaagacgtatgttgagatcatagcaaaagcttaagaaga 4860
QY 4861 agatctgggtggaatgtgtatggtatggtggtgttccctgtgtgtcagtaatactcaag 4920
|||||
Db 4861 agatctgggtggaatgtgtatggtatggtggtgttccctgtgtgtcagtaatactcaag 4920
QY 4921 cacttcctcagtcagaaatgaatgaatgacatcaacaacaaatgaagaacacctaagc 4980
|||||

Db 4921 cacttcctcagtcagaaatgaatgaatgacatcaacaacaaatgaagaacacctaagc 4980
QY 4981 tggccaagagacagttctctgagatcagatctcacaacagcttggaaagattatgacagac 5040
|||||
Db 4981 tggccaagagacagttctctgagatcagatctcacaacagcttggaaagattatgacagac 5040
QY 5041 tggacaaccaagaataatgtcaaggtgtgtgtlcaataacaagggctgtgcatcaagct 5100
|||||
Db 5041 tggacaaccaagaataatgtcaaggtgtgtgtlcaataacaagggctgtgcatcaagct 5100
QY 5101 cttcctcagatgtcacaacaatgtcattctcggggccaacctgtgaagaaggagaaac 5160
|||||
Db 5101 cttcctcagatgtcacaacaatgtcattctcggggccaacctgtgaagaaggagaaac 5160
QY 5161 ctgaccatataggaattactgtcttcaatcactccctgaatccctcacaagcagactct 5220
|||||
Db 5161 ctgaccatataggaattactgtcttcaatcactccctgaatccctcacaagcagactct 5220
QY 5221 cagaggtgtctgtatgacacatacagtggaatggtcctgtgtcattgtctgtctgt 5280
|||||
Db 5221 cagaggtgtctgtatgacacatacagtggaatggtcctgtgtcattgtctgtctgt 5280
QY 5281 caatgtcctcgtcccaagcagcttctgtcgtatctcctgataccagagcggtlcaagcaag 5340
|||||
Db 5281 caatgtcctcgtcccaagcagcttctgtcgtatctcctgataccagagcggtlcaagcaag 5340
QY 5341 caaaacacctgaatgtcaatcagtggaatggaagcctgtatctactcgtctcattttg 5400
|||||
Db 5341 caaaacacctgaatgtcaatcagtggaatggaagcctgtatctactcgtctcattttg 5400
QY 5401 tctgggataatgacaaatgaagttccctgccaacactgtcatatcaatctcactcgt 5460
|||||
Db 5401 tctgggataatgacaaatgaagttccctgccaacactgtcatatcaatctcactcgt 5460
QY 5461 tcccaagagaatgccatgtgtcctccacaactcgtcgtgtcgtacgaccttactttgc 5520
|||||
Db 5461 tcccaagagaatgccatgtgtcctccacaactcgtcgtgtcgtacgaccttactttgc 5520
QY 5521 tgtatgggtgtgtcaatcacaactctcactgtaacacagcctccttgtgtcaagatccca 5580
|||||
Db 5521 tgtatgggtgtgtcaatcacaactctcactgtaacacagcctccttgtgtcaagatccca 5580
QY 5581 gcaacgactatgtgtgtcctacacagctgaaactcttcattgtgcatatgacagctgtg 5640
|||||
Db 5581 gcaacgactatgtgtgtcctacacagctgaaactcttcattgtgcatatgacagctgtg 5640
QY 5641 ccaacttgtgtgtgagctgttccacgacaataagctgtgaataataatgatatcctga 5700
|||||
Db 5641 ccaacttgtgtgtgagctgttccacgacaataagctgtgaataataatgatatcctga 5700
QY 5701 agtccgttcttctgtcttccacaacttctgtcgtggaaggggtcactgacatgtlga 5760
|||||
Db 5701 agtccgttcttctgtcttccacaacttctgtcgtggaaggggtcactgacatgtlga 5760
QY 5761 aaacacaggaacatgtgtgtcctctggaaggttctgggaagatcgtgtgtccacat 5820
|||||
Db 5761 aaacacaggaacatgtgtgtcctctggaaggttctgggaagatcgtgtgtccacat 5820
QY 5821 tatcttggagctgtgtggaagaaactctcgcataatgacgtgtggaaggggtgtgtct 5880
|||||
Db 5821 tatcttggagctgtgtggaagaaactctcgcataatgacgtgtggaaggggtgtgtct 5880
QY 5881 tctcattactgttctgtctcagtaacagatcttccataccagccagacgtgtgaatgcaa 5940
|||||
Db 5881 tctcattactgttctgtctcagtaacagatcttccataccagccagacgtgtgaatgcaa 5940
QY 5941 agctatcctcctctgaatgaatgaatgaatgtggaagcggaagacagagaactcttg 6000
|||||
Db 5941 agctatcctcctctgaatgaatgaatgaatgtggaagcggaagacagagaactcttg 6000
QY 6001 atgtgtggaagcagaatgacatcttgaagaatcaaggggtgtgacaagaatlatagaaga 6060
|||||

Dh	6001	atggtggaagcccaagatgacattctttaagaatacaaggaagtgaacgaatataataagaaga	6060
Qy	6061	agcggaaagccctgctgtgtgacaagagattbgtgtgagcattccctctgtgtgagtgctttggcc	6120
Dh	6061	agcggaaagccctgctgtgtgacaagagattbgtgtgagcattccctctgtgtgagtgctttggcc	6120
Qy	6121	tccctggagattaatggtggtctggaataatcatcaacttcaagaatgttaacagagatacca	6180
Dh	6121	tccctggagattaatggtggtctggaataatcatcaacttcaagaatgttaacagagatacca	6180
Qy	6181	ctgttaccagaagagatgcttcttccctaacaanaaatagatctatcaacaatccaataaag	6240
Dh	6181	ctgttaccagaagagatgcttcttccctaacaanaaatagatctatcaacaatccaataaag	6240
Qy	6241	tacatcagaacacatgaggtctactgcccctcaatttgatgccaatcaagaagtggttgacttgga	6300
Dh	6241	tacatcagaacacatgaggtctactgcccctcaatttgatgccaatcaagaagtggttgacttgga	6300
Qy	6301	gagaaacagtgtgagtgcttcttgcccttttgaagagagctcccaagagaagaagtltggcaag	6360
Dh	6301	gagaaacagtgtgagtgcttcttgcccttttgaagagagctcccaagagaagaagtltggcaag	6360
Qy	6361	tgtgtgagtggtggcgatcttcggaaaacttggcgctctgtgaagtatgagaaataatgctgtga	6420
Dh	6361	tgtgtgagtggtggcgatcttcggaaaacttggcgctctgtgaagtatgagaaataatgctgtga	6420
Qy	6421	actatagtgagaggaacaaacacgcaagctctctctacagccaatggtcttgaatggcggtctc	6480
Dh	6421	actatagtgagaggaacaaacacgcaagctctctctacagccaatggtcttgaatggcggtctc	6480
Qy	6481	ctgtgtgtgttctctgatalyaaacccaccacacagagatgatalcccaaaagcccggtgtctgt	6540
Dh	6481	ctgtgtgtgttctctgatalyaaacccaccacacagagatgatalcccaaaagcccggtgtctgt	6540
Qy	6541	gggaattgtgccccaagagtggttgaagaagggagagatcagtagtcttcatcatctcatagta	6600
Dh	6541	gggaattgtgccccaagagtggttgaagaagggagagatcagtagtcttcatcatctcatagta	6600
Qy	6601	tggagaagaatgtgaagcgctcttgcacacagatgtgccaatctgttcaatggaaagtgctcaggt	6660
Dh	6601	tggagaagaatgtgaagcgctcttgcacacagatgtgccaatctgttcaatggaaagtgctcaggt	6660
Qy	6661	gacctgtgacagtgctccagcatcttaaaaaaataggttttgagatggttatacaatagtlgtac	6720
Dh	6661	gacctgtgacagtgctccagcatcttaaaaaaataggttttgagatggttatacaatagtlgtac	6720
Qy	6721	gaatatgacaggtgtccaacccggagaccttgaagcctgttccagaatttcttggacttgcatttc	6780
Dh	6721	gaatatgacaggtgtccaacccggagaccttgaagcctgttccagaatttcttggacttgcatttc	6780
Qy	6781	ctggaagagtggtcttaaaagagaanaacacccggaacatgttaataatcagaagttccattcat	6840
Dh	6781	ctggaagagtggtcttaaaagagaanaacacccggaacatgttaataatcagaagttccattcat	6840
Qy	6841	tatcttctctgccaagataatlaagcatcctctccacagacgaanaagagttccacatag	6900
Dh	6841	tatcttctctgccaagataatlaagcatcctctccacagacgaanaagagttccacatag	6900
Qy	6901	aagactactcgtttctccagacaacaacttgcacaagatatttgtgaactlttgcacaagacc	6960
Dh	6901	aagactactcgtttctccagacaacaacttgcacaagatatttgtgaactlttgcacaagacc	6960
Qy	6961	aaagtgaatgagaccactttaaagaagctctcattacaanaaaacagaagatagtgagcg	7020
Dh	6961	aaagtgaatgagaccactttaaagaagctctcattacaanaaaacagaagatagtgagcg	7020
Qy	7021	ttagcagttctacaatcttcttctcagatgagatgagaagtgaagaagaagctatgtatgaaga	7080
Dh	7021	ttagcagttctacaatcttcttctcagatgagatgagaagtgaagaagaagctatgtatgaaga	7080
Qy	7081	tccgttataacgggtgtgcttgaagaagttaaaggaagaaactagaacttcccttgcacaatg	7140
Dh	7081	tccgttataacgggtgtgcttgaagaagttaaaggaagaaactagaacttcccttgcacaatg	7140

[illegible]

QY	8221	ttattttctatgtaagtttgatatacgtacatgctagctgctcagaagaacatgctat	8220
Db	8221	ttattttctatgtaagtttgatatacgtacatgctagctgctcagaagaacatgctat	8280
QY	8281	gtctcaggtctcagacaatatatttgagtttcttcacatcatttaagatacttcaat	8340
Db	8281	gtctcaggtctcagacaatatatttgagtttcttcacatcatttaagatacttcaat	8340
QY	8341	ctcacttcaatcaatcaatatatttttgagtgtaatgctgtagctgagaagaatgtaagta	8400
Db	8341	ctcacttcaatcaatcaatatatttttgagtgtaatgctgtagctgagaagaatgtaagta	8400
QY	8401	cgataaagactcagagagaatatlaagctctcagtaacctctctgtagcaatgtaattcagctc	8460
Db	8401	cgataaagactcagagagaatatlaagctctcagtaacctctctgtagcaatgtaattcagctc	8460
QY	8461	actggtttaacaatatagtgctgtctgtgtgtgtagagcccaactgtacaatatgtggtc	8520
Db	8461	actggtttaacaatatagtgctgtctgtgtgtgtagagcccaactgtacaatatgtggtc	8520
QY	8521	agcccttttttttttttttttaattgtgcaacatgcagaagccagaagaatataagagttac	8580
Db	8521	agcccttttttttttttttttaattgtgcaacatgcagaagccagaagaatataagagttac	8580
QY	8581	aagtttaacaatgtaattcttccaacaggggaaacagctagctgtgaaactgtctgtgaaaaa	8640
Db	8581	aagtttaacaatgtaattcttccaacaggggaaacagctagctgtgaaactgtctgtgaaaaa	8640
QY	8641	cacaactgtgtttatgagcttttagaccttccaacttaaatgtgcttgagaatattgtata	8700
Db	8641	cacaactgtgtttatgagcttttagaccttccaacttaaatgtgcttgagaatattgtata	8700
QY	8701	ccccattaaactctgacagctccaacttttcatcctcttcaatccactagtcgaagaaaaa	8760
Db	8701	ccccattaaactctgacagctccaacttttcatcctcttcaatccactagtcgaagaaaaa	8760
QY	8761	taaaaaacaacaataacttccaatbtggagcaatttttcagagtttcttaacccaagttcatt	8820
Db	8761	taaaaaacaacaataacttccaatbtggagcaatttttcagagtttcttaacccaagttcatt	8820
QY	8821	tttctagtcgaataacactgtglaaaaaactgttccacaaactaactactgttaactgtct	8880
Db	8821	tttctagtcgaataacactgtglaaaaaactgttccacaaactaactactgttaactgtct	8880
QY	8881	tgagagaaagaaaaaataatgagagaactatgttttggggaagttcaaatgtacttcaat	8940
Db	8881	tgagagaaagaaaaaataatgagagaactatgttttggggaagttcaaatgtacttcaat	8940
QY	8941	atcatttaactctctccacacttttccaanaatttgaatattaaagccaaaggcgtataga	9000
Db	8941	atcatttaactctctccacacttttccaanaatttgaatattaaagccaaaggcgtataga	9000
QY	9001	ctcagatttcaaatcaatcttctcataltttttaatttaacagataatataaaccca	9060
Db	9001	ctcagatttcaaatcaatcttctcataltttttaatttaacagataatataaaccca	9060
QY	9061	ctgtctgaaaaaagaaaaaagaatgtgttttagaagaattaaagtaacatgattttaaata	9120
Db	9061	ctgtctgaaaaaagaaaaaagaatgtgttttagaagaattaaagtaacatgattttaaata	9120
QY	9121	aagtaatgaaagcatatttccaataactagtgatatgcatcggttgaactttacagttac	9180
Db	9121	aagtaatgaaagcatatttccaataactagtgatatgcatcggttgaactttacagttac	9180
QY	9181	ttcaaaaaatacagaatttatagataataattccctccatttaatatattttccaanaacag	9240
Db	9181	ttcaaaaaatacagaatttatagataataattccctccatttaatatattttccaanaacag	9240
QY	9241	ttatggtttcccatatttactaaacatcgatctcaatccatccatataatagtaaacatgta	9300
Db	9241	ttatggtttcccatatttactaaacatcgatctcaatccatccatataatagtaaacatgta	9300
QY	9301	gcaacttccattctcggttctctgtattccaaggccatatatttaaaaaatacaaaaggcac	9360

[illegible]

```

Db 10381 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 10440
QY 10441 aa 10442
    ||
Db 10441 aa 10442

```

RESULT 2

ID	AAE24702	standard; DNA; 10442 BP.
1	1	1

AC AAF24702;

DT 20-APR-2001 (first entry)

DE Nucleotide sequence of a human ABC1 polypeptide

Human, adenosine triphosphate binding cassette protein 1; ABC1;
apolipoprotein-mediated mobilisation; cholesterol; Tangier disease

KW atherosclerosis

OS Homo sapiens

FH	key	Location/qualifiers
FT	CDS	391 2075

```
FT /product= "ABC1 polypeptide"
```

PN WO2000078971-
XX

PD 28-DEC-2000.

16-JUN-2000; 2000WO-0516591.

PR	18-JUN-1999;	99US-0140264.
PR	14-SEP-1999;	99US-0153872

PR 19-NOV-1999; 9905-01665/3.
XX
XXPA (CVTH-) CV THERAPEUTICS INC.
PA (INTW) INTV WASHINGTON

xx
PT
Law PM
Made D
Ogram .TF

AA
DB
WPT: 2001-137811/14

DR P-PSDB; AABJ1303.
XX

PT Adenosine triphosphate (ATP),
polynucleotides and polynucleo-

PT and other disorders associated with hypercholesterolemia and atherosclerosis -

Claim 3: Page 117-123: 211pp: English

CC The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC membranes and utilises ATP hydrolysis to transport a wide variety of
CC substrates across the plasma membrane. ABC1 is a pivotal protein in
CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC stores. ABC1 is defective in Tangier disease, a genetic disorder
CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC useful for developing pharmaceutical agents for the treatment of heart
CC disease and other disorders associated with hypercholesterolemia and
CC atherosclerosis. The genes are useful for developing screening assays to
CC screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC are also useful as diagnostic indicators of cardiovascular disease and
CC other disorders associated with hypercholesterolemia.

SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match	100.0%	Score 10438;	DB 22;	Length 10442;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 10442; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0.

QY	1	gggagcgagcccgagagcgacgagcccttctcccgagctgagcgagcgagcg	60
Db	1	ggcccgagacccgagagcgccgagccgcccctctcccgagctgagcgagcgcg	60
QY	61	ggaagctccgagcccaacagagcggttctcagggcgcttgctcctgttttcccg	120
Db	61	ggagctccgagcccaacagagcggttctcagggcgcttgctcctgttttcccg	120
QY	121	gttcgttttctcccttctccgaaagcttgtcaagggttagaggaaagagcgcaac	180
Db	121	gttcgttttctcccttctccgaaagcttgtcaagggttagaggaaagagcgcaac	180
QY	181	acaaagatggaagacagttatagacagccagcgggcgctccctgctgtagcttgcgc	240
Db	181	acaaagatggaagacagttatagacagccagcgggcgctccctgctgtagcttgcgc	240
QY	241	tgccctccagggctcccgagccacacgctggcgctgtgcgtcagggagaaatgctgtt	300
Db	241	tgccctccagggctcccgagccacacgctggcgctgtgcgtcagggagaaatgctgtt	300
QY	301	ggcctcagcgaggttgctgtctgtgaagaaactcaacttccaggaagagcaaaatctc	360
Db	301	ggcctcagcgaggttgctgtctgtgaagaaactcaacttccaggaagagcaaaatctc	360
QY	361	agctgttaactcgtgaagctgtgcctgtgcctctatattctccgtactgtctgtgcg	420
Db	361	agctgttaactcgtgaagctgtgcctgtgcctctatattctccgtactgtctgtgcg	420
QY	421	tgaagatcccaacctatgaaacaacagaaatgcattttccaataaagcctatgccttg	480
Db	421	tgaagatcccaacctatgaaacaacagaaatgcattttccaataaagcctatgccttg	480
QY	481	caggaacaacttccttggtgttcacagggatatactgtatgtccacaacaccctgttcgct	540
Db	481	caggaacaacttccttggtgttcacagggatatactgtatgtccacaacaccctgttcgct	540
QY	541	accgcgactcctggggagagctcccgagctgtgttggaactttacaacatccattgtgctc	600
Db	541	accgcgactcctggggagagctcccgagctgtgttggaactttacaacatccattgtgctc	600
QY	601	ggcgtgtctcagaagctcccgagagctctcttttatacagccagaagaacacccagatgaaag	660
Db	601	ggcgtgtctcagaagctcccgagagctctcttttatacagccagaagaacacccagatgaaag	660
QY	661	acatgctgcgaaggtctctgaagacaattacagcagatcaagaataccagctcaaatctgaagc	720
Db	661	acatgctgcgaaggtctctgaagacaattacagcagatcaagaataccagctcaaatctgaagc	720
QY	721	ttcaagatctccgtgtgagacaatgaaactctctgtgttctctatatatacaacccctctc	780
Db	721	ttcaagatctccgtgtgagacaatgaaactctctgtgttctctatatatacaacccctctc	780
QY	781	ttccaaagctcaactgttgacaagaatcgtgagggctatgttcaattctccaaagctattt	840
Db	781	ttccaaagctcaactgttgacaagaatcgtgagggctatgttcaattctccaaagctattt	840
QY	841	tgcgaagctacagttacatttgaacaagtcgtgcaatgagatcaaaatcagaagaatga	900
Db	841	tgcgaagctacagttacatttgaacaagtcgtgcaatgagatcaaaatcagaagaatga	900
QY	901	ttcaactgttgaccgaagaaggttcttgagcttgtgtgcttaccacaaggagaaactgctgt	960
Db	901	ttcaactgttgaccgaagaaggttcttgagcttgtgtgcttaccacaaggagaaactgctgt	960
QY	961	cagcagagcgagtaattcgtttccaacaatgacatccctgaaagccaatcccgagaaacataa	1020
Db	961	cagcagagcgagtaattcgtttccaacaatgacatccctgaaagccaatcccgagaaacataa	1020
QY	1021	actctacatcttccctccgagcaaggagctgtgaaagccacaataaattgtcgtcata	1080

```
Db 1021 actcaactccctccctcccgagagagctgcttgaaagcccaaaaacattgtctgata 1080
Qy 1081 gtcttggaactctggcccaagagctgttcaagcatgaaagctgagatgacatgacagag 1140
Db 1081 gtcttggaactctggcccaagagctgttcaagcatgaaagctgagatgacatgacagag 1140
Qy 1141 agtatgtttcttaccaatgtgaacagctcagctcctcccaaccaatcacagagctg 1200
Db 1141 agtgagatcttcgaccaaagtggaacagctccacctccccaacaaatccaaagctg 1200
Qy 1201 tgtctgfatgtctggcgagcatcccgagagaggggcttgaaagataagcttccaaat 1260
Db 1201 tgtctgfatgtctggcgagcatcccgagagaggggcttgaaagataagcttccaaat 1260
Qy 1261 ggtatgagacaacaacaacaagcctcttggagagcaatgagcctgaggaagaatgctg 1320
Db 1261 ggtatgagacaacaacaacaagcctcttggagagcaatgagcctgaggaagaatgctg 1320
Qy 1321 aaactctatgacaactcaactcaactccttaacttgcaatgatttgaagaatttgagt 1380
Db 1321 aaactctatgacaactcaactcaactccttaacttgcaatgatttgaagaatttgagt 1380
Qy 1381 ctatgctctcttcccgcaatctcgaagaagctcgaagcgcgtctgcttgaggagaatcc 1440
Db 1381 ctatgctctcttcccgcaatctcgaagaagctcgaagcgcgtctgcttgaggagaatcc 1440
Qy 1441 tgtataacctggaacatcccgacgaagcgacatgctgctgagagtgaaacagacttcc 1500
Db 1441 tgtataacctggaacatcccgacgaagcgacatgctgctgagagtgaaacagacttcc 1500
Qy 1501 aggaactgctgtgttccatgatctggaagagcatgttgaggagaaactcagcccaagatc 1560
Db 1501 aggaactgctgtgttccatgatctggaagagcatgttgaggagaaactcagcccaagatc 1560
Qy 1561 ggaacttcacatgagaaacagccaaagaaatggaacttgcctgagatgctgttgagacagcag 1620
Db 1561 ggaacttcacatgagaaacagccaaagaaatggaacttgcctgagatgctgttgagacagcag 1620
Qy 1621 acaatgacacatcttgggaacagacagatgtgagctgagattggagacagcccaagacatc 1680
Db 1621 acaatgacacatcttgggaacagacagatgtgagctgagattggagacagcccaagacatc 1680
Qy 1681 tggcgttcttggcccaagcaccagagagatgtccagctcagtaatgcttctgttacaact 1740
Db 1681 tggcgttcttggcccaagcaccagagagatgtccagctcagtaatgcttctgttacaact 1740
Qy 1741 ggaagaagaagctttaaagagagacttaacaggaatccgagacatctcgcgttcatagagt 1800
Db 1741 ggaagaagaagctttaaagagagacttaacaggaatccgagacatctcgcgttcatagagt 1800
Qy 1801 gttcacaacttgaaacaagctagaacccaatagcaacagaagctgctgctatcaacaagatcca 1860
Db 1801 gttcacaacttgaaacaagctagaacccaatagcaacagaagctgctgctatcaacaagatcca 1860
Qy 1861 tggagctgcgtgagatgaaagagatcttctgggctggttattgttcaactgaggaattacccag 1920
Db 1861 tggagctgcgtgagatgaaagagatcttctgggctggttattgttcaactgaggaattacccag 1920
Qy 1921 gcaacatctggcgtgcccccatcagtcaagtacaagaatccgaatgagacatggaatgtag 1980
Db 1921 gcaacatctggcgtgcccccatcagtcaagtacaagaatccgaatgagacatggaatgtag 1980
Qy 1981 agagagacaataaataatcaagatgagctgagctgggagccctgtgctcgagctgaccccttg 2040
Db 1981 agagagacaataaataatcaagatgagctgagctgggagccctgtgctcgagctgaccccttg 2040
Qy 2041 agagacatgagctgagctgagctgggagctgagctgagctgagctgagctgagctgagctg 2100
Db 2041 agagacatgagctgagctgagctgggagctgagctgagctgagctgagctgagctgagctg 2100
Qy 2101 tcatcaggtgctgagcggagcagcagagaagaataatggtgtctatagcaacatgacct 2160
Db 2101 tcatcaggtgctgagcggagcagcagagaagaataatggtgtctatagcaacatgacct 2160
Db 2161 atccctgttaacgttgaatgacatcttctcgggtgagtgagccggtcaatgcccccttca 2220
Qy 2161 atccctgttaacgttgaatgacatcttctcgggtgagtgagccggtcaatgcccccttca 2220
Db 2221 tgaagctgagcgtgagatcttcaatgagctgagatcaatcaagagcatctgtatgagaag 2280
Qy 2221 tgaagctgagcgtgagatcttcaatgagctgagatcaatcaagagcatctgtatgagaag 2280
Db 2281 aggaacgctgaaagaaagaaacatgagcagatcatgagccttgaaacaaagcatactctgtta 2340
Qy 2281 aggaacgctgaaagaaagaaacatgagcagatcatgagccttgaaacaaagcatactctgtta 2340
Db 2341 gctgtgtcaattagtagcctcaatctctctctgtgagcgtgagcgtgagctgagctgagct 2400
Qy 2341 gctgtgtcaattagtagcctcaatctctctctgtgagcgtgagcgtgagctgagctgagct 2400
Db 2401 tgaagctgaaagaaacgtgagcctcaatgagcagatgagcagcgtgtgttcttccctgctc 2460
Qy 2401 tgaagctgaaagaaacgtgagcctcaatgagcagatgagcagcgtgtgttcttccctgctc 2460
Db 2401 tgaagctgaaagaaacgtgagcctcaatgagcagatgagcagcgtgtgttcttccctgctc 2460
Qy 2461 tgttctgttggtagaacaatcccgacatgctgctctgattagcaacatcttcccaagacca 2520
Db 2461 tgttctgttggtagaacaatcccgacatgctgctctgattagcaacatcttcccaagacca 2520
Qy 2521 acctggcagcagcctgtgagggagcatcaatcaactcaactcagctgactgctgctgct 2580
Db 2521 acctggcagcagcctgtgagggagcatcaatcaactcaactcagctgactgctgctgctgct 2580
Qy 2581 gtaggacatgagcagcagcctgtgagggagcatcaatcaactcagctgactgctgctgct 2640
Db 2581 gtaggacatgagcagcagcctgtgagggagcatcaatcaactcagctgactgctgctgctgct 2640
Qy 2641 ctgtgcttctgtggttggctgagtaacttgccttcttggagagcagggagcttggag 2700
Db 2641 ctgtgcttctgtggttggctgagtaacttgccttcttggagagcagggagcttggag 2700
Qy 2701 tgcagtgaggaaacacgttggagagctcgtgaggaagagatgagcttcaatccacatt 2760
Db 2701 tgcagtgaggaaacacgttggagagctcgtgaggaagagatgagcttcaatccacatt 2760
Qy 2761 cgaatcccaatgagctgcttggacacatccctcaatgagggatgagcagctgagctgag 2820
Db 2761 cgaatcccaatgagctgcttggacacatccctcaatgagggatgagcagctgagctgag 2820
Qy 2821 ctgtcttccagcagatgaggaattcccaagcctgtgatttccctgacccaagtctc 2880
Db 2821 ctgtcttccagcagatgaggaattcccaagcctgtgatttccctgacccaagtctc 2880
Qy 2881 actgtgttggcagagaaatgagtgaggaagagcgaacccgtgttccaaacagaagaagatgt 2940
Db 2881 actgtgttggcagagaaatgagtgaggaagagcgaacccgtgttccaaacagaagaagatgt 2940
Qy 2941 cagaatctcagcagtgaggaaggaaccccaacatctgaagcgttggcgtgttccaaacaga 3000
Db 2941 cagaatctcagcagtgaggaaggaaccccaacatctgaagcgttggcgtgttccaaacaga 3000
Qy 3001 tggtaaaatgtaacagagatgagtgaggaagtgagcgtgagcgttggcgttggcgttggcgt 3060
Db 3001 tggtaaaatgtaacagagatgagtgaggaagtgagcgtgagcgttggcgttggcgttggcgt 3060
Qy 3061 atgagggcagagatcaactcctctctgtggcccaatgagcgggaggaagacagacacatgt 3120
Db 3061 atgagggcagagatcaactcctctctgtggcccaatgagcgggaggaagacagacacatgt 3120
Qy 3121 caatccctgagcgggtgtgttcccccagactcgggagcagcagcagcagcagcagcagcag 3180
Db 3121 caatccctgagcgggtgtgttcccccagactcgggagcagcagcagcagcagcagcagcag 3180
Qy 3181 ttcgctcagagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3240
Db 3181 ttcgctcagagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3240
```


D	b	5401	ttctgggatatgtgcgaattacgcttgccttcgacacgtggtcattatcatcttcacgtct	5460
Q	y	5461	tcacagcaagaatccctatgtgtctccacccaattctgcctgtgtagcccttcactttgc	5520
D	b	5461	tcacagcaagaatccctatgtgtctccacccaattctgcctgtgtagcccttcactttgc	5520
Q	y	5521	tgatatgggtggtcattcaatacctcttcacgtatccagccctctctgtgttcaagaatccca	5580
D	b	5521	tgatatgggtggtcattcaatacctcttcacgtatccagccctctctgtgttcaagaatccca	5580
Q	y	5581	gacagcccatctgtgtgtccacacagcgtgaaccccttcattctgtcatctatgcagcgttg	5640
D	b	5581	gacagcccatctgtgtgtccacacagcgtgaaccccttcattctgtcatctatgcagcgttg	5640
Q	y	5641	ccaactttgtctgtcgtgaagctgttccacgcaataagctgaaataataatcaatgatctctga	5700
D	b	5641	ccaactttgtctgtcgtgaagctgttccacgcaataagctgaaataataatcaatgatctctga	5700
Q	y	5701	agtcggtgtctctgtatcttccacaattttgcctgggacgagggctcatcgacatgttga	5760
D	b	5701	agtcggtgtctctgtatcttccacaattttgcctgggacgagggctcatcgacatgttga	5760
Q	y	5761	aaaaccaggccaatgtgcgtatgctcctggaagaagtttggggagaatcgctttgttcacacat	5820
D	b	5761	aaaaccaggccaatgtgcgtatgctcctggaagaagtttggggagaatcgctttgttcacacat	5820
Q	y	5821	tatcttgggaactgtgtggacgaataacctcttcgcatctgcgttggaagggtgtgtctct	5880
D	b	5821	tatcttgggaactgtgtggacgaataacctcttcgcatctgcgttggaagggtgtgtctct	5880
Q	y	5881	tcctcatctactgttctgtatccaglaacagatcttccatcagcccgagccctgtlaaatgcaa	5940
D	b	5881	tcctcatctactgttctgtatccaglaacagatcttccatcagcccgagccctgtlaaatgcaa	5940
Q	y	5941	agcctatccctctgtatgaatgaagaatgaagaatgtgagcggggaagaagacagaattcttg	6000
D	b	5941	agcctatccctctgtatgaatgaagaatgaagaatgtgagcggggaagaagacagaattcttg	6000
Q	y	6001	atggtgtggagccagatgacatcttgaagaatcaaggaagttgacgaagatataatagaagga	6060
D	b	6001	atggtgtggagccagatgacatcttgaagaatcaaggaagttgacgaagatataatagaagga	6060
Q	y	6061	agcggaaacccgtgtgtgacaggaatttgcgtggcatccctccgtgagatgcttgggc	6120
D	b	6061	agcggaaacccgtgtgtgacaggaatttgcgtggcatccctccgtgagatgcttgggc	6120
Q	y	6121	tccttggaggttaatgtgggcttggaataatcatcaactttcaaatgtttacaaggaatcca	6180
D	b	6121	tccttggaggttaatgtgggcttggaataatcatcaactttcaaatgtttacaaggaatcca	6180
Q	y	6181	ctgtttacccaagagagaatgcttcttcttaacaaaatagtatattcatcaacaatccatgaag	6240
D	b	6181	ctgtttacccaagagagaatgcttcttcttaacaaaatagtatattcatcaacaatccatgaag	6240
Q	y	6241	tacatcagaacaatgtgactgcgctcagtttgaatgcacatcacagaagctgttgcctggga	6300
D	b	6241	tacatcagaacaatgtgactgcgctcagtttgaatgcacatcacagaagctgttgcctggga	6300
Q	y	6301	gagaacacgtgagatgttcttgccttcttgagaagagttccacgaaagaagaatttgcagaag	6360
D	b	6301	gagaacacgtgagatgttcttgccttcttgagaagagttccacgaaagaagaatttgcagaag	6360
Q	y	6361	ttgtgtgaattgggcgaattccgaaacttggccctcgtaagaattatgggaaataataatgtcgtta	6420
D	b	6361	ttgtgtgaattgggcgaattccgaaacttggccctcgtaagaattatgggaaataataatgtcgtta	6420
Q	y	6421	actatagatggagggacaacaacgcaagctctctacagccaatggcctttatatgcgggcctc	6480
D	b	6421	actatagatggagggacaacaacgcaagctctctacagccaatggcctttatatgcgggcctc	6480
Q	y	6481	ctgtgtgttcttctgtatgaaccacccaacagcatgtgattcccaaacccggcgttcttgt	6540
D	b	6481	ctgtgtgttcttctgtatgaaccacccaacagcatgtgattcccaaacccggcgttcttgt	6540

QY 7621 accttgtgaaagctgctcgtcctcagagctctatcaaatgtgatatcaagttgacagaatg 7680
|||||
Db 7621 accttgtgaaagctgctcgtcctcagagctctatcaaatgtgatatcaagttgacagaatg 7680
QY 7681 gtgcagatgcgtgtgtaacatcctgcttgcctccctcgtatgaagctgtctgtgtgcagt 7740
|||||
Db 7681 gtgcagatgcgtgtgtaacatcctgcttgcctccctcgtatgaagctgtctgtgtgcagt 7740
QY 7741 aacatgcacaaaagtggtgtgtcctcagcagcggaaactgtgtccatgtgtatatt 7800
|||||
Db 7741 aacatgcacaaaagtggtgtgtcctcagcagcggaaactgtgtccatgtgtatatt 7800
QY 7801 gtccctatgcctcagcagcagtggtgtctacaggtcctatagagactcttaataatact 7860
|||||
Db 7801 gtccctatgcctcagcagcagtggtgtctacaggtcctatagagactcttaataatact 7860
QY 7861 agatcctgtgaagaagcagaacatcaacagccaactgctgggtgcagagctgtcgaag 7920
|||||
Db 7861 agatcctgtgaagaagcagaacatcaacagccaactgctgggtgcagagctgtcgaag 7920
QY 7921 ccagggcagatggatgaagaagatgtgcgtctcaaaccttagggagcctgtgccattgt 7980
|||||
Db 7921 ccagggcagatggatgaagaagatgtgcgtctcaaaccttagggagcctgtgccattgt 7980
QY 7981 ccgagactgtcgttaacatgtgtacactgtcctcaagatgtttatctgcacaaagtgtat 8040
|||||
Db 7981 ccgagactgtcgttaacatgtgtacactgtcctcaagatgtttatctgcacaaagtgtat 8040
QY 8041 taattcgtgcttctgtgaatctcgaagaatgaagaagatgagtgatatttgacaaaa 8100
|||||
Db 8041 taattcgtgcttctgtgaatctcgaagaatgaagaagatgagtgatatttgacaaaa 8100
QY 8101 atcttctgtacttttattgtattgttgaaatttgaatttcatcagagacttctgaactct 8160
|||||
Db 8101 atcttctgtacttttattgtattgttgaaatttgaatttcatcagagacttctgaactct 8160
QY 8161 taagaatgcctcttctgaagacctgtgtagatagagagatgtgcacgtcccaactatt 8220
|||||
Db 8161 taagaatgcctcttctgaagacctgtgtagatagagagatgtgcacgtcccaactatt 8220
QY 8221 ttatttcttactgtgaagtttgacatacagtcagtcagtcagtcagtcagtcagtcagtc 8280
|||||
Db 8221 ttatttcttactgtgaagtttgacatacagtcagtcagtcagtcagtcagtcagtcagtc 8280
QY 8281 ggtcagagatctcagcatattattgtgatttcttccagatctcagatcttcaat 8340
|||||
Db 8281 ggtcagagatctcagcatattattgtgatttcttccagatctcagatcttcaat 8340
QY 8341 ctcaactcacaatcaaatatttctgtgagtgatgctgtatgctgaaagatgatatcgta 8400
|||||
Db 8341 ctcaactcacaatcaaatatttctgtgagtgatgctgtatgctgaaagatgatatcgta 8400
QY 8401 cgtataagactagagatattgaagtcagtaactcctgtgcagtattatcagctc 8460
|||||
Db 8401 cgtataagactagagatattgaagtcagtaactcctgtgcagtattatcagctc 8460
QY 8461 actggtttacaataatagtggt 8520
|||||
Db 8461 actggtttacaataatagtggt 8520
QY 8521 agccttt 8580
|||||
Db 8521 agccttt 8580
QY 8581 aagtttaacaatgaatctctcaacaggggaaacagctagcttgaaactgtgtgaaaaa 8640
|||||
Db 8581 aagtttaacaatgaatctctcaacaggggaaacagctagcttgaaactgtgtgaaaaa 8640
QY 8641 caaacactgtgttatgtgagcttgaagacttcaaatgaatgtgtgtgtgtgtgtgtgtgtgt 8700
|||||
Db 8641 caaacactgtgttatgtgagcttgaagacttcaaatgaatgtgtgtgtgtgtgtgtgtgtgt 8700
QY 8701 ccccatlaactgtgacagctcacaatlttctcatctctcaactgcagtcagaagaaaaa 8760
|||||
Db 8701 ccccatlaactgtgacagctcacaatlttctcatctctcaactgcagtcagaagaaaaa 8760
QY 8761 taaaacaacaataactctccatagagacatttctcagagtttcttaacccagctctat 8820
|||||
Db 8761 taaaacaacaataactctccatagagacatttctcagagtttcttaacccagctctat 8820
QY 8821 ttctcagtcagtaaacatttgtaaaataactgttccaaataacttaactactgttaactgt 8880
|||||
Db 8821 ttctcagtcagtaaacatttgtaaaataactgttccaaataacttaactactgttaactgt 8880
QY 8881 tgaagaaagaaagaaataatgaagacatattgttggggaagtcgaagtccttcaat 8940
|||||
Db 8881 tgaagaaagaaagaaataatgaagacatattgttggggaagtcgaagtccttcaat 8940
QY 8941 atcattactaactcttccacttctccaaatttgaatattgaacgtcaagtgatgaa 9000
|||||
Db 8941 atcattactaactcttccacttctccaaatttgaatattgaacgtcaagtgatgaa 9000
QY 9001 cttcagattcacaatlaactcttctataattttaaatttcaagaataataataaccca 9060
|||||
Db 9001 cttcagattcacaatlaactcttctataattttaaatttcaagaataataataaccca 9060
QY 9061 ctgctgaaagaaagaaagaaatgtgtttagaagttaaagtcgaatgtatatttcaat 9120
|||||
Db 9061 ctgctgaaagaaagaaagaaatgtgtttagaagttaaagtcgaatgtatatttcaat 9120
QY 9121 aagtaatgaagacatatttccaaataactagtgatagtcacgttgcatttcaagatc 9180
|||||
Db 9121 aagtaatgaagacatatttccaaataactagtgatagtcacgttgcatttcaagatc 9180
QY 9181 ttcaaaaatacagaatttatagaataatttcccaatttcaatatttcaaaaatacaga 9240
|||||
Db 9181 ttcaaaaatacagaatttatagaataatttcccaatttcaatatttcaaaaatacaga 9240
QY 9241 ttatgttctcctcatcttcaataaactgtatctcaatctcattatagtaaatctatga 9300
|||||
Db 9241 ttatgttctcctcatcttcaataaactgtatctcaatctcattatagtaaatctatga 9300
QY 9301 gcaactccttactcgtgttctcctgtatctcaagcgaatattttaaataataaagagac 9360
|||||
Db 9301 gcaactccttactcgtgttctcctgtatctcaagcgaatattttaaataataaagagac 9360
QY 9361 tgtgaactatttgaagaaacagacatttcaatcagatgtgaagagcctctctgaa 9420
|||||
Db 9361 tgtgaactatttgaagaaacagacatttcaatcagatgtgaagagcctctctgaa 9420
QY 9421 gctagaanaacatctatgtatatacttcaatlaactgtgttaactttaaataagta 9480
|||||
Db 9421 gctagaanaacatctatgtatatacttcaatlaactgtgttaactttaaataagta 9480
QY 9481 atttttcaatttccgtgttaaaccttaatgtgtgaagaatttctaacactctatct 9540
|||||
Db 9481 atttttcaatttccgtgttaaaccttaatgtgtgaagaatttctaacactctatct 9540
QY 9541 caatcaagcaaatcttctgtatatactcctgtgtgaatgtaactatgtgtgtgtgtgtgt 9600
|||||
Db 9541 caatcaagcaaatcttctgtatatactcctgtgtgaatgtaactatgtgtgtgtgtgtgt 9600
QY 9601 ctcaaatatcgtgtcacaataatttctgtcttgcatacttgggacactcagaanaactta 9660
|||||
Db 9601 ctcaaatatcgtgtcacaataatttctgtcttgcatacttgggacactcagaanaactta 9660
QY 9661 ttaacaactgtgtatataatgagaataatcagaagaaataataagcctctatataatgac 9720
|||||
Db 9661 ttaacaactgtgtatataatgagaataatcagaagaaataataagcctctatataatgac 9720
QY 9721 ccagcaaatctatgttttaaaaaaacacaaaccccaactacactgtatttcatatctgt 9780
|||||
Db 9721 ccagcaaatctatgttttaaaaaaacacaaaccccaactacactgtatttcatatctgt 9780
QY 9781 actgaagcaaatgtcttgtgactataatgtgtgacatcatcatcttcaactgtatagta 9840
|||||

Db	454	gagctaccccccctatgaaacaacatgaaatgccaatttcccaataaagccagtcctctgc	513
Oy	482	aggaacaccttcccttgggttccaagggtatctctgtaatgccaaacccctgttccgtta	541
Db	514	aggaacaccttcccttgggttccaagggtatctctgtaatgccaacacccctgttccgtta	573
Oy	542	cccgactctcgggagagctccccggagttgttggaaacttaacaattcaattgtgtctcg	601
Db	574	cccgactccctcgggagagctccccggagttgttggaaacttaacaattcaattgtgtctcg	633
Oy	602	cccttctcaagatgctcccgagagcttcttttatacggcccaagaagaccacagcatgaaaga	661
Db	634	ccgttctccagatgctcccgagagcttcttttatacagccagaagaagaccacagcatgaaaga	693
Oy	662	catgcgaaaagtctctgagaacattacaagaaga tcaagaatccagctccaacttgaagct	721
Db	694	catgcgaaaagtctctgagaacattacaagaaga tcaagaatccagctccaacttgaagct	753
Oy	722	tcaagaattccctgtgtgacaatgaaacctctctctgtgttctctatatctcaacctctctc	781
Db	754	tcaagaattccctgtgtgacaatgaaacctctctctgtgttctctatatctcaacctctctc	813
Oy	782	cccaaatctacactgttgacaaga tgcctcggggcctgacatgcatctcccaagatatttt	841
Db	814	cccaaatctacactgttgacaaga tgcctcggggcctgacatgcatctcccaagatatttt	873
Oy	842	gcaaggtctaccagttacatttgacaagctctgtgcaattgcatcaaaatcagaagaatgat	901
Db	874	gcaaggtctaccagttacatttgacaagctctgtgcaattgcatcaaaatcagaagaatgat	933
Oy	902	tcaactgtgtgacccaagaagaattttctgaagcttgtgcccacaaaggagaaactgtgtgc	961
Db	934	tcaactgtgtgacccaagaagaattttctgaagcttgtgcccacaaaggagaaactgtgtgc	993
Oy	962	agcagagcagagttacttgtttcccaacaatggaacatcctgaaagccaactctgtgaacaactaa	1021
Db	994	agcagagcagagttacttgtttcccaacaatggaacatcctgaaagccaactctgtgaacaactaa	1053
Oy	1022	ctctacaatctccctcccgagcaagagactgtgcttgaaagcccaaaaacattgtcgtcatag	1081
Db	1054	ctctacaatctccctcccgagcaagagactgtgcttgaaagcccaaaaacattgtcgtcatag	1113
Oy	1082	tctctggagactgtgcccaagagagctgtgtccagcatgaaagaactgtgagcatgtgcacaga	1141
Db	1114	tctctggagactgtgcccaagagagctgtgtccagcatgaaagaactgtgagcatgtgcacaga	1173
Oy	1142	ggtgatgtttcttgaccaaattgtaacagctcccaagctctctccaccaaatctaccagctgt	1201
Db	1174	ggtgatgtttcttgaccaaattgtaacagctcccaagctctctccaccaaatctaccagctgt	1233
Oy	1202	gtctcgtatttctcgggggatacccgagggagggggtcgtgaagatccaagtctctcaactg	1261
Db	1234	gtctcgtatttctcgggggatacccgagggagggggtcgtgaagatccaagtctctcaactg	1293
Oy	1262	gtatgaggaacaacaactacaagaagcctcttggaggcaatggtcactgaggaagtgtctga	1321
Db	1294	gtatgaggaacaacaactacaagaagcctcttggaggcaatggtcactgaggaagtgtctga	1353
Oy	1322	aaactctatgaacaactcaacaactcttaactcttaactgtaattgtaagaagaatttggagtc	1381
Db	1354	aaactctatgaacaactcaacaactcttaactcttaactgtaattgtaagaagaatttggagtc	1413
Oy	1382	tagtctcttctccggcatatctctgaaagctctgaaagccgctgtcgttbggaagatccct	1441
Db	1414	tagtctcttctccggcatatctctgaaagctctgaaagccgctgtcgttbggaagatccct	1473
Oy	1442	gtaataccttgaactctccagccaagaagcgtcatggtctggagtgtaaaaaactcttca	1501
Db	1474	gtaataccttgaactctccagccaagaagcgtcatggtctggagtgtaaaaaactcttca	1533
Oy	1502	ggaactgtcctgttccatgatctcggaaagcattgtggaggaactcaagcccaagatctg	1561

Db	1534	ggagctgctgtgttccatgatactctggaagcaatgtggtggaagcaatccagccccaagatctg	1593
Qy	1562	gaccttaatvgagaacagccagaatctgaccttgtccgatactgtcttgacagcaaggga	1621
Db	1594	gaccttcatgtgagacagccaaagaataatgtgaacctcttccgatactgtcttgacagcaaggga	1653
Qy	1622	caatgacccaacttttgggaagaacagatctgatacttgatcttgataagcccaagaacatcgt	1681
Db	1654	caatgacccaacttttgggaagaacagcaagtctgatacttgatcttgataagcccaagaacatcgt	1713
Qy	1682	ggcgtttcttgcccaagacaccagaagatgtccagtcacgaataatgtgtctgttgaacctg	1741
Db	1714	ggcgtttcttgcccaagacaccagaagatgtccagtcacgaataatgtgtctgttgaacctg	1773
Qy	1742	gagagaagctttcaacagagataccagagcaatcccgagccatactctgccttccatggagtg	1801
Db	1774	gagagaagctttcaacagagataccagagcaatcccgagccatactctgccttccatggagtg	1833
Qy	1802	tgtcaaaccttgacaagctctagaacccaatagacaacagaagctgtgtccatcaacaagaatcat	1861
Db	1834	tgtcaaaccttgacaacagctctagaacccaatagacaacagaagctgtgtccatcaacaagaatcat	1893
Qy	1862	ggagctctgtctgatacgagagaagttctggtgcttgatctgttcaactgtgaattccaaag	1921
Db	1894	ggagctctgtctgatacgagagaagttctggtgcttgatctgttcaactgtgaattccaaag	1953
Qy	1922	cagcaattgagctgtgcccatatgacatactgacaagataccgaatggagcaattgaaatgttga	1981
Db	1954	cagcaattgagctgtgcccatatgacatactgacaagataccgaatggagcaattgaaatgttga	2013
Qy	1982	gaggaacaataaataatcaagatactgtgatactgtgacccctgtgtccctgagctgaaaccccttga	2041
Db	2014	gaggaacaataaataatcaagatactgtgatactgtgacccctgtgtccctgagctgaaaccccttga	2073
Qy	2042	ggacaatgcgatacgtctcgtggggggggtctgcgctaactgtgcagagatgtgtgtggagcaggcaat	2101
Db	2074	ggacaatgcgatacgtctcgtggggggggtctgcgctaactgtgcagagatgtgtgtggagcaggcaat	2133
Qy	2102	gatacaggtgtctcgaagggcacaacggagaagaataactgtgtctatatacgacaagaatcccta	2161
Db	2134	gatacaggtgtctcgaagggcacaacggagaagaataactgtgtctatatacgacaagaatcccta	2193
Qy	2162	tccctgttaacgttgatgacatccttctcggggtgtatagagccgtgtaagccctcttcatt	2221
Db	2194	tccctgttaacgttgatgacatccttctcggggtgtatagagccgtgtaagccctcttcatt	2253
Qy	2222	gacgcctggccctggatatttaactaagtgagctgtgtgataccaagaagagatcgtgtatagaaga	2281
Db	2254	gacgcctggccctggatatttaactaagtgagctgtgtgataccaagaagagatcgtgtatagaaga	2313
Qy	2282	ggcacagcgtcgaagaagacaacatgctgagatcatalgagggcctgtgaaacaacagatactctgtttag	2341
Db	2314	ggcacagcgtcgaagaagacaacatgctgagatcatalgagggcctgtgaaacaacagatactctgtttag	2373
Qy	2342	cgtgttcaattagtgccctcatctctctctcttcttggaagcctggggcctctagtgtaacct	2401
Db	2374	cgtgttcaattagtgccctcatctctctctctcttcttggaagcctggggcctctagtgtaacct	2433
Qy	2402	gaagtttaggaacacctgtccatcaacatgtaaccagaagtgtagttgtcttccgtccgt	2461
Db	2434	gaagtttaggaacacctgtccatcaacatgtaaccagaagtgtagttgtcttccgtccgt	2493
Qy	2462	gttttgcgtgtgtgaaatactctgcgaagtgcttccatgaatagaacacttttccagaagccaa	2521
Db	2494	gttttgcgtgtgtgaaatactctgcgaagtgcttccatgaatagaacacttttccagaagccaa	2553
Qy	2522	ccctggaagcagccttgggggacatactaacttcaacgtcttacctccccaagtctctg	2581
Db	2554	ccctggaagcagccttgggggacatactaacttcaacgtcttacctccccaagtctctg	2613
Qy	2582	tgtgtgacatgacgaactacgtgtgggttccaacatcaagaatcttcgtcagccgtctctcc	2641
Db	2614	tgtgtgacatgacgaactacgtgtgggttccaacatcaagaatcttcgtcagccgtctctcc	2673

```
QY 2642 tttgtgcttttggttttggtcgtgtgtaacttttccttttttgagagcaaggatcttgagt 2701
Db 2674 tttgtgcttttggttttggtcgtgtgtaacttttccttttttgagagcaaggatcttgagt 2733
QY 2702 gcaagtggacaacgtgttttaagagtcctgtgtgaggaagatggtcttaactcaccacttc 2761
Db 2734 gcaagtggacaacgtgttttaagagtcctgtgtgaggaagatggtcttaactcaccacttc 2793
QY 2762 gatctccaatgactgttttgacaaccttcctctatgtgggtgtatgtactgtgtacattgagc 2821
Db 2794 gatctccaatgactgttttgacaaccttcctctatgtgggtgtatgtactgtgtacattgagc 2853
QY 2822 tttctttccagcgcagaaagaaatctcccaagccttgatctttcctctgacaagaagcccta 2881
Db 2854 tttctttccagcgcagaaagaaatctcccaagccttgatctttcctctgacaagaagcccta 2913
QY 2882 ctggtttgagagaaagtatgagaagaagccacctgtgttcccaaccagaaagaaatgtc 2941
Db 2914 ctggtttgagagaaagtatgagaagaagccacctgtgttcccaaccagaaagaaatgtc 2973
QY 2942 agaaatctgataatgagagaaagaaaccccaacttgaagctgtggcgctgttccatcagaacct 3001
Db 2974 agaaatctgataatgagagaaagaaaccccaacttgaagctgtggcgctgttccatcagaacct 3033
QY 3002 ggtaaaaagctacccagatgtggaatgaaggtgtgtcgtatggtcgtgacctgaattttta 3061
Db 3034 ggtaaaaagctacccagatgtggaatgaaggtgtgtcgtatggtcgtgacctgaattttta 3093
QY 3062 tgaaggccagatacactcctctctgtggccaacaatgagagcgaggaaagacacacatactc 3121
Db 3094 tgaaggccagatacactcctctctgtggccaacaatgagagcgaggaaagacacacatactc 3153
QY 3122 aatcccgaaacgggtttttcccccagacccctcgagcaccgctctatactcttgagaaagacct 3181
Db 3154 aatcccgaaacgggtttttcccccagacccctcgagcaccgctctatactcttgagaaagacct 3213
QY 3182 tgcgtctgagatgagacacatacccgagaaactgtgggtgtctgttcccaacataacgtgtc 3241
Db 3214 tgcgtctgagatgagacacatacccgagaaactgtgggtgtctgttcccaacataacgtgtc 3273
QY 3242 gtttgacatgtcgtactgtctgaagaacacatactgtctctatgtcccgctgtgaaaggctctc 3301
Db 3274 gtttgacatgtcgtactgtctgaagaacacatactgtctctatgtcccgctgtgaaaggctctc 3333
QY 3302 tgaagaagcagtgaaagcgagagatgagacagatgagccctgagatgtgtgtttccatcaag 3361
Db 3334 tgaagaagcagtgaaagcgagagatgagacagatgagccctgagatgtgtgtttccatcaag 3393
QY 3362 caagctgaaaaagcaaaacaaagccagctgtcaggtgaaatgacagagaaactatctgtgac 3421
Db 3394 caagctgaaaaagcaaaacaaagccagctgtcaggtgaaatgacagagaaactatctgtgac 3453
QY 3422 ctgtgacctgtctcgaggagataaagtgttcaatctgtgatacccaacagctgtgtgga 3481
Db 3454 ctgtgacctgtctcgaggagataaagtgttcaatctgtgatacccaacagctgtgtgga 3513
QY 3482 ccccttactcccgagaggagataatgagagctgtctgtgtaataccgaagaagccgacat 3541
Db 3514 ccccttactcccgagaggagataatgagagctgtctgtgtaataccgaagaagccgacat 3573
QY 3542 tattctctacacacacacatgagatgaaagcgagctcctgtgggagacagatgtgcatcat 3601
Db 3574 tattctctacacacacacatgagatgaaagcgagctcctgtgggagacagatgtgcatcat 3633
QY 3602 cttcccaatgaaagctgtgtgtgtgtgtgtgtcctcctcctgtttctgaaagaacagctvggaac 3661
Db 3634 cttcccaatgaaagctgtgtgtgtgtgtgtgtcctcctcctgtttctgaaagaacagctvggaac 3693
QY 3662 aggtactactacccgtactgtgtcaagaagaatgtgaaatcctccctcagttccttgagaa 3721
Db 3694 aggtactactacccgtactgtgtcaagaagaatgtgaaatcctccctcagttccttgagaa 3753

QY 3722 cagtagtagcaactgtgttataccttgaaaaagagaaagatgttttctcaagagacttctga 3781
Db 3754 cagtagtagcaactgtgttataccttgaaaaagagaaagatgttttctcaagagacttctga 3813
QY 3782 tgtgtgctggcgaaagcacaatgaaagatgacacgtcaacatctgatctctgtatctc 3841
Db 3814 tgtgtgctggcgaaagcacaatgaaagatgacacgtcaacatctgatctctgtatctc 3873
QY 3842 caacctcatcagaaagcatgtgtctgaaagcccggtctgtgtgaagacataagggcatagact 3901
Db 3874 caacctcatcagaaagcatgtgtctgaaagcccggtctgtgtgaagacataagggcatagact 3933
QY 3902 gaacctatgtctgcacataatgaagctgtcctaaggaagagacctttgtgaacctttctatga 3961
Db 3934 gaacctatgtctgcacataatgaagctgtcctaaggaagagacctttgtgaacctttctatga 3993
QY 3962 gatgatgacccgctcctcagaccccttgagacttactagatgatgacatcccaagagacacct 4021
Db 3994 gatgatgacccgctcctcagaccccttgagacttactagatgatgacatcccaagagacacct 4053
QY 4022 ggaagaataatctctcaaggtgtgcccgaagagatgtgggtgtgatagtcagacatcagatg 4081
Db 4054 ggaagaataatctctcaaggtgtgcccgaagagatgtgggtgtgatagtcagacatcagatg 4113
QY 4082 tactctgcagcaagacaaacagcgagcctctggggagacaagaagctgtcttgccc 4141
Db 4114 tactctgcagcaagacaaacagcgagcctctggggagacaagaagctgtcttgccc 4173
QY 4142 gtccaatgaaatgagtgtgtgtatccaatgatactctgacataaaccacaatccaaga 4201
Db 4174 gtccaatgaaatgagtgtgtgtatccaatgatactctgacataaaccacaatccaaga 4233
QY 4202 gacagactgtctcagtgagatgagatgagcaagaggtcctaccaggtgaaagctgtgaaact 4261
Db 4234 gacagactgtctcagtgagatgagatgagcaagaggtcctaccaggtgaaagctgtgaaact 4293
QY 4262 tacacagcaaacagttgtgtgcccctttgtgaaagaagactctaaatgtccagacagagctg 4321
Db 4294 tacacagcaaacagttgtgtgcccctttgtgaaagaagactctaaatgtccagacagagctg 4353
QY 4322 gaaagatctttgtcctcaagatgtctgtcagcagctgtgtgtgtcgtacatgtccctgtgt 4381
Db 4354 gaaagatctttgtcctcaagatgtctgtcagcagctgtgtgtgtcgtacatgtccctgtgt 4413
QY 4382 cagcctgactgtgcccacccctttggcaagatgaccccaagccttgaaacttaagccctgagtga 4441
Db 4414 cagcctgactgtgcccacccctttggcaagatgaccccaagccttgaaacttaagccctgagtga 4473
QY 4442 caacgaacagatcacattgtgtcaagcaatgatagtctcctgtgagacacggaacccctggaact 4501
Db 4474 caacgaacagatcacattgtgtcaagcaatgatagtctcctgtgagacacggaacccctggaact 4533
QY 4502 ctlaaagcctcacaagaagacccctgtctcggaagcccgctgtatgtgaagaaacccaat 4561
Db 4534 ctlaaagcctcacaagaagacccctgtctcggaagcccgctgtatgtgaagaaacccaat 4593
QY 4562 cccagacacagcctcgtccagacaggggaggaagatggaacacacgcccagatctcccaag 4621
Db 4594 cccagacacagcctcgtccagacaggggaggaagatggaacacacgcccagatctcccaag 4653
QY 4622 catcatgtgacctcttccaagatggaagctggaacatgtcagaacacccctcaacctgtcatgcca 4681
Db 4654 catcatgtgacctcttccaagatggaagctggaacatgtcagaacacccctcaacctgtcatgcca 4713
QY 4682 gtgtagcagcgacaataatcaagaagatgtcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4741
Db 4714 gtgtagcagcgacaataatcaagaagatgtcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4773
QY 4742 ggcctcccaaaaagaaacaaaacatgagataltccttcagagacttaacaaagaaaga 4801
Db 4774 ggcctcccaaaaagaaacaaaacatgagataltccttcagagacttaacaaagaaaga 4833
QY 4802 cattcgatcatctgtgtgaagacgtatgtgcagatcatagccaaaagctttaagaacaa 4861
```

Db 4834 caticcgatlatcigtgagagacgfatgugcaatcatagccaagaacttaagaacaa 4893
QY 4862 gatctgggagatgagtttagtataggcggtcttccctgggtgtcagtataactaaagc 4921
Db 4894 gatctgggagatgagtttagtataggcggtcttccctgggtgtcagtataactaaagc 4953
QY 4922 actctccgaatcgaaggttaatagtatccatcaacaagaagaacacttaagtc 4981
Db 4954 actctccgaatcgaaggttaatagtatccatcaacaagaagaacacttaagtc 5013
QY 4982 ggcacagagacgtctcgcagatcgatcttccacaacagcttgggagaattatgacagact 5041
Db 5014 ggcacagagacgtctcgcagatcgatcttccacaacagcttgggagaattatgacagact 5073
QY 5042 ggcacacgaataatgltcaaggtgtgtgttcaataacaagggtcgtgcaltgcactc 5101
Db 5074 ggcacacgaataatgltcaaggtgtgtgttcaataacaagggtcgtgcaltgcactc 5133
QY 5102 ttcccgatgtatcaataacaatgccaattctccggggccaacccgtgcaaaaggagagacc 5161
Db 5134 ttcccgatgtatcaataacaatgccaattctccggggccaacccgtgcaaaaggagagacc 5193
QY 5162 tagccatlatggaatbactgcttccatcatccctgaaatccacaagcagacgctc 5221
Db 5194 tagccatlatggaatbactgcttccatcatccctgaaatccacaagcagacgctc 5253
QY 5222 agaggtggtctcgtatgacaacatcaagtgaagtctcctgtgtccatctgttgcactcttgc 5281
Db 5254 agaggtggtctcgtatgacaacatcaagtgaagtctcctgtgtccatctgttgcactcttgc 5313
QY 5282 aatgtctctcgtcccgacagcttctgtctatctccgacccaaggcggtgaagcaagc 5341
Db 5314 aatgtctctcgtcccgacagcttctgtctatctccgacccaaggcggtgaagcaagc 5373
QY 5342 aaaaacccgtcagttcaatcagtggaagtgaagcctgtcactaactcgtcctcctcaatttgc 5401
Db 5374 aaaaacccgtcagttcaatcagtggaagtgaagcctgtcactaactcgtcctcctcaatttgc 5433
QY 5402 ctggggtatgtgcaataatgaatgttccctgcacaaatgtgtcattatcatcttcatctgc 5461
Db 5434 ctggggtatgtgcaataatgaatgttccctgcacaaatgtgtcattatcatcttcatctgc 5493
QY 5462 ccagcgaagtcctatgtgtctcccaacatctgcctgtgcagccctcctccttgc 5521
Db 5494 ccagcgaagtcctatgtgtctcccaacatctgcctgtgcagccctcctccttgc 5553
QY 5522 gtaatgggtgltcaatcaacactcctcaatgtacccagcctccttgtgttcaaatccag 5581
Db 5554 gtaatgggtgltcaatcaacactcctcaatgtacccagcctccttgtgttcaaatccag 5613
QY 5582 ccaagcctatgtgtgtgtcctacagcggtgaacactcctcattgtgcattatgtcagcggtgc 5641
Db 5614 ccaagcctatgtgtgtgtcctacagcggtgaacactcctcattgtgcattatgtcagcggtgc 5673
QY 5642 ccaacttgcgtgagcgtgttcaacgacaataagctgaataatataatgatatactaa 5701
Db 5674 ccaacttgcgtgagcgtgttcaacgacaataagctgaataatataatgatatactaa 5733
QY 5702 gtccgtgtcttgcattctccacatttgccttggagcgaagggtcctacatgcatagttga 5761
Db 5734 gtccgtgtcttgcattctccacatttgccttggagcgaagggtcctacatgcatagttga 5793
QY 5762 aaaaacgaagatggtcgtatgcccctggaaaaggttgggagaatcgcttgtgtcacat 5821
Db 5794 aaaaacgaagatggtcgtatgcccctggaaaaggttgggagaatcgcttgtgtcacat 5853
QY 5822 atcttggacctgtgtggaacgaacactcctgcatagtgcgtggaagggtgttctt 5881
Db 5854 atcttggacctgtgtggaacgaacactcctgcatagtgcgtggaagggtgttctt 5913
QY 5882 cctcatctactgttctgcatacagtatccttcatcaggcccaaacctgttaatgcaaa 5941

Db 5914 cctcatctactgttctgcatacagtatccttcatcagccccaagcctgttaatgcaaa 5973
QY 5942 gctatctcctcgtgaatgataagatgaaagctgtgagcgggaaaagacagagatcttga 6001
Db 5974 gctatctcctcgtgaatgataagatgaaagctgtgagcgggaaaagacagagatcttga 6033
QY 6002 tgggtgagggccaagatgacatctttagaaaatcaagaggtgtgcagagatataatagaagaa 6061
Db 6034 tgggtgagggccaagatgacatctttagaaaatcaagaggtgtgcagagatataatagaagaa 6093
QY 6062 gggagagcctcgtgtgacagagattgtgtggacatccctcctgtgtgtgttgggt 6121
Db 6094 gggagagcctcgtgtgacagagattgtgtggacatccctcctgtgtgtgttgggt 6153
QY 6122 ccttggagttatggggcttggaaaatcacaacttcaagatgttaacagagataccac 6181
Db 6154 ccttggagttatggggcttggaaaatcacaacttcaagatgttaacagagataccac 6213
QY 6182 tgttccagagagagatgtcttcccttaaaaaatagtatcttcatcaaacatccatgaagt 6241
Db 6214 tgttccagagagagatgtcttcccttaaaaaatagtatcttcatcaaacatccatgaagt 6273
QY 6242 acatcagaacatlggagctactgcccctgaattgtatgccaacagagcgtgtgactggag 6301
Db 6274 acatcagaacatlggagctactgcccctgaattgtatgccaacagagcgtgtgactggag 6333
QY 6302 agaacacgttgagttccttgccttltgagagagatcccaagaaaaggttggcaagt 6361
Db 6334 agaacacgttgagttccttgccttltgagagagatcccaagaaaaggttggcaagt 6393
QY 6362 tgggtgaggtggcgtatggaacatcggtcctgtgaagtatgagaaaatatcgtgttaa 6421
Db 6394 tgggtgaggtggcgtatggaacatcggtcctgtgaagtatgagaaaatatcgtgttaa 6453
QY 6422 ctatagttgagggcaacaacagcctctctacagccaatggtcttgcgtgcggctcc 6481
Db 6454 ctatagttgagggcaacaacagcctctctacagccaatggtcttgcgtgcggctcc 6513
QY 6482 tgtgtgttcttggatgaaacccaacgaagcatggtatcccaaaagccggcggttctgtg 6541
Db 6514 tgtgtgttcttggatgaaacccaacgaagcatggtatcccaaaagccggcggttctgtg 6573
QY 6542 gaattgtcccttaaggtgtgtcgaaggaggagatgaagtgttatacctataat 6601
Db 6574 gaattgtcccttaaggtgtgtcgaaggaggagatgaagtgttatacctataat 6633
QY 6602 ggaagaaatgtgaagccttltgacatagatgagcaatcatggtcaatgtgaaggttcaagt 6661
Db 6634 ggaagaaatgtgaagccttltgacatagatgagcaatcatggtcaatgtgaaggttcaagt 6693
QY 6662 ccttggcaggttccagcatcctaaataaagtttggagatggttatacaatagttgaag 6721
Db 6694 ccttggcaggttccagcatcctaaataaagtttggagatggttatacaatagttgaag 6753
QY 6722 aatagcaaggtccaaacccggacccgtgaagcctgtcccaagatttcttggacttgcattcc 6781
Db 6754 aatagcaaggtccaaacccggacccgtgaagcctgtcccaagatttcttggacttgcattcc 6813
QY 6782 tggaggtgttctaaagaagaacacccggaacatctcacaatcacagcttccattcat 6841
Db 6814 tggaggtgttctaaagaagaacacccggaacatctcacaatcacagcttccattcat 6873
QY 6842 atcttctcgtgcagagatlatcagcatcctcctccagaagaacaaagcgtatccacataga 6901
Db 6874 atcttctcgtgcagagatlatcagcatcctcctccagaagaacaaagcgtatccacataga 6933
QY 6902 agactactgttctcgaagaacacttgcagaaagtattgtgaacttgcagaagaa 6961
Db 6934 agactactgttctcgaagaacacttgcagaaagtattgtgaacttgcagaagaa 6993
QY 6962 aagtgatgatgaccacttaaaagcctctcatlacaaaaaacagacaatagtgagct 7021
Db 6994 aagtgatgatgaccacttaaaagcctctcatlacaaaaaacagacaatagtgagct 7053


```

|||||
Db 9214 tcaaaatacagaatttaagaataattccctccatttaataattttccaataatcgaat 9273
Qy 9242 tatgtttcccatcttaataatcgtatcttaattcttcattatagaatactatgag 9301
Db 9274 tatgtttcccatcttaataatcgtatcttaattcttcattatagaatactatgag 9333
Qy 9302 caaccctactcgttctcctcgtatctcaagcgcatatttaaaaaatcaaaaggcact 9361
Db 9334 caaccctactcgttctcctcgtatctcaagcgcatatttaaaaaatcaaaaggcact 9393
Qy 9362 gtgaactattttgaagaacacacgacattttaatacagattgaaggacctcttcgaag 9421
Db 9394 gtgaactattttgaagaacacacgacattttaatacagattgaaggacctcttcgaag 9453
Qy 9422 ctagaacaacatagatcatatcatctcattatacagtggttaaccctttaaataagtaa 9481
Db 9454 ctagaacaacatagatcatatcatctcattatacagtggttaaccctttaaataagtaa 9513
Qy 9482 ttttttaatttccctgtgtaaacctaattgtgtagaataattttaccaactatctc 9541
Db 9514 ttttttaatttccctgtgtaaacctaattgtgtagaataattttaccaactatctc 9573
Qy 9542 aatcaagcaaaattctgtatatactccctgtggaatgtacattgtgaattcagaattc 9601
Db 9574 aatcaagcaaaattctgtatatactccctgtggaatgtacattgtgaattcagaattc 9633
Qy 9602 tcaaaatacagtggtcaaaatctcgtcttgcattcttggagacacctcagaanaactat 9661
Db 9634 tcaaaatacagtggtcaaaatctcgtcttgcattcttggagacacctcagaanaactat 9693
Qy 9662 taacaactgtgaatagagaataacagaagaataaataaagccctctataataatagcc 9721
Db 9694 taacaactgtgaatagagaataacagaagaataaataaagccctctataataatagcc 9753
Qy 9722 caagcaattcatctgttaaaaaaacacacacacacacacacacacacacacacacacac 9781
Db 9754 caagcaattcatctgttaaaaaaacacacacacacacacacacacacacacacacacac 9813
Qy 9782 ctgaagcaaatgtcttgcattataatgttgcacatcatcttaactgtatagtaa 9841
Db 9814 ctgaagcaaatgtcttgcattataatgttgcacacacacacacacacacacacacacacac 9873
Qy 9842 tcatctactaaagcactctgtctgttctctcctgtgtgtnatatactcaagtaata 9901
Db 9874 tcatctactaaagcactctgtctgttctctcctgtgtgtnatatactcaagtaata 9933
Qy 9902 ttttccaagcagctgtcatgtaatactgaaccttgcattgtagacattattg 9961
Db 9934 ttttccaagcagctgtcatgtaatactgaaccttgcattgtagacattattg 9993
Qy 9962 gacctgtgatactactagataaataatgtaatactgnaagaataatgtctcaattctt 10021
Db 9994 gacctgtgatactactagataaataatgtaatactgnaagaataatgtctcaattctt 10053
Qy 10022 caaaatgttccatcccttaaaangttcatttcataagattagttcttatccc 10081
Db 10054 caaaatgttccatcccttaaaangttcatttcataagattagttcttatccc 10113
Qy 10082 ttctataccctaagatgaagctgttttgcctcttgcattcatcttgccctcatcc 10141
Db 10114 ttctataccctaagatgaagctgttttgcctcttgcattcatcttgccctcatcc 10173
Qy 10142 aagcaacttaagctgtctgaatgagatctattttgcacatgtaatacttggaatttga 10201
Db 10174 aagcaacttaagctgtctgaatgagatctattttgcacatgtaatacttggaatttga 10233
Qy 10202 aaactagaacaaagttcacaaacagatttcaagttaaatcatttcatttaaaaggaana 10261
Db 10234 aaactagaacaaagttcacaaacagatttcaagttaaatcatttcatttaaaaggaana 10293
Qy 10262 aagaaaaaaatttgaatgtcaataacttatatgaagattaaaatgcatatttctat 10321
|||||

```

```

Db 10294 aagaaaaaaatttgaatgtcaataacttatatgaagttataaagtcatattctat 10353
Qy 10322 gtgttaataatagtcacaaataagctgtgacagttctgtttaaaaaaaaaaaaaa 10381
Db 10354 gtgttaataatagtcacaaataagctgtgacagttctgtttaaaaaaaaaaaaaa 10413
Qy 10382 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 10441
Db 10414 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 10473
Qy 10442 a 10442
Db 10474 a 10474

RESULT 4
AAF24686
ID AAF24686 standard; DNA; 10474 BP.
XX
AC AAF24686;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX
OS Homo sapiens.
XX
FH Key 323..7108
FT CDS /tag= a
FT /product= "defective ABC1 polypeptide"
XX
PN MO200078972-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000: 2000MO-US16765.
XX
PR 18-JUN-1999; 990S-0140264.
PR 14-SEP-1999; 990S-0153872.
PR 19-NOV-1999; 990S-0166573.
XX
PA (CVTH-) CV THERAPEUTICS INC.
XX
PI Lawn RM, Wade D, Garvin M;
XX
DR WPI: 2001-137812/14.
XX
PT Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT useful for the development of agents for the treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
PS Disclosure: Page 170-176; 215pp: English.
XX
CC The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide, and is isolated from
CC a Tangier disease patient. ABC1 resides in cell membranes and utilises
CC ATP hydrolysis to transport a wide variety of substrates across the
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC Tangier disease, a genetic disorder characterised by abnormal
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC 9q22-9q31. The ABC1 genes and proteins are useful for developing
CC pharmaceutical agents for the treatment of heart disease and other
CC disorders associated with hypercholesterolemia and atherosclerosis. The
CC genes are useful for developing screening assays to screen for compounds
CC that regulate the expression of genes associated with cholesterol

```

[illegible]

Db	934	tcaacttggctgaccaaagaaagttcttgagctcttctggtccctaccaaaggaagaaacttgctgc	993
QY	962	agcagaagcagatacttctgtcccaacatgagacatccctgaagccaaactctgagaaactaa	1021
Db	994	agcagaagcagatacttctgtcccaacatgagacatccctgaagccaaactctgagaaactaa	105
QY	1022	ctctaatctccctcccgagcaaggaagctgctgaaagccacaanaacatgtgcctatag	1081
Db	1054	ctctaatctccctcccgagcaaggaagctgctgaaagccacaanaacatgtgcctatag	1113
QY	1082	tcttggagactcgtgcccggagcgtttcaagatagaaagcttgaaagtgcacatgacgacga	1144
Db	1114	tcttggagactcgtgcccggagcgtttcaagatagaaagcttgaaagtgcacatgacgacga	1173
QY	1142	ggttgatggttctgaccaaagtgaacagctccaggtccctccacccaatctacaaagcgtgt	1201
Db	1174	ggttgatggttctgaccaaagtgaacagctccaggtccctccacccaatctacaaagcgtgt	1233
QY	1202	gtctcgatgtgtcgtcgagcattcccgaggagggggcgtaagatataagttctctaactg	1261
Db	1234	gtctcgatgtgtcgtcgagcattcccgaggagggggcgtaagatataagttctctaactg	1293
QY	1262	gtacgaaggaacaaactacaagaagccctctcttggaaagcgaatggacatgaaagaaatgtcga	1321
Db	1294	gtacgaaggaacaaactacaagaagccctcttggaaagcgaatggacatgaaagaaatgtcga	1353
QY	1322	aacctctcatgaacactctcaaaactctctctgtcaatgatttgatgaagaatttggagctc	1381
Db	1354	aacctctcatgaacactctcaaaactctctctgtcaatgatttgatgaagaatttggagctc	1413
QY	1382	tagtctctcttccgcattactctgaaagcgtctcgaagccgcgtcgtctggaagaatctc	1441
Db	1414	tagtctctcttccgcattactctgaaagcgtctcgaagccgcgtcgtctggaagaatctc	1473
QY	1442	gtaatacacttgaacactccagcccaagggcaggtcattgagctgagtgatgaaacaaagacctcca	1501
Db	1474	gtaatacacttgaacactccagcccaagggcaggtcattgagctgagtgatgaaacaaagacctcca	1533
QY	1502	ggaaactgtgctgtgtcccaatcatctctgaaagcagatgttgaggagaaactcccaagaatctg	1561
Db	1534	ggaaactgtgctgtgtcccaatcatctctgaaagcagatgttgaggagaaactcccaagaatctg	1593
QY	1562	gaaccttaatgaaagaaacagccaaagaatgtgaactctgtccgatalgtctgttgaacagagga	1621
Db	1594	gaaccttaatgaaagaaacagccaaagaatgtgaactctgtccgatalgtctgttgaacagagga	1653
QY	1622	caatgaacaaacttctggaaagaaagcagatgttgattagatttgaaagcccaagaacatcgt	1681
Db	1654	caatgaacaaacttctggaaagaaagcagatgttgattagatttgaaagcccaagaacatcgt	1713
QY	1682	ggcgttttttggccaagcaccacagaggaatgtccagttccaaatagttctgtgtgaacactg	1741
Db	1714	ggcgttttttggccaagcaccacagaggaatgtccagttccaaatagttctgtgtgaacactg	1773
QY	1742	gagaggaagcttcaacagagcttaacaaagggcaatccggagccatatctcggtctcatagaggtg	1801
Db	1774	gagaggaagcttcaacagagcttaacaaagggcaatccggagccatatctcggtctcatagaggtg	1833
QY	1802	tgttaacctgaacaagaactagaaaccaatagcaagaagtctgtgtctatcaacaagtccat	1861
Db	1834	tgttaacctgaacaagaactagaaaccaatagcaagaagtctgtgtctatcaacaagtccat	1893
QY	1862	ggaactgtctgaagaaagaaagttctggggctgttatgtgttcaacttgaaattactccagg	1921
Db	1894	ggaactgtctgaagaaagaaagttctggggctgttatgtgttcaacttgaaattactccagg	1953
QY	1922	cagcattgagctgtcccatcatgttcaaaatagaaagctccgaatggacaatttgaacaatttga	1981
Db	1954	cagcattgagctgtcccatcatgttcaaaatagaaagctccgaatggacaatttgaacaatttga	2013
QY	1982	gaggaacaataaataaagatagggttactgtggaccctgtgtctcagagctgaacctttga	2041
Db	2014	gaggaacaataaataaagatagggttactgtggaccctgtgtctcagagctgaacctttga	2073

QY	2042	ggaacatgcgtacgtctctgagggggctctccgactctgcagagatgtgtgtgagcagagcaat	2101
Db	2074	ggaacatgcgtacgtctctgagggggctctccgactctgcagagatgtgtgtgagcagagcaat	2133
QY	2102	catcaagggtctgtacgcggccacccgagaagaacatgctgtctctatactgaacaagatgtcccta	2161
Db	2134	catcaagggtctgtacgcggccacccgagaagaacatgctgtctctatactgaacaagatgtcccta	2193
QY	2162	tcocctgttaacgtcttatgtacacatctctctgcgggtgtatagccgggtcaaatgtccctctccat	2221
Db	2194	tcocctgttaacgtcttatgtacacatctctctgcgggtgtatagccgggtcaaatgtccctctccat	2253
QY	2222	gaacgttcgcctcgatcttatctcaagtgtgctgtatcaaccaaggccaatgtgtatagaagga	2281
Db	2254	gaacgttcgcctcgatcttatctcaagtgtgctgtatcaaccaaggccaatgtgtatagaagga	2313
QY	2282	ggcagcgtcttgaaagagaccatgcggatcatatgagcgctctggacaacagcatctctgtgttag	2341
Db	2314	ggcagcgtcttgaaagagaccatgcggatcatatgagcgctctggacaacagcatctctgtgttag	2373
QY	2342	ctggtctcatcttagccctccatctctctctgtgtagcgtctgcctgttagtgtgtacatcct	2401
Db	2374	ctggtctcatcttagccctccatctctctctgtgtagcgtctgcctgttagtgtgtacatcct	2433
QY	2402	gaagttagaagaaacctgtcgtccctacagtatccagtcggtgtgttctctctgtccgt	2461
Db	2434	gaagttagaagaaacctgtcgtccctacagtatccagtcggtgtgttctctctgtccgt	2493
QY	2462	gtttgctgtctgttgaaacaatcctgcagctgtctctcttagtagcaacatctctctccaaagccaa	2521
Db	2494	gtttgctgtctgttgaaacaatcctgcagctgtctctcttagtagcaacatctctctccaaagccaa	2553
QY	2522	cctgcgcagcaacccgtctgagggggcacatcatctaacacgctgtacacgtccctacgtccctgtg	2581
Db	2554	cctgcgcagcaacccgtctgagggggcacatcatctaacacgctgtacacgtccctacgtccctgtg	2613
QY	2582	tgtgtgcacgtgcaggaactcgtgtggtctccacaactcaagaatctcgtcgtcgtctctcc	2641
Db	2614	tgtgtgcacgtgcaggaactcgtgtggtctccacaactcaagaatctcgtcgtcgtctctcc	2673
QY	2642	tgtggtcttttggtgttgctgtgagttactcttgcctcttttagaaggacgggcattgtgaat	2701
Db	2674	tgtggtcttttggtgttgctgtgagttactcttgcctcttttagaaggacgggcattgtgaat	2733
QY	2702	gcaagtgcgggacaacccgttttgtagagtcctgtgtgaggaagatgtcctcaatctccacaacttc	2761
Db	2734	gcaagtgcgggacaacccgttttgtagagtcctgtgtgaggaagatgtcctcaatctccacaacttc	2793
QY	2762	gactcccatatgctgttttgtaacaacctctctatgtggtgtatgtacacgtgtatcttagagc	2821
Db	2794	gactcccatatgctgttttgtaacaacctctctatgtggtgtatgtatgtacacgtgtatcttagagc	2853
QY	2822	tgtctcttcacagccagatccgaattcccaaggccctgtgattcttctctggacaacagttccta	2881
Db	2854	tgtctcttcacagccagatccgaattcccaaggccctgtgattcttctctggacaacagttccta	2913
QY	2882	ctgtgtcttgccgagagaaatgtatgtagaagaagccacccctgtgtctcaaacccagaagaatgttc	2941
Db	2914	ctgtgtcttgccgagagaaatgtatgtagaagaagccacccctgtgtctcaaacccagaagaatgttc	2973
QY	2942	agaataatctgcatagtgagggaggaaccccaaccttgaaagctgtgcgtgtctcatcaagaacct	3001
Db	2974	agaataatctgcatagtgagggaggaaccccaaccttgaaagctgtgcgtgtctcatcaagaacct	3033
QY	3002	ggttaaaatctctacccagaaatgtgaatgtgctgtctcatatgacctgcggtaagattttta	3061
Db	3034	ggttaaaatctctacccagaaatgtgaatgtgctgtctcatatgacctgcggtaagattttta	3093
QY	3062	tgaaggccagatcatcctctctctctgtggccacaatgtgagccggggaggaagcaacacacatgttc	3121
Db	3094	tgaaggccagatcatcctctctctctgtggccacaatgtgagccggggaggaagcaacacacatgttc	3153

OY 6422 ctatagtgaagcaacaaacgaagctctctacagccatggtcttgatcggcggtcc 6481
|||||
DB 6454 ctatagtgaagcaacaaacgaagctctctacagccatggtcttgatcggcggtcc 6513
6482 tctgtgtctcttgatgaagccacacacagagcatggtatcccaaaagccggcggtctgtg 6541
DB 6514 tctgtgtctcttgatgaagccacacacagagcatggtatcccaaaagccggcggtctgtg 6573
OY 6542 gaattgtgccttaagtgtgttcgaagaggagagatcagtaagtcttatactatagat 6601
DB 6574 gaattgtgccttaagtgtgttcgaagaggagatcagtaagtcttatactatagat 6633
OY 6602 ggaagaatgtgaagctctcttgacatgagatgacatcatggtcaatgaaggtccaggtg 6661
DB 6634 ggaagaatgtgaagctctcttgacatgagatgacatcatggtcaatgaaggtccaggtg 6663
OY 6662 ccttgagcgtgtccagcactcaaaaataagttctgagatggtatatacaatagtgtacg 6721
DB 6694 ccttgagcgtgtccagcactcaaaaataagttctgagatggtatatacaatagtgtacg 6753
OY 6722 aatagcaggtgccaaacccgagcctggaagcctgtccaggaattcttggactgtcatctc 6781
DB 6754 aatagcaggtgccaaacccgagcctggaagcctgtccaggaattcttggactgtcatctc 6813
OY 6782 tggaggtgtcttaaaaggaagaaacccggaacatgctacatcacagctccatcttcatt 6841
DB 6814 tggaggtgtcttaaaaggaagaaacccggaacatgctacatcacagctccatcttcatt 6873
OY 6842 atctctctgcaggaatatacgaatcctctccagagcaaaaagcgactccacataga 6901
DB 6874 atctctctgcaggaatatacgaatcctctccagagcaaaaagcgactccacataga 6933
OY 6902 agactactcctgttctcagacaacacacttgaccgaagtatttgtgaacttgcgaagagca 6961
DB 6934 agactactcctgttctcagacaacacacttgaccgaagtatttgtgaacttgcgaagagca 6993
OY 6962 aagtgatgatgacacacttaaaagacactctcatcacaaaaacagacagatgagtgagact 7021
DB 6994 aagtgatgatgacacacttaaaagacactctcatcacaaaaacagacagatgagtgagact 7053
OY 7022 tgcagttctcacatcttctctacaggaatgagaagtgaaaagactatgatatgaagat 7081
DB 7054 tgcagttctcacatcttctctacaggaatgagaagtgaaaagactatgatatgaagat 7113
OY 7082 cctgttcttaaggggtgtgtctgaaagtaaaaggaactgacttcccttgcacatgtga 7141
DB 7114 cctgttcttaaggggtgtgtctgaaagtaaaaggaactgacttcccttgcacatgtga 7173
OY 7142 agtgtgtggagaaagagccagaaagtgtatgtggaagaaagttaaaactgatactgtact 7201
DB 7174 agtgtgtggagaaagagccagaaagtgtatgtggaagaaagttaaaactgatactgtact 7233
OY 7202 gatactatcataatgcaatgcaatccaatgcaatgcaatgcaatgcaatgcaatgcaatgcaat 7261
DB 7234 gatactatcataatgcaatgcaatccaatgcaatgcaatgcaatgcaatgcaatgcaatgcaat 7293
OY 7262 tgccttgaagcctatgctgtatgcttcaagtgtgaagaaactggaattgaattttta 7321
DB 7294 tgccttgaagcctatgctgtatgcttcaagtgtgaagaaactggaattgaattttta 7353
OY 7322 cctataactatgtaaacctcattatgtaaacccaatgtaaacatgtaaacatgtaaacatgtaaac 7381
DB 7354 cctataactatgtaaacctcattatgtaaacccaatgtaaacatgtaaacatgtaaacatgtaaac 7413
OY 7382 tttttttttttttttgtcctgtgtatctcatctgggggtgcaacaataatcataagt 7441
DB 7414 tttttttttttttttgtcctgtgtatctcatctgggggtgcaacaataatcataagt 7473
OY 7442 aatcagtcgagcgatattgatcaaaatcaaaaggtatgcatcctccttactcaag 7501
DB 7474 aatcagtcgagcgatattgatcaaaatcaaaaggtatgcatcctccttactcaag 7533

OY 7502 ccatgcatgcccagagagatggttcccggtgacacatccattgtctgcaaatgtagtg 7561
DB 7534 ccatgcatgcccagagagatggttcccggtgacacatccattgtctgcaaatgtagtg 7593
OY 7562 ccagagttaatggtcccaagtttccagaagtttgaagaacatggtgtgtcaagtcca 7621
DB 7594 ccagagttaatggtcccaagtttccagaagtttgaagaacatggtgtgtcaagtcca 7653
OY 7622 ctttttggaagctgtcttgcctcagaagttcatalcaaatggaatcaattggaagagag 7681
DB 7654 ctttttggaagctgtcttgcctcagaagttcatalcaaatggaatcaattggaagagag 7713
OY 7682 tgcacatgctgtgtaacatcctgtcttgatccctctgataagctgttctgtgtgagta 7741
DB 7714 tgcacatgctgtgtaacatcctgtcttgatccctctgataagctgttctgtgtgagta 7773
OY 7742 acatgcaacaaaatgtggtgtctcctgaagcacggaacactgtgtccattgtatctg 7801
DB 7774 acatgcaacaaaatgtggtgtctcctgaagcacggaacactgtgtccattgtatctg 7833
OY 7802 tcttatgtcttcgagccatggtgtctacaggtgtcatccttataagacttataactta 7861
DB 7834 tcttatgtcttcgagccatggtgtctacaggtgtcatccttataagacttataactta 7893
OY 7862 gatccctgtgaagggcgaagaatccaacagccaactgcgtgggtcgaagctgtgaagc 7921
DB 7894 gatccctgtgaagggcgaagaatccaacagccaactgcgtgggtcgaagctgtgaagc 7953
OY 7922 caaggcatggaatlaaagagatgtgcgttcaaaactgaaggaaagcctgtgccattgtc 7981
DB 7954 caaggcatggaatlaaagagatgtgcgttcaaaactgaaggaaagcctgtgccattgtc 8013
OY 7982 ctgactgtctgtaaatgtagtaacatgtagcactcctaagaattttatctgcaacaagtgtat 8041
DB 8014 ctgactgtctgtaaatgtagtaacatgtagcactcctaagaattttatctgcaacaagtgtat 8073
OY 8042 attctgtccttcttgaaatatactagaaaaatgaaaagatgagttgtattcttgacaanaa 8101
DB 8074 attctgtccttcttgaaatatactagaaaaatgaaaagatgagttgtattcttgacaanaa 8133
OY 8102 tgtttgacttcttaatgttaatttggaatttgaattctatcaagtgactctgaaatcctt 8161
DB 8134 tgtttgacttcttaatgttaatttggaatttgaattctatcaagtgactctgaaatcctt 8193
OY 8162 agaatggcctcttcttgaaacccctgtgtgtagaagagtagtgccactgccccactatt 8221
DB 8194 agaatggcctcttcttgaaacccctgtgtgtagaagagtagtgccactgccccactatt 8253
OY 8222 ttaattctatgtaagtttgcatatcaagtcagactagtccttagaagaacatgtgatg 8281
DB 8254 ttaattctatgtaagtttgcatatcaagtcagactagtccttagaagaacatgtgatg 8313
OY 8282 gtcaagatcctatgacatlatatctgagttctcttcagatcaatcttagaactcttaac 8341
DB 8314 gtcaagatcctatgacatlatatctgagttctcttcagatcaatcttagaactcttaac 8373
OY 8342 tcaacttcaatcaaatatttttttgagtgtatgctgtgactgtgaagaagatgtagtaag 8401
DB 8374 tcaacttcaatcaaatatttttttgagtgtatgctgtgactgtgaagaagatgtagtaag 8433
OY 8402 gtaaaagactagagataatlaagttcagatcaactcctgtgcaatgttatcagctca 8461
DB 8434 gtaaaagactagagataatlaagttcagatcaactcctgtgcaatgttatcagctca 8493
OY 8462 ctggtttaacaataataggtgtgtgtgtgtgtaggaagcccaactgttaacaatattggca 8521
DB 8494 ctggtttaacaataataggtgtgtgtgtgtgtaggaagcccaactgttaacaataattggca 8553
OY 8522 ggccttttttttttttttttaattgtaacaaatgcaaaaagccaagaagtataaggtgtcaca 8581
DB 8554 ggccttttttttttttttttaattgtaacaaatgcaaaaagccaagaagtataaggtgtcaca 8613
OY 8582 agttaaacaatgaaattcttcaacacagggaanaacagtagcttgaanaactgtgtgaanaac 8641

```

|||||
Db 8614 agttaacaatgaattcttcaacaggaacagctagcttgaacactgtcgtaaac 8673
Qy 8642 acaactgtgtttatgcatcttagtacctcaataatgtgcttgcaagtatgatac 8701
Db 8674 acaactgtgtttatgcatcttagtacctcaataatgtgcttgcaagtatgatac 8733
Qy 8702 cccattaaatcagcaagctcccaatttttcaatcctcaatcactagtcagaataat 8761
Db 8734 cccattaaatcagcaagctcccaatttttcaatcctcaatcactagtcagaataat 8793
Qy 8762 aaaaaacaataatctccatagtgagcatttttcagagtttctaaccagcttatt 8821
Db 8794 aaaaaacaataatctccatagtgagcatttttcagagtttctaaccagcttatt 8853
Qy 8822 ttctagtcagtaaacatttgaataaatactgttcaactaactagtcagtaactgt 8881
Db 8854 ttctagtcagtaaacatttgaataaatactgttcaactaactagtcagtaactgt 8913
Qy 8882 gagagaaagaaataatgtgagagaaactatgtttgaggaagttcaagttcaata 8941
Db 8914 gagagaaagaaataatgtgagagaaactatgtttgaggaagttcaagttcaata 8973
Qy 8942 tcaatctaacctcttccactcttcccaaatgtgaataatgaagcgtgaagtgagac 9001
Db 8974 tcaatctaacctcttccactcttcccaaatgtgaataatgaagcgtgaagtgagac 9033
Qy 9002 ttcaagattcaaatlaacttctctataatttttaaatlttaagaataatataaacccac 9061
Db 9034 ttcaagattcaaatlaacttctctataatttttaaatlttaagaataatataaacccac 9093
Qy 9062 tgcctgaaagaaataatgtatgttttaagaagttgaagcgaatattgaatttaata 9121
Db 9094 tgcctgaaagaaataatgtatgttttaagaagttgaagcgaatattgaatttaata 9153
Qy 9122 agtaataagcgaatttccaataactagtgatagtcacgttgcgaattacagatctc 9181
Db 9154 agtaataagcgaatttccaataactagtgatagtcacgttgcgaattacagatctc 9213
Qy 9182 tcaaaatacagaattatagaataatttcccaatttaataattttcaaaatacaagt 9241
Db 9214 tcaaaatacagaattatagaataatttcccaatttaataattttcaaaatacaagt 9273
Qy 9242 tatgttccctcatcttaccataaactgtatctcaattctcatatagtaactctgag 9301
Db 9274 tatgttccctcatcttaccataaactgtatctcaattctcatatagtaactctgag 9333
Qy 9302 caactccttaactcgttccctcgtatccaagccatattttaaaaaatcaaaagcact 9361
Db 9334 caactccttaactcgttccctcgtatccaagccatattttaaaaaatcaaaagcact 9393
Qy 9362 gtgaactatttgaagaacacgacatttaatacagattgaagaagcctctctgaag 9421
Db 9394 gtgaactatttgaagaacacgacatttaatacagattgaagaagcctctctgaag 9453
Qy 9422 ctgaagaacatctatagttatactctcaatctcaatctgttaccctttaaataagtaa 9481
Db 9454 ctgaagaacatctatagttatactctcaatctcaatctgttaccctttaaataagtaa 9513
Qy 9482 ttttttaacatttccctgtgaacactaatgtgtgtagaataattttcaaacctatactc 9541
Db 9514 ttttttaacatttccctgtgaacactaatgtgtgtagaataattttcaaacctatactc 9573
Qy 9542 aatcaagcaaaatttctgtatattcctcgtggaatgtaactatgtatgttgaagaatcc 9601
Db 9574 aatcaagcaaaatttctgtatattcctcgtggaatgtaactatgtatgttgaagaatcc 9633
Qy 9602 tcaaaatacgttcaaaaattcctcgttcttgcatcttggcagacctgaagaactttat 9661
Db 9634 tcaaaatacgttcaaaaattcctcgttcttgcatcttggcagacctgaagaactttat 9693
Qy 9662 taacaactgtgaatgtgaagaatacagaagaataaataagccctctatacataatggcc 9721
|||||

```

```

Db 9694 taacaactgtgataatgaagaatacagaagaataataaagccctctatacataatggcc 9753
Qy 9722 cagcaaatctatgtttaaaaaaacacacacacacacacacacacacacacacacacacacac 9781
Db 9754 cagcaaatctatgtttaaaaaaacacacacacacacacacacacacacacacacacacacac 9813
Qy 9782 ctgaagaacaaatgtcttgtaactataatgttgacacacacacacacacacacacacacacac 9841
Db 9814 ctgaagaacaaatgtcttgtaactataatgttgacacacacacacacacacacacacacacac 9873
Qy 9842 tcaatgacaaagccatttgcgtgttttctctctgtgmgatataatgaagaataa 9901
Db 9874 tcaatgacaaagccatttgcgtgttttctctctgtgmgatataatgaagaataa 9933
Qy 9902 ttttccaaagagccatgtgtcatgaataactgaaccccttgataattgaacataatttg 9961
Db 9934 ttttccaaagagccatgtgtcatgaataactgaaccccttgataattgaacataatttg 9993
Qy 9962 gaccccttgatatactactagaataatgtataactgnaagaataatgtcttaattctt 10021
Db 9994 gaccccttgatatactactagaataatgtataactgnaagaataatgtcttaattctt 10053
Qy 10022 caaatgtgtacatccccccttaaaagtctatcttccaaagattgaactgtctatccc 10081
Db 10054 caaatgtgtacatccccccttaaaagtctatcttccaaagattgaactgtctatccc 10113
Qy 10082 tttctataccctaagaatgaagcgtttttgtgctcttgttcaatcattgcccctcattcc 10141
Db 10114 tttctataccctaagaatgaagcgtttttgtgctcttgttcaatcattgcccctcattcc 10173
Qy 10142 aagcactttagcgtgtcgtatgtgatacttttttgacccggaatctgaagaatgca 10201
Db 10174 aagcactttagcgtgtcgtatgtgatacttttttgacccggaatctgaagaatgca 10233
Qy 10202 aaactagacaaagtttcaacaacagatctcaagttaataatcttcaatlaaaggagaaa 10261
Db 10234 aaactagacaaagtttcaacaacagatcttcaagttaataatcttcaatlaaaggagaaa 10293
Qy 10262 aagaaataaataatgtgtatgtcaataacttataatgaatgaatgaatgaatgaatgaat 10321
Db 10294 aagaaataaataatgtgtatgtcaataacttataatgaatgaatgaatgaatgaatgaat 10353
Qy 10322 gtgtgaataataatgtgtcaaaataaagcgtgtgaagttctgttaaaaaaaataaaaaa 10381
Db 10354 gtgtgaataataatgtgtcaaaataaagcgtgtgaagttctgttaaaaaaaataaaaaa 10413
Qy 10382 aaaaaataaataaataaataaataaataaataaataaataaataaataaataaataaataa 10441
Db 10414 aaaaaataaataaataaataaataaataaataaataaataaataaataaataaataaataa 10473
Qy 10442 a 10442
Db 10474 a 10474

```

RESULT 5
 AAF24707
 ID AAF24707 standard; DNA; 10474 BP.

AAF24707;
 20-APR-2001 (first entry)

DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.

KW Human; adenosine triphosphate binding cassette protein 1; ABC1;

KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;

KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;

KW atherosclerosis; cholesterol transport; ss.

OS Homo sapiens.

XX Key

Location/Qualifiers

FT CDS 323..7108
 FT /tag= a
 FT /product= "defective ABC1 polypeptide"
 PN MO200078971-A2.
 XX 28-DEC-2000.
 PD
 XX
 XX 16-JUN-2000; 2000MO-US16591.
 XX
 XX 18-JUN-1999; 99US-0140264.
 PR 14-SEP-1999; 99US-0153872.
 PR 19-NOV-1999; 99US-0166573.
 XX
 PA (CVTH-) CV THERAPEUTICS INC.
 PA (UNIV) UNIV WASHINGTON.
 PI
 XX Lawn RM, Wade D, Oram JF, Garvin M;
 DR WPI; 2001-137811/14.
 DR P-SDB; AAB31366.
 XX
 XX
 PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
 PT polynucleotides and polypeptides, useful for treatment of heart disease
 PT and other disorders associated with hypercholesterolemia and
 PT atherosclerosis -
 XX
 XX
 PS Claim 27; Page 144-150; 211pp; English.
 XX
 XX The present sequence encodes a human adenosine triphosphate (ATP)
 CC binding cassette protein (ABC) 1 polypeptide, and is isolated from
 CC a Tangier disease patient. ABC1 resides in cell membranes and utilises
 CC ATP hydrolysis to transport a wide variety of substrates across the
 CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
 CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
 CC Tangier disease, a genetic disorder characterised by abnormal
 CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
 CC 9q22-9q31. The ABC1 genes and proteins are useful for developing
 CC pharmaceutical agents for the treatment of heart disease and other
 CC disorders associated with hypercholesterolemia and atherosclerosis. The
 CC genes are useful for developing screening assays to screen for compounds
 CC that regulate the expression of genes associated with cholesterol
 CC transport. The genes and proteins are also useful for are also useful
 CC as diagnostic indicators of cardiovascular disease and other disorders
 CC associated with hypercholesterolemia.
 CC
 XX
 XX Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;
 SQ

Query Match 99.9%; Score 10429; DB 22; Length 10474;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 10436; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 gccggagccgcgacgagccgacccctctccggcgctgcgagcgagcgcg 61
 DB 34 ggcacgagccgcgacgagccgacccctctccggcgctgcgagcgagcg 93
 QY 62 gagctccgcgacgagcgagcgctctcagcgctgtgtctgttttccgg 121
 DB 94 gagctccgcgacgagcgagcgctctcagcgctgtgtctgttttccgg 153
 QY 122 ttctgtttctccctctccgagagctgtcagaggttagagaaagacgaa 181
 DB 154 ttctgtttctccctctccgagagctgtcagaggttagagaaagacgaa 213
 QY 182 caaaagtggaaacagtaattgaccagccagcggtctccctgtgtgagct 241
 DB 214 caaaagtggaaacagtaattgaccagccagcggtctccctgtgtgagct 273
 QY 242 gccctcagagctccgagcagcagcgctgctgctgaggaagacatgtgt 301
 DB 274 gccctcagagctccgagcagcagcgctgctgctgaggaagacatgtgt 333

QY 302 gccctcagctgaggtgtgtgtgtgaaagacccctcctcagaaagacaaatgtca 361
 DB 334 gccctcagctgaggtgtgtgtgtgaaagacccctcctcagaaagacaaatgtca 393
 QY 362 gctgttactggaagtgtgctgtgctcttattctcctgactgtgtgtgtgt 421
 DB 394 gctgttactggaagtgtgctgtgctcttattctcctgactgtgtgtgtgt 453
 QY 422 gagctaccacccctatgaaacacatgaaatgccatttccaaataaagcagccctctgc 481
 DB 454 gagctaccacccctatgaaacacatgaaatgccatttccaaataaagcagccctctgc 513
 QY 482 aggaacacttctgt 541
 DB 514 aggaacacttctgt 573
 QY 542 cccgactcctggggagctcccgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 601
 DB 574 cccgactcctggggagctcccgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 633
 QY 602 cctgttctcagatgt 661
 DB 634 cctgttctcagatgt 693
 QY 662 catgacgaagttctgagacattacagacatcagaacatccagctcaactgtgaagt 721
 DB 694 catgacgaagttctgagacattacagacatcagaacatccagctcaactgtgaagt 753
 QY 722 tcaagattctctgt 781
 DB 754 tcaagattctctgt 813
 QY 782 cccaaagtctatgt 841
 DB 814 cccaaagtctatgt 873
 QY 842 gaaaggtaccagttacattgtacaaagtctgtgtgtgtgtgtgtgtgtgtgtgtgt 901
 DB 874 gaaaggtaccagttacattgtacaaagtctgtgtgtgtgtgtgtgtgtgtgtgtgt 933
 QY 902 tcaactgt 961
 DB 934 tcaactgt 993
 QY 962 agcagagcaggtactgt 1021
 DB 994 agcagagcaggtactgt 1053
 QY 1022 ctctacatctccctcccgagagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1081
 DB 1054 ctctacatctccctcccgagagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1113
 QY 1082 tcttggagactgt 1141
 DB 1114 tcttggagactgt 1173
 QY 1142 ggtgagttctgt 1201
 DB 1174 ggtgagttctgt 1233
 QY 1202 gttctgtattgt 1261
 DB 1234 gttctgtattgt 1293
 QY 1262 gttctgtattgt 1321
 DB 1294 gttctgtattgt 1353
 QY 1322 aacctctatgaaacattacaaacttcttactgtgtgtgtgtgtgtgtgtgtgtgtgt 1381
 DB 1354 aacctctatgaaacattacaaacttcttactgtgtgtgtgtgtgtgtgtgtgtgtgt 1413
 QY 1382 tagtctcttctcccgatattctgtgaagctctgtgaagcgcgtgtgtgtgtgaagatct 1441

Db 1414 tagtccctccctccgcatlactlgnaaagcctcgaagcctcgtctgcttggaaagatcct 1473
QY 1442 gtataccctgaactccagccacaagaagcagatcgtctgaagtgaaagacttcca 1501
Db 1474 gtataccctgaactccagccacaagaagcagatcgtctgaagtgaaagacttcca 1533
QY 1502 ggaactgctgtctcactgactcgtgaagcactgtggaaggaactcagcccaagactcgt 1561
Db 1534 ggaactgctgtctcactgactcgtgaagcactgtggaaggaactcagcccaagactcgt 1593
QY 1562 gaacttcagtgagaacagccaagaatggaactgtcctgagctgtctgttgaagaacagga 1621
Db 1594 gaacttcagtgagaacagccaagaatggaactgtcctgagctgtctgttgaagaacagga 1653
QY 1622 caatgacacacttctggagacagcagttgagctgactgagttggaacagcccaagacatcgt 1681
Db 1654 caatgacacacttctggagacagcagttgagctgactgagttggaacagcccaagacatcgt 1713
QY 1682 ggcgttttggccaagcaccagaagagatgtccagttccagtaa tggcttctgttgaacctg 1741
Db 1714 ggcgttttggccaagcaccagaagagatgtccagttccagtaa tggcttctgttgaacctg 1773
QY 1742 gagaagaacttccaagagactaaccaggaatccaggaacatccatctgacttgaagagtg 1801
Db 1774 gagaagaacttccaagagactaaccaggaatccaggaacatccatctgacttgaagagtg 1833
QY 1802 tgtcaacctgaacaagctagaagaccatagaacaagaagctgtgtctca tcaacaagttccat 1861
Db 1834 tgtcaacctgaacaagctagaagaccatagaacaagaagctgtgtctca tcaacaagttccat 1893
QY 1862 ggaactcgtgagtagaaggaaggtctcgtgactgtgactgttcaacttgaacttaccag 1921
Db 1894 ggaactcgtgagtagaaggaaggtctcgtgactgtgactgttcaacttgaacttaccag 1953
QY 1922 caagcatgtgagctgcccacatcagctcaagtaacagatccgaattggaacatgaatgtgga 1981
Db 1954 caagcatgtgagctgcccacatcagctcaagtaacagatccgaattggaacatgaatgtgga 2013
QY 1982 gaggacaataaataaataaagatgtgtatctgtggaacccctggtccctccagactgaaccccttga 2041
Db 2014 gaggacaataaataaataaagatgtgtatctgtggaacccctggtccctccagactgaaccccttga 2073
QY 2042 ggaactgctgtacgtctcgtgagggggtctcgtcacttgcagagatgtgtgtgagcagagcaat 2101
Db 2074 ggaactgctgtacgtctcgtgagggggtctcgtcacttgcagagatgtgtgtgagcagagcaat 2133
QY 2102 catcaaggtgtctgacggtgacccggaagaaactgtgtctataatgcaacagatgtcccta 2161
Db 2134 catcaaggtgtctgacggtgacccggaagaaactgtgtctataatgcaacagatgtcccta 2193
QY 2162 tccctgtttagcttgatatacctcttctcgtggtgtgagtagccgttcaatgccccttctcat 2221
Db 2194 tccctgtttagcttgatatacctcttctcgtggtgtgagtagccgttcaatgccccttctcat 2253
QY 2222 gaagctgtgctgtgacttactcaggtgtgtatcatcaatgaaggaatcgtgtatgaagaagga 2281
Db 2254 gaagctgtgctgtgacttactcaggtgtgtatcatcaatgaaggaatcgtgtatgaagaagga 2313
QY 2282 ggaacggtctgaagaagacatctgagatgagctgtgagacacagacatatactcgtgtttag 2341
Db 2314 ggaacggtctgaagaagacatctgagatgagctgtgagacacagacatatactcgtgtttag 2373
QY 2342 ctgtgttaatagtagactcacttctcttctgtgagcgtctgagctgaagtgactaact 2401
Db 2374 ctgtgttaatagtagactcacttctcttctgtgagcgtctgagctgaagtgactaact 2433
QY 2402 gaagtagaagaacactgtctgcccataagatgccacagctgtgtgttgccttccgtccgt 2461
Db 2434 gaagtagaagaacactgtctgcccataagatgccacagctgtgtgttgccttccgtccgt 2493
QY 2462 gtttgtgtgtgtgacaaatccgtgagctgtccgtgattagaacacttctccagaagccaa 2521
Db 2494 gtttgtgtgtgtgacaaatccgtgagctgtccgtgattagaacacttctccagaagccaa 2553
QY 2522 cctggcagacagcctgtgtgggggagacatactacttcaagcgtactccgtccctaagctctgtg 2581
Db 2554 cctggcagacagcctgtgtgggggagacatactacttcaagcgtactccgtccctaagctctgtg 2613
QY 2582 tgtgacatgtgacagactagctgtggtctcactcaagatctctcgtactgactgtctcc 2641
Db 2614 tgtgacatgtgacagactagctgtggtctcactcaagatctctcgtactgactgtctcc 2673
QY 2642 tgtgtgttttgggttgggtgtgacttgccttcttggagggcagggcattggaggt 2701
Db 2674 tgtgtgttttgggttgggtgtgacttgccttcttggagggcagggcattggaggt 2733
QY 2702 gcaagtggacaacctgttgaagctccttggagaggaatgtgtcactcaatctcaacactc 2761
Db 2734 gcaagtggacaacctgttgaagctccttggagaggaatgtgtcactcaatctcaacactc 2793
QY 2762 gactccatgactgtcttgaacacttccctcactagtggtgtatgactgttgaactgtgagc 2821
Db 2794 gactccatgactgtcttgaacacttccctcactagtggtgtatgactgttgaactgtgagc 2853
QY 2822 tgtcttccagggccagtagaattccagggccctgtgatttctcttgcacaaagttcccta 2881
Db 2854 tgtcttccagggccagtagaattccagggccctgtgatttctcttgcacaaagttcccta 2913
QY 2882 ctgtgttggcaggaagaatgtatgaagaagcaccctgtgtccaacccaagaagaatgtc 2941
Db 2914 ctgtgttggcaggaagaatgtatgaagaagcaccctgtgtccaacccaagaagaatgtc 2973
QY 2942 agaaatctgtcaltgagaggaagaaacccacacttgaagctgtgctgtccatcagaacct 3001
Db 2974 agaaatctgtcaltgagaggaagaaacccacacttgaagctgtgctgtccatcagaacct 3033
QY 3002 ggtcaaaagctacccagatgagatgaaggtgtgtctgcatgagccctgacagaaatttcta 3061
Db 3034 ggtcaaaagctacccagatgagatgaaggtgtgtctgcatgagccctgacagaaatttcta 3093
QY 3062 tgaagggtcagatccactcctcctcgtggcccaatvggaagcggggaagcagaccacatgtc 3121
Db 3094 tgaagggtcagatccactcctcctcgtggcccaatvggaagcggggaagcagaccacatgtc 3153
QY 3122 aatcttgacaggggtgtgttcccccagcactcgggacccgctcactacatccctgggaaagaat 3181
Db 3154 aatcttgacaggggtgtgttcccccagcactcgggacccgctcactacatccctgggaaagaat 3213
QY 3182 tgcgtctgagatvgagacacatcccgacagaacctgtgggtctgtctcccgacataacgtgtc 3241
Db 3214 tgcgtctgagatvgagacacatcccgacagaacctgtgggtctgtctcccgacataacgtgtc 3273
QY 3242 gtttgaacatgctgactgtcgaagaacacatgtgttctatgcccgtttgaaaggctctc 3301
Db 3274 gtttgaacatgctgactgtcgaagaacacatgtgttctatgcccgtttgaaaggctctc 3333
QY 3302 tgaagaagcagctgaaaggtgagatgagacagatgagccctgagatgtgtgttgcacataag 3361
Db 3334 tgaagaagcagctgaaaggtgagatgagacagatgagccctgagatgtgtgttgcacataag 3393
QY 3362 caagcttgaagaagcnaaacaagccagctgtcaggtgtgaatgtcagagaagaatcactgtggtc 3421
Db 3394 caagcttgaagaagcnaaacaagccagctgtcaggtgtgaatgtcagagaagaatcactgtggtc 3453
QY 3422 ctgtgcttctgtcggggagatcctaaggtgtgactctgtgataacccaacagctgtgtgga 3481
Db 3454 ctgtgcttctgtcggggagatcctaaggtgtgactctgtgataacccaacagctgtgtgga 3513
QY 3482 ccttactcccgaggggaatatavggaagctgtcgtgaataatccgaagaagccgcacat 3541
Db 3514 ccttactcccgaggggaatatavggaagctgtcgtgaataatccgaagaagccgcacat 3573
QY 3542 tatctctctacacacacacatgagatgaagcagagctcctgtgggagacagattgcacat 3601
Db 3574 tatctctctacacacacacatgagatgaagcagagctcctgtgggagacagattgcacat 3633

[illegible]

OY	4682	gtctagcagcgacaaatcagaagaagctgctccgtgtgtgtccccaaggcgaggggct	4741
Db	4714	gtctagcagcgacaaatcagaagaagctgctccgtgtgtgtccccaaggcgaggggct	4773
OY	4742	gctccctccacaagaanaaanaaacctgcagatctccctcaaggacctgcagagaagaa	4801
Db	4774	gctccctccacaagaanaaanaaacctgcagatctccctcaaggacctgcagagaagaa	4833
OY	4802	cattcgatctatctgtgtgaagacgtatgtgagatcatalagccaaagcttaagaaca	4861
Db	4834	cattcgatctatctgtgtgaagacgtatgtgagatcatalagccaaagcttaagaaca	4893
OY	4862	gattctggtaataagttttagttgattgaggggtttcccggtgtgcataactcaagc	4921
Db	4894	gattctggtaataagttttagttgattgaggggtttcccggtgtgcataactcaagc	4953
OY	4922	actctctccgattcaagaagtttaataatgctcattcaacaataatgaagaacctaaagct	4961
Db	4954	actctctccgattcaagaagtttaataatgctcattcaacaataatgaagaacctaaagct	5013
OY	4982	ggccaaggacagttctcgaatcgattcttcaacagcttgggaagaatttagaagagct	5041
Db	5014	ggccaaggacagttctcgaatcgattcttcaacagcttgggaagaatttagaagagct	5073
OY	5042	ggaaccaagaataatgttcaaggltgtgttcaataaacaagggtctggcatactcagctc	5101
Db	5074	ggaaccaagaataatgttcaaggltgtgttcaataaacaagggtctggcatactcagctc	5133
OY	5102	ttctctgaatgtcatcaacaatgccaattctcgggcaccaacctgcaaaaggagagaaacc	5161
Db	5134	ttctctgaatgtcatcaacaatgccaattctcgggcaccaacctgcaaaaggagagaaacc	5193
OY	5162	tagcattatgaataatactcttccaatacctccctgaaatccacaacagcagcagctctc	5221
Db	5194	tagcattatgaataatactcttccaatacctccctgaaatccacaacagcagcagctctc	5253
OY	5222	agaaggtgctctgtatgacacatcagttgatatgtctgtgtccatctgltcatctttgc	5261
Db	5254	agaaggtgctctgtatgacacatcagttgatatgtctgtgtccatctgltcatctttgc	5313
OY	5282	aatgtccttgctccacgcagagcttgtgcgattctcgtatccgatacgaaggcggttaacgaagc	5341
Db	5314	aatgtccttgctccacgcagagcttgtgcgattctcgtatccgatacgaaggcggttaacgaagc	5373
OY	5342	aaaacacctgtgaatctacgtaggagtgaagccctgtcatctactctgctctctaatttgt	5401
Db	5374	aaaacacctgtgaatctacgtaggagtgaagccctgtcatctactctgctctctaatttgt	5433
OY	5402	ctgggatatgtgaattacgtttgtctcctgcgaacatcggtcattatcatcttaatttgtt	5461
Db	5434	ctgggatatgtgaattacgtttgtctcctgcgaacatcggtcattatcatcttaatttgtt	5493
OY	5462	ccagagaagaatccctatgtgtctcctccaaatctgcgctgtgcagccctctacttttgtc	5521
Db	5494	ccagagaagaatccctatgtgtctcctccaaatctgcgctgtgtgcagccctctacttttgtc	5553
OY	5522	gtaatgggtgtgtcaatcacacctctcatgtatccagctccctctgtgtgttcaagaacctcag	5561
Db	5554	gtaatgggtgtgtcaatcacacctctcatgtatccagctccctctgtgtgttcaagaacctcag	5613
OY	5582	cacagccatattgtgtgtccacacgcgtgaacacctctcatattgagataatgaagacgttgcc	5641
Db	5614	cacagccatattgtgtgtccacacgcgtgaacacctctcatattgagataatgaagacgttgcc	5673
OY	5642	cacacttltgtctgagagctgtttcaacgcgaataaagctgtgaataatcatcagatatctcgaa	5701
Db	5674	cacacttltgtctgagagctgtttcaacgcgaataaagctgtgaataatcatcagatatctcgaa	5733
OY	5702	gtccgtgtctctgtatctctccacaattttgcctcgggaacgaaggctcatctgacaatgtgtgaa	5761
Db	5734	gtccgtgtctctgtatctctccacaattttgcctcgggaacgaaggctcatctgacaatgtgtgaa	5793
OY	5762	aaacacagcaatgtgcttatgacctcggaanaagtttgaggaanaatcagctttgttcaacctt	5821

```
Db 5794 aaaccagcattgcttgaatgccccggaaggttggggaatctgcttctgaccatt 5853
QY 5822 atcttggacttggtaggaagaacctctccgcatgacggttggaagggtgtgtctt 5881
Db 5854 atcttggacttggtaggaagaacctctccgcatgacggttggaagggtgtgtctt 5913
QY 5882 cctcatctgcttctgacagtaacagattcttcacagccagaccgtglaaaycaaa 5941
Db 5914 cctcatctgcttctgacagtaacagattcttcacagccagaccgtglaaaycaaa 5973
QY 5942 gctatctccttgaatgatgaagaatgtagggcggaaggaagcagaattcttga 6001
Db 5974 gctatctccttgaatgatgaagaatgtagggcggaaggaagcagaattcttga 6033
QY 6002 tggtagggccagaaatgacatcttagaatacaaggatltgacgaagatalatagaagaa 6061
Db 6034 tggtagggccagaaatgacatcttagaatacaaggatltgacgaagatalatagaagaa 6093
QY 6062 ggggaagccgtgcttggacagatttgcgtgggcatctcctcgtgtgattgttggct 6121
Db 6094 ggggaagccgtgcttggacagatttgcgtgggcatctcctcgtgtgattgttggct 6153
QY 6122 cctggaggttaattggggttggaaatcattcaacttcaagatgttacaaggataccac 6181
Db 6154 cctggaggttaattggggttggaaatcattcaacttcaagatgttacaaggataccac 6213
QY 6182 tgttaccagagagatgcttctcttaaaaaaatagatattcattacaacatcagaat 6241
Db 6214 tgttaccagagagatgcttctcttaaaaaaatagatattcattacaacatcagaat 6273
QY 6242 acatcagaataatggctactgacctcagtttgaatgcatcacagaagcttgaactggag 6301
Db 6274 acatcagaataatggctactgacctcagtttgaatgcatcacagaagcttgaactggag 6333
QY 6302 agaacacgttggaattcttggccctttagagagagatcccaagaaagaaatgttgcgaagt 6361
Db 6334 agaacacgttggaattcttggccctttagagagagatcccaagaaagaaatgttgcgaagt 6393
QY 6362 tggtaggttggcgaattcgggaacttggcccttgaagatltggaagaaatatgctgttaa 6421
Db 6394 tggtaggttggcgaattcgggaacttggcccttgaagatltggaagaaatatgctgttaa 6453
QY 6422 ctatagtggaggaacaacaacgcaagctctctacagccatgtcttgcgcgggctcc 6481
Db 6454 ctatagtggaggaacaacaacgcaagctctctacagccatgtcttgcgcgggctcc 6513
QY 6482 tgtgtgttcttctgataaaccacacagcagatgatacccaagcccggttcttgg 6541
Db 6514 tgtgtgttcttctgataaaccacacagcagatgatacccaagcccggttcttgg 6573
QY 6542 gaattgtgcccataagtgctcaagagagagatcagtagtcttatactcattat 6601
Db 6574 gaattgtgcccataagtgctcaagagagagatcagtagtcttatactcattat 6633
QY 6602 ggaagaatgtgaagccttctgacatagatgagatcattcgtcaatgtgaagtccaagt 6661
Db 6634 ggaagaatgtgaagccttctgacatagatgagatcattcgtcaatgtgaagtccaagt 6693
QY 6662 ccttggcagtgctcagcattcaaaaaataggttggagatgtttatataatgttgaag 6721
Db 6694 ccttggcagtgctcagcattcaaaaaataggttggagatgtttatataatgttgaag 6753
QY 6722 aatagcaggttccaaaccggaactggaagcctgtlccaggaattcttctgtgacttcc 6781
Db 6754 aatagcaggttccaaaccggaactggaagcctgtlccaggaattcttctgtgacttcc 6813
QY 6782 tgggaatgttcttaaaagaagaacacgggaacatgtctacataccagcttccattcatt 6841
Db 6814 tgggaatgttcttaaaagaagaacacgggaacatgtctacataccagcttccattcatt 6873
QY 6842 atcttctcggcagatattcagatcctctccagaaacaaaggcgtccacataga 6901
|||||

Db 6874 atcttctcggcagatattcagatcctctccagaaacaaaggcgtccacataga 6933
QY 6902 aagactactctgttctcagacaacacattgacaagatttggacttggcaaggaca 6961
Db 6934 aagactactctgttctcagacaacacattgacaagatttggacttggcaaggaca 6993
QY 6962 aagtgatgtgacacacttaaaagacctctcattacaacaaaaacagacagatgtgacgt 7021
Db 6994 aagtgatgtgacacacttaaaagacctctcattacaacaaaaacagacagatgtgacgt 7053
QY 7022 tgcagttctcacatcttctcagagatgagaaagttagaaagaagcattgataaagat 7081
Db 7054 tgcagttctcacatcttctcagagatgagaaagttagaaagaagcattgataaagat 7113
QY 7082 cctgttcaacgggttggctgaaagttagaaagtagaacttctccttggacatttga 7141
Db 7114 cctgttcaacgggttggctgaaagttagaaagtagaacttctccttggacatttga 7173
QY 7142 agtgttgggaagaaagcgccagaagtgatgtgggaagaaatgaactgtgatactgact 7201
Db 7174 agtgttgggaagaaagcgccagaagtgatgtgggaagaaatgaactgtgatactgact 7233
QY 7202 gatactattcaatgtgaaatgcaattcaatgtgaaatgcaaaatctcattacagggcag 7261
Db 7234 gatactattcaatgtgaaatgcaattcaatgtgaaatgcaaaatctcattacagggcag 7293
QY 7262 tgccttgttaagcctatgtctgtatgctctcaagtgaaagacttgaattgtttta 7321
Db 7294 tgccttgttaagcctatgtctgtatgctctcaagtgaaagacttgaattgtttta 7353
QY 7322 cctataactatgtgaaatcattatgaaacccaatgtgacataggttggaaactcac 7381
Db 7354 cctataactatgtgaaatcattatgaaacccaatgtgacataggttggaaactcac 7413
QY 7382 ttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt 7441
Db 7414 ttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt 7473
QY 7442 aatcatggccagcagattatgtatcaaaaatcaaaaagaaatgaaatcctcattacaag 7501
Db 7474 aatcatggccagcagattatgtatcaaaaatcaaaaagaaatgaaatcctcattacaag 7533
QY 7502 ccatgtgcaatggccagagactgtttcccggtgacacatccatgtctgcaatgtgtg 7561
Db 7534 ccatgtgcaatggccagagactgtttcccggtgacacatccatgtctgcaatgtgtg 7593
QY 7562 ccagagattatagtgccaagtttttcaagaagtttgaagcaacatgtgtgtcatgtca 7621
Db 7594 ccagagattatagtgccaagtttttcaagaagtttgaagcaacatgtgtgtcatgtca 7653
QY 7622 ctttgtgaagaagctgtctgtcagagatctatacaaatgtaatatcagttgacagaatg 7681
Db 7654 ctttgtgaagaagctgtctgtcagagatctatacaaatgtaatatcagttgacagaatg 7713
QY 7682 tgcacatgtgtgtcaacatctctgttgaatcctctgtataagctgttctgtgtgcaatga 7741
Db 7714 tgcacatgtgtgtcaacatctctgttgaatcctctgtataagctgttctgtgtgcaatga 7773
QY 7742 acatgtcaacaaaaatgttgggtgtctctgaagcaagggaaactgtttccattgtataat 7801
Db 7774 acatgtcaacaaaaatgttgggtgtctctgaagcaagggaaactgtttccattgtataat 7833
QY 7802 tctatgtctcgaagcatttgggtctacaggttcaatccttataagacttataactta 7861
Db 7834 tctatgtctcgaagcatttgggtctacaggttcaatccttataagacttataactta 7893
QY 7862 gatcctgttaagaggaagaagaatcaacagccaactgtctgggtcgaagctgtgaagc 7921
Db 7894 gatcctgttaagaggaagaagaatcaacagccaactgtctgggtcgaagctgtgaagc 7953
QY 7922 caggagcttgagataaagagatgtgtgttcaaaccttaaggagacgtgttccattgttc 7981
Db 7954 caggagcttgagataaagagatgtgtgttcaaaccttaaggagacgtgttccattgttc 8013
```



```

Db 10174 aagccttaccgctgctgtaagggatctatttgcacggaatctgaattgca 10233
QY 10202 aaactagacaaagttcacacagattctcaagttcaatcatcatttaaaagga 10261
Db 10234 aaactagacaaagttcacacagattctcaagttcaatcatcatttaaaagga 10293
QY 10262 aagaaaaaatttctgtatgcaatacttataagtaataatgcatattctat 10321
Db 10294 aagaaaaaatttctgtatgcaatacttataagtaataatgcatattctat 10353
QY 10322 gtgttaataatgacacaaataaagctgtacagttctgttaaaaaa 10381
Db 10354 gtgttaataatgacacaaataaagctgtacagttctgttaaaaaa 10413
QY 10382 aaaaaaataaataaataaataaataaataaataaataaataa 10441
Db 10414 aaaaaaataaataaataaataaataaataaataaataaataa 10473
QY 10442 a 10442
Db 10474 a 10474

```

RESULT 6
AAF24708 standard; DNA: 10474 BP.

AAF24708:

20-APR-2001 (first entry)

Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.

Human: adenosine triphosphate binding cassette protein 1; ABC1;
Kw apolipoprotein mediated mobilisation; cholesterol; Tangier disease;
Kw chromosome 9q22-9q31; heart disease; hypercholesterolemia;
Kw atherosclerosis; cholesterol transport; ss.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 323..7108

FT /tag= a

FT /product= "defective ABC1 polypeptide"

XX MO200078971-A2.

XX 28-DEC-2000.

XX 16-JUN-2000; 2000MO-US16591.

XX 18-JUN-1999; 99US-0140264.

XX 14-SEP-1999; 99US-0153872.

XX 19-NOV-1999; 99US-0166573.

XX (CVT4-) CV THERAPEUTICS INC.

XX (UNIV) UNIV WASHINGTON.

XX Lawn RM, Wade D, Oram JF, Garvin M;

XX WPI, 2001-137811/14.

XX P-SPDH; AAB31367.

XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1

XX PT polynucleotides and polypeptides, useful for treatment of heart disease

XX PT and other disorders associated with hypercholesterolemia and

XX PT atherosclerosis -

XX Claim 30; Page 165-172; 21pp; English.

XX The present sequence encodes a human adenosine triphosphate (ATP)

XX binding cassette protein (ABC) 1 polypeptide, and is isolated from

CC binding cassette protein (ABC) 1 polypeptide, and is isolated from

CC a Tangier disease patient. ABC1 resides in cell membranes and utilizes
CC ATP hydrolysis to transport a wide variety of substrates across the
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
CC Tangier disease, a genetic disorder characterised by abnormal
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
CC 9q22-9q31. The ABC1 genes and proteins are useful for developing
CC pharmaceutical agents for the treatment of heart disease and other
CC disorders associated with hypercholesterolemia and atherosclerosis. The
CC genes are useful for developing screening assays to screen for compounds
CC that regulate the expression of genes associated with cholesterol
CC transport. The genes and proteins are also useful for are also useful
CC as diagnostic indicators of cardiovascular disease and other disorders
CC associated with hypercholesterolemia.

XX Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

Query Match 99.9%; Score 10429; DB 22; Length 10474;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10436; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY 2 gccggagcccgagagccgagccgacccctctcccggtcgcgagcgagcg 61
Db 34 ggcacgagccgagagccgagccgagccgacccctctcccggtcgcgagcgagcg 93
QY 62 gagctcgcgcacacacagagccggtctcaggcgcttgcctgttttcccg 121
Db 94 gagctcgcgcacacacagagccggtctcaggcgcttgcctgttttcccg 153
QY 122 ttctgtttcccccctcccgagagcgcttgcaggggttgaggaagagacgaaca 181
Db 154 ttctgtttcccccctcccgagagcgcttgcaggggttgaggaagagacgaaca 213
QY 182 caaaagtgaagaaacagtaataagacacagcgccctctgtgtgagcctgcgcgt 241
Db 214 caaaagtgaagaaacagtaataagacacagcgccctctgtgtgagcctgcgcgt 273
QY 242 gccctccagagctcccgagccacagcgctggcgctgtgcaggggaacagctgtg 301
Db 274 gccctccagagctcccgagccacagcgctggcgctgtgcaggggaacagctgtg 333
QY 302 gccctcagctgaagctgtctgtgtgtggaagaacccctccttcagaaagaacaatgtca 361
Db 334 gccctcagctgaagctgtctgtgtgtggaagaacccctccttcagaaagaacaatgtca 393
QY 362 gctgttactggaagtgagcctgtgctcttattcttctgtatcctgtactctgttggct 421
Db 394 gctgttactggaagtgagcctgtgctcttattcttctgtatcctgtactctgttggct 453
QY 422 gagctaccacccctatgaaacaacagatgacatttccaataaagcagcctctgc 481
Db 454 gagctaccacccctatgaaacaacagatgacatttccaataaagcagcctctgc 513
QY 482 aggaacacttctgtgtgtcagggatatactgtatgccaacaacccctgtttccgltta 541
Db 514 aggaacacttctgtgtgtcagggatatactgtatgccaacaacccctgtttccgltta 573
QY 542 cccgactcctggggaggtcccgaggtgtgtggaacttaacaatcattgtggtcgc 601
Db 574 cccgactcctggggaggtcccgaggtgtgtggaacttaacaatcattgtggtcgc 633
QY 602 cctgttccagatgctcgagagctccttcttatacagccagaagaacccagatgagga 661
Db 634 cctgttccagatgctcgagagctccttcttatacagccagaagaacccagatgagga 693
QY 662 catgcgcaagttctggaacattacagcagataagaatccagctcagctaaacttgaagct 721
Db 694 catgcgcaagttctggaacattacagcagataagaatccagctcagctaaacttgaagct 753
QY 722 tcaagattcctgtgtggaacattacagcagataagaatccagctcagctaaacttgaagct 781
Db 754 tcaagattcctgtgtggaacattacagcagataagaatccagctcagctaaacttgaagct 813

```


QY	782	cccaagctctactctgtgacaaagatctgtagaggtctgatacttctccaaagattttt	841
QY	814	cccaagctctactctgtgacaaagatctgtagaggtctgatacttctccaaagattttt	873
QY	842	gcaaggtctaccagttatcatatttgacaagctctgtgcaatgatatccaatctaaagaagtgt	901
DB	874	gcaaggtctaccagttatcatatttgacaagctctgtgcaatgatatccaatctaaagaagtgt	933
QY	902	tcaactgtgtgacaaagaagttcttgagctttgtgacctaacaaaggagaactgctgc	961
DB	934	tcaactgtgtgacaaagaagttcttgagctttgtgacctaacaaaggagaactgctgc	993
QY	962	agcagagcgaagtactcgttccacaatggaacctctgaaagccaactctgagaactaa	1021
DB	994	agcagagcgaagtactcgttccacaatggaacctctgaaagccaactctgagaactaa	1053
QY	1022	ctctacactctccctcccgagaaagagctgtgtbaagcccaaaaacattgtgcatag	1081
DB	1054	ctctacactctccctcccgagaaagagctgtgtbaagcccaaaaacattgtgcatag	1113
QY	1082	tctgtggaactctgtcccaagagctgttccagcatgaaagctgtgagatgacatgacagga	1141
DB	1114	tctgtggaactctgtcccaagagctgttccagcatgaaagctgtgagatgacatgacagga	1173
QY	1142	gggtgagtcttctgacccaatgttgacaagctcccaagctccctcccaacccaatctaacaggtgt	1201
DB	1174	gggtgagtcttctgacccaatgttgacaagctcccaagctccctcccaacccaatctaacaggtgt	1233
QY	1202	gtcccgatctgtctgcgagatccccaaggagggggtctgaaagatccaagtctccaactg	1261
DB	1234	gtcccgatctgtctgcgagatccccaaggagggggtctgaaagatccaagtctccaactg	1293
QY	1262	gtatgaggaacaacaatacaagaagcctctttggaggaatgacatgtgaggaagtctga	1321
DB	1294	gtatgaggaacaacaatacaagaagcctctttggaggaatgacatgtgaggaagtctga	1353
QY	1322	aacctctatgaacaactctcaactcctcttactgacaaatgatttgaaagaatttgagatc	1381
DB	1354	aacctctatgaacaactctcaactcctcttactgacaaatgatttgaaagaatttgagatc	1413
QY	1382	taagtctctctccgcatactatctgaaagctctgaaagccgctgctgtcttggaagaacct	1441
DB	1414	taagtctctctccgcatactatctgaaagctctgaaagccgctgctgtcttggaagaacct	1473
QY	1442	gtatacactctgaacctcccaagccaagagcgtcagctgtgaggtgaaacaagaacctcca	1501
DB	1474	gtatacactctgaacctcccaagccaagagcgtcagctgtgaggtgaaacaagaacctcca	1533
QY	1502	ggaactctgctgtgtcccatatctctgaaagcatgtgaggagaactcaagccccaagatctg	1561
DB	1534	ggaactctgctgtgtcccatatctctgaaagcatgtgaggagaactcaagccccaagatctg	1593
QY	1562	gacctctatggaagaacggccaagaatagagcctctgtccggaatgctgttgaaagaagga	1621
DB	1594	gacctctatggaagaacggccaagaatagagcctctgtccggaatgctgttgaaagaagga	1653
QY	1622	caatgacaacttttgggacaagcagctgtgagatggctctagaattggaacagcccaagatcgt	1681
DB	1654	caatgacaacttttgggacaagcagctgtgagatggctctagaattggaacagcccaagatcgt	1713
QY	1682	ggcgttttttggccaagcaccagaagatgtcccaagttccagtatgttctgtgtataacctg	1741
DB	1714	ggcgttttttggccaagcaccagaagatgtcccaagttccagtatgttctgtgtataacctg	1773
QY	1742	ggagagaagctttccaacgagataaccggaatccogaaatccatactccgctttcatggaagt	1801
DB	1774	ggagagaagctttccaacgagataaccggaatccogaaatccatactccgctttcatggaagt	1833
QY	1802	tgtcaactctgaacaagcttagaacccaatagcaacagaagctgtgctctatcaacaagtctcat	1861
DB	1834	tgtcaactctgaacaagcttagaacccaatagcaacagaagctgtgctctatcaacaagtctcat	1893

QY	1862	ggaacgtcctgatacgaagagaagttctctgggcctgatactgctgtltaactgtgaattactccagg	1921
Db	1884	ggagctctgctgatacgaagagaagttctctgggcctgatactgctgtltaactgtgaattactccagg	1953
QY	1922	cagcatctgagctccccatcatgataagtataaagatccgaattggaactgtgaacatgttga	1981
Db	1954	cagcatctgagctccccatcatgataagataaagatccgaattggaactgtgaacatgttga	2013
QY	1982	gaggacaataaagataagatctggtactgtggaacctgtgctctgagcttgagcttgacccttttga	2041
Db	2014	gaggacaataaagataagatctggtactgtggaacctgtgctctgagcttgagcttgacccttttga	2073
QY	2042	ggacaatgcgtatacgtctcgggggggcttcgcctactctgaggaatgttggttgagaagacat	2101
Db	2074	ggacaatgcgtatacgtctcgggggggcttcgcctactctgaggaatgttggttgagaagacat	2133
QY	2102	catcaaggctcctagcgggacccgaagaagaacatctgttcatatgtcaacaagatggcccta	2161
Db	2134	catcaaggctcctagcgggacccgaagaagaacatctgttcatatgtcaacaagatggcccta	2193
QY	2162	lcccggttaccgtltgatacatacttcttcgcyggttgatagagccggtcaatgtccctcttcat	2221
Db	2194	lcccggttaccgtltgatacatacttcttcgcyggttgatagagccggtcaatgtccctcttcat	2253
QY	2222	gaacgtcgtccctggaatttaccatggctgtgtatgatacaaggacatctgtatataagaaga	2281
Db	2254	gaacgtcgtccctggaatttaccatcagttgcctgtgtatcaacaaggacatctgtatataagaaga	2313
QY	2282	ggcaacgctctgaaagaagacacatgtagatactgagcccttgagacacagacatactcgttttag	2341
Db	2314	ggcaacgctctgaaagaagacacatgtagatactgagcccttgagacacagacatactcgttttag	2373
QY	2342	ctggttcaatagatagcctcaattccctctctctgtgagcgcttgccgtgagtgatcatccct	2401
Db	2374	ctggttcaatagatagcctcaattccctctctctgtgtgagcgcgctgacagtgatcatccct	2433
QY	2402	ggaagttaagaaacctgtcgtccctacacagtatcccaagcgtgtgttctgtctctgttcgct	2461
Db	2434	ggaagttaagaaacctgtcgtccctacacagtatcccaagcgtgtgttctgtctctgttcgct	2493
QY	2462	gtttgcctgtgtgatacaactcctgcagatgcttccctgatactgacaacctctctccaaagacaa	2521
Db	2494	gtttgcctgtgtgatacaactcctgcagatgcttccctgatactgacaacctctctccaaagacaa	2553
QY	2522	cctgcgaacgaacgtgtggyggacatactactcaacgcgtgataccgcgcctacagctcctgtg	2581
Db	2554	cctgcgaacgaacgtgtggyggacatactactcaacgcgtgataccgcgcctacagctcctgtg	2613
QY	2582	tgtgtgatacgcaggaactcgttgggtctacacatccaaagatccttcgtatacctgcgtctctcc	2641
Db	2614	tgtgtgatacgcaggaactcgttgggtctacacatccaaagatccttcgtatacctgcgtctctcc	2673
QY	2642	tggtggttttgggttttgctgtgtgagtaacttggcccttttctggagagcagggcatttggagt	2701
Db	2674	tggtggttttgggttttgctgtgtgagtaacttggcccttttctggagagcagggcatttggagt	2733
QY	2702	gcagttgagacaacccgtttttagagatccctgttggagagatagtgcttcaatccacagatcttc	2761
Db	2734	gcagttgagacaacccgtttttagagatccctgttggagagatagtgcttcaatccacagatcttc	2793
QY	2762	gactccatagatgcgttttggacaccttccctctctatctgggtgtgatacgaacctgtgataatgagcc	2821
Db	2794	gactccatagatgcgttttggacaccttccctctctatctgggtgtgatacgaacctgtgataatgagcc	2853
QY	2822	tgtcttcccaagcccgatacgaagaattcccaagccctggatatttctctgtgaccaagatcccta	2881
Db	2854	tgtcttcccaagcccgatacgaagaattcccaagccctggatatttctctgtgaccaagatcccta	2913
QY	2882	ctggttttggcggagaaagtgtatggagaagaagccacccgtgttcccaacccagaagaagatgttc	2941
Db	2914	ctggttttggcggagaaagtgtatggagaagaagccacccgtgttcccaacccagaagaagatgttc	2973
QY	2942	agaacatctcatagagagggagaaccacacacatttgaagctgttggcggtgtcatatcagaacct	3001

Db	2974	agaatcttcgacgagaggaacccacccttgaagcttggggtgttccattccagaact	3033
QY	3002	ggttaaaagttctaacgagatctgggataaaggttggtctgtcatgtgccttggacattgaatttca	3061
Db	3034	ggttaaaagttctaacgagatctgggataaaggttggtctgtcatgtgccttggacattgaatttca	3093
QY	3062	ttgggagccagatcaactctctcttctgggacaaatggggcggggaaagaaagacaacattgtc	3121
Db	3094	ttgggagccagatcaactctctcttctgggacaaatggggcggggaaagaaagacaacattgtc	3153
QY	3122	aatctcgacccgggtgtgttctcccccgaacctctggggacccgcttcatatcttggagaaagacat	3181
Db	3154	aatctcgacccgggtgtgttctcccccgaacctctggggacccgcttcatatcttggagaaagacat	3213
QY	3182	ttgcctctggagatgagacacatctccgacgaaccttgggggttctgtgtccccaataaagtgct	3241
Db	3214	ttgcctctggagatgagacacatctccgacgaaccttgggggttctgtgtccccaataaagtgct	3273
QY	3242	gtttgacatctgtacatctgtctcgaagaagacaacatctgtttctatggcccgctttgaagggcttc	3301
Db	3274	gtttgacatctgtacatctgtctcgaagaagacaacatctgtttctatggcccgctttgaagggcttc	3333
QY	3302	ttggagagccggtggaagcgggagatctgggacagatctggcccggtatgtgtgttctgtccataag	3361
Db	3334	ttggagagccggtggaagcgggagatctgggacagatctggcccggtatgtgtgttctgtccataag	3393
QY	3362	caagctgaaagacaacaacaagaccagctgtctcaagttggaatctgacagaaagaaatctctgtgc	3421
Db	3394	caagctgaaagacaacaacaagaccagctgtctcaagttggaatctgacagaaagaaatctctgtgc	3453
QY	3422	ctttgaccttgtctgggggatacttaaggtttcatcttctggatgaaaccaacagctgtgtgtga	3481
Db	3454	ctttgaccttgtctgggggatacttaaggtttcatcttctggatgaaaccaacagctgtgtgtga	3513
QY	3482	cccttaactcccgacggggaatatgttgagctgcctgcctgaaatactccacaagccgcagacat	3541
Db	3514	cccttaactcccgacggggaatatgttgagctgcctgcctgaaatactccacaagccgcagacat	3573
QY	3542	tattctctctacaacaacaacatctgaaatggaagcgtctccctgggggacaagattgcacatct	3601
Db	3574	tattctctctacaacaacaacatctgaaatggaagcgtctccctgggggacaagattgcacatct	3633
QY	3602	ctcccaatgggaagctctgtgcgttgttggggtctctccctgtttctgaaagacacagctgggaac	3661
Db	3634	ctcccaatgggaagctctgtgcgttgttggggtctctccctgtttctgaaagacacagctgggaac	3693
QY	3662	aggctactacacttgacacttggttcacaagaagaatgtggaatctctccctcagattctctcaga	3721
Db	3694	aggctactacacttgacacttggttcacaagaagaatgtggaatctctccctcagattctctcaga	3753
QY	3722	caggtgtgtagcactgtgtctcatacttgaaaaagagagacagtgttctcagagcagttctga	3781
Db	3754	caggtgtgtagcactgtgtctcatacttgaaaaagagagacagtgttctcagagcagttctga	3813
QY	3782	ttgttgcccttggcgacgacacatgaaggttaacagctctgacacatctgaatgtctctgtatctc	3841
Db	3814	ttgttgcccttggcgacgacacatgaaggttaacagctctgacacatctgaatgtctctgtatctc	3873
QY	3842	caacctcatcaggaagcattgtctctgaagccgggtctgttgaagaacataagagcttagct	3901
Db	3874	caacctcatcaggaagcattgtctctgaagccgggtctgttgaagaacataagagcttagct	3933
QY	3902	gacctatgtctgcacatatgaagaactctgaaggagagaccttttgaacctctttcatga	3961
Db	3934	gacctatgtctgcacatatgaagaactctgaaggagagaccttttgaacctctttcatga	3993
QY	3962	gattgatgacccggtctcacaagaccttggcatttctcagttatgtgcatctccaagagccacct	4021
Db	3994	gattgatgacccggtctcacaagaccttggcatttctcagttatgtgcatctccaagagccacct	4053
QY	4022	ggaagaatttctctcaaggttggccggaagaggttggtgtgatatctcagaacctcaatgg	4081

QY 5162 tagccatattgtaattactgctttaaattcatatccctgaattcctacaaagcaagctcttc 5221
DB 5194 taagcatattgtaattactgctttaaattcatatccctgaattcctacaaagcaagctcttc 5253
QY 5222 aagagtggtctctgattacacacatcaatgagatgtctcttgatcatctgtgcatctcttc 5281
DB 5254 aagagtggtctctgattacacacatcaatgagatgtctcttgatcatctgtgcatctcttc 5313
QY 5282 aatgtccctctgtcccaagcagctttgtctgtaattcctgtatccagagcgaggtcagcaaacg 5341
DB 5314 aatgtccctctgtcccaagcagctttgtctgtaattcctgtatccagagcgaggtcagcaaacg 5373
QY 5342 aaaaaccccgaggttatcaatgagagtgagagctgtcatctactgtgtctcttaattttt 5401
DB 5374 aaaaaccccgaggttatcaatgagagtgagagctgtcatctactgtgtctcttaattttt 5433
QY 5402 ctggagatattgtaattactgcttgcctccagacatgtgcatattatcatctgtct 5461
DB 5434 ctggagatattgtaattactgcttgcctccagacatgtgcatattatcatctgtct 5493
QY 5462 ccagcaagaagtcctatgtgtctcccaacatctgctgtgtagccctctacttctgtct 5521
DB 5494 ccagcaagaagtcctatgtgtctcccaacatctgctgtgtagccctctacttctgtct 5553
QY 5522 gtaagtggtgtgtaattacacacatctctatgtacccagctctcttggtttaaagatcccgag 5581
DB 5554 gtaagtggtgtgtaattacacacatctctatgtacccagctctcttggtttaaagatcccgag 5613
QY 5582 caaagcctatgtgtgtctcaacacagcttgaaacctctcatctgtcaatattgtagcggtgag 5641
DB 5614 caaagcctatgtgtgtctcaacacagcttgaaacctctcatctgtcaatattgtagcggtgag 5673
QY 5642 caaccttggtgtgagactgtttacacgaataaagctgtaataatataatagatatctctga 5701
DB 5674 caaccttggtgtgagactgtttacacgaataaagctgtaataatataatagatatctctga 5733
QY 5702 gtccggtctctgtatctctccacatcttgcctgtagcagagagctcatcgatgtgtga 5761
DB 5734 gtccggtctctgtatctctccacatcttgcctgtagcagagagctcatcgatgtgtga 5793
QY 5762 aaacacagcaatgtgctgtacgtccctgaaaggtttgtaggaatcgtctgtacacatt 5821
DB 5794 aaacacagcaatgtgctgtacgtccctgaaaggtttgtaggaatcgtctgtacacatt 5853
QY 5822 atcttgagactgtgtgtagcagaaactctctgcacatgtgcgtgtaggaaggtgtgtctct 5881
DB 5854 atcttgagactgtgtgtagcagaaactctctgcacatgtgcgtgtaggaaggtgtgtctct 5913
QY 5882 cctcatattactgtctgtatccagatcctcatctcatcagccacagcctgtlaaatgcaaa 5941
DB 5914 cctcatattactgtctgtatccagatcctcatctcatcagccacagcctgtlaaatgcaaa 5973
QY 5942 gctatctcctctgtaatgtatgaagaatgtgtagcgaggaagaaagacagaaattctctga 6001
DB 5974 gctatctcctctgtaatgtatgaagaatgtgtagcgaggaagaaagacagaaattctctga 6033
QY 6002 tggtagagagcagaatgacatcttaagaatacaagaggttgtagcaaaatataatagaagaa 6061
DB 6034 tggtagagagcagaatgacatcttaagaatacaagaggttgtagcaaaatataatagaagaa 6093
QY 6062 gcggaagcctgtctgtgacagagattgtgtagcattccctcctgtaggtgtgtgtgtgt 6121
DB 6094 gcggaagcctgtctgtgacagagattgtgtagcattccctcctgtaggtgtgtgtgtgtgt 6153
QY 6122 cctgtagagatlaatgtgagctgtgaaataatcaacttccaagaatgttaacagagataccac 6181
DB 6154 cctgtagagatlaatgtgagctgtgaaataatcaacttccaagaatgttaacagagataccac 6213
QY 6182 ttttaacagagagatgtctctcttaacaaaatagatatcttaacaaatcaataaagt 6241
DB 6214 ttttaacagagagatgtctctcttaacaaaatagatatcttaacaaatcaataaagt 6273

QY 6242 aatcagaacatggtgctactgtccctcagtttgatgtccatcaacagagctgtgtagtgag 6301
DB 6274 aatcagaacatggtgctactgtccctcagtttgatgtccatcaacagagctgtgtagtgag 6333
QY 6302 agaaacgtgtgagttcttgcctcttgtagagaggtcccaagagaagaagttgcaaggt 6361
DB 6334 agaaacgtgtgagttcttgcctcttgtagagaggtcccaagagaagaagttgcaaggt 6393
QY 6362 tggtagagagcaggttccggaacgtggtgtgtagatgtgtaggaataaataatgtgttaa 6421
DB 6394 tggtagagagcaggttccggaacgtggtgtgtagatgtgtaggaataaataatgtgttaa 6453
QY 6422 ctatagtgtaggcaacaaacgaagctctctacagcagatgtgtcttgatcgtgagcctcc 6481
DB 6454 ctatagtgtaggcaacaaacgaagctctctacagcagatgtgtcttgatcgtgagcctcc 6513
QY 6482 tgtgtgttcttgtagtaaaccccaacagagcatgtatcccaaaagccggtgtctgtg 6541
DB 6514 tgtgtgttcttgtagtaaaccccaacagagcatgtatcccaaaagccggtgtctgtg 6573
QY 6542 gaattgtcccttaagtgtgttcaagagagagatcaagtagtgtttatcatctcaatgat 6601
DB 6574 gaattgtcccttaagtgtgttcaagagagagatcaagtagtgtttatcatctcaatgat 6633
QY 6602 ggaagaaatgtgaagctcttgcacttagatgtgcaatcatgtatcaatgtgaaggtlcaaggtg 6661
DB 6634 ggaagaaatgtgaagctcttgcacttagatgtgcaatcatgtatcaatgtgaaggtlcaaggtg 6693
QY 6662 ccttgtagctgtccagcatcttaaaaaataggtttgtagagatgtgtatacatagtttagt 6721
DB 6694 ccttgtagctgtgtccagcatcttaaaaaataggtttgtagagatgtgtatacatagtttagt 6753
QY 6722 aatagcaaggtgtccaaacccgagcctgtgaagctgtgtccagagttcttgtagactgtatcc 6781
DB 6754 aatagcaaggtgtccaaacccgagcctgtgaagctgtgtccagagttcttgtagactgtatcc 6813
QY 6782 tggagagtttcttaaaagaaacacacggaacatgtctaaatataacagcttccatctcat 6841
DB 6814 tggagagtttcttaaaagaaacacacggaacatgtctaaatataacagcttccatctcat 6873
QY 6842 atcttctctgtccagagatattcagatctctctccagagcaaaagagactccacataga 6901
DB 6874 atcttctctgtccagagatattcagatctctctccagagcaaaagagactccacataga 6933
QY 6902 agactacactgttctctcagacaacactgtgacaagattttgtgaacttgcgaagagaca 6961
DB 6934 agactacactgttctctcagacaacactgtgacaagattttgtgaacttgcgaagagaca 6993
QY 6962 aagtgtatgtgacacacttaaaagacctctcatltaacaaaaacagacagtagtggagct 7021
DB 6994 aagtgtatgtgacacacttaaaagacctctcatltaacaaaaacagacagtagtggagct 7053
QY 7022 tgcagttctcaacatcttcttcaacagatgagagatgtgaagaagaatctatgtatagaagt 7081
DB 7054 tgcagttctcaacatcttcttcaacagatgagagatgtgaagaagaatctatgtatagaagt 7113
QY 7082 cctgttcaatagcgggtgtgtgtgaagtaaaaggaactgagacttcccttgacacatgtga 7141
DB 7114 cctgttcaatagcgggtgtgtgtgaagtaaaaggaactgagacttcccttgacacatgtga 7173
QY 7142 agtgtgtgtgagaaagaagccagaagttgtatgtgtaggaagtaaaactgtgactgtact 7201
DB 7174 agtgtgtgtgagaaagaagccagaagttgtatgtgtaggaagtaaaactgtgactgtact 7233
QY 7202 gatactattcaatgtcaatgtcaattcaatgtcaatgtgaataaataatctcatcaagggag 7261
DB 7234 gatactattcaatgtcaatgtcaattcaatgtcaatgtgaataaataatctcatcaagggag 7293
QY 7262 tgcctttagcctatgtctgtgtatagcgtctcaagtgaagaagctgtgaatttagttttta 7321
DB 7294 tgcctttagcctatgtctgtgtatagcgtctcaagtgaagaagctgtgaatttagttttta 7353
QY 7322 cctatacctatgtgaaactctatltgaaacccaatgtgacalattgtgttgaactcacac 7381

[illegible]


```
Db 248 tgccttcacaggtcccgagccacacgctgggggtgctgctgaggaatggttgc 307
QY 301 ggcctcagctgaggtgctgctgtggaagaacctcattcagaagaagacacatg 360
Db 308 ggcctcagctgaggtgctgctgtggaagaacctcattcagaagaagacacatg 367
QY 361 agctgtactggaagtgctgctgcttatttcttcctgacccctgctgctgcgc 420
Db 368 agctgtactggaagtgctgctgcttatttcttcctgacccctgctgctgcgc 427
QY 421 tgaagtaaccacotatgaacaacatgatgacatttcccaataaagccatcctc 480
Db 428 tgaagtaaccacotatgaacaacatgatgacatttcccaataaagccatcctc 487
QY 481 caggaaactcctctgtgttcagaggatattcgttaatgcacaacccctgttcc 540
Db 488 caggaaactcctctgtgttcagaggatattcgttaatgcacaacccctgttcc 547
QY 541 acccgatcctgggagagctcccgaggtgttggaacttaacatcatctgtgc 600
Db 548 acccgatcctgggagagctcccgaggtgttggaacttaacatcatctgtgc 607
QY 601 ggcctgtctcagatgctcggaggtcttcttatacagcagaagaacacagatga 660
Db 608 ggcctgtctcagatgctcggaggtcttcttatacagcagaagaacacagatga 667
QY 661 acatgcgcaaatgtctgagaaacttccagagatcagaatccagatcaacttga 720
Db 668 acatgcgcaaatgtctgagaaacttccagagatcagaatccagatcaacttga 727
QY 721 ttaagaatttcctggtggaacaatgaaacctctgtgttccatatacaacctct 780
Db 728 ttaagaatttcctggtggaacaatgaaacctctgtgttccatatacaacctct 787
QY 781 tcccaaggtctactgtggaacaagtctgaaggctgaatctcctcacaagtatt 840
Db 788 tcccaaggtctactgtggaacaagtctgaaggctgaatctcctcacaagtatt 847
QY 841 tggcaaggtccagattacatttgacaagtctgtgcaatgatcaataatagaaga 900
Db 848 tggcaaggtccagattacatttgacaagtctgtgcaatgatcaataatagaaga 907
QY 901 ttaacttggtggaacaagaatttctgaagctgtggtcctcacaagaaggaaact 960
Db 908 ttaacttggtggaacaagaatttctgaagctgtggtcctcacaagaaggaaact 967
QY 961 cagcagagcagagctactgttccacatgacatccttgaaagccaatccctga 1020
Db 968 cagcagagcagagctactgttccacatgacatccttgaaagccaatccctga 1027
QY 1021 actataatcccttcctcagcagaaggagctgtgaagccaacaacattgtgca 1080
Db 1028 actataatcccttcctcagcagaaggagctgtgaagccaacaacattgtgca 1087
QY 1081 gttcttgagctcggcccgaggagctgttcaagcatgagaagctggtgcaatg 1140
Db 1088 gttcttgagctcggcccgaggagctgttcaagcatgagaagctggtgcaatg 1147
QY 1141 agctgaatgttctgacaaatgttaacagctccagctccccaacccaactccag 1200
Db 1148 agctgaatgttctgacaaatgttaacagctccagctccccaacccaactccag 1207
QY 1201 tgtctgatatgtctgagggcatcccgaggagggggtctgaagatcaagtctca 1260
Db 1208 tgtctgatatgtctgagggcatcccgaggagggggtctgaagatcaagtctca 1267
QY 1261 ggtataggaacaacaactcaaacgcttcttgaggagcaatgacatgaggaatg 1320
Db 1268 ggtataggaacaacaactcaaacgcttcttgaggagcaatgacatgaggaatg 1327
QY 1321 aaacttcatgacaactcaactccttactgcatatttgatgaagattggagt 1380
Db 1328 aaacttcatgacaactccttactgcatatttgatgaagattggagt 1387
QY 1381 ctatgctctcttcccgacatctctggaagctcgaagcgtctgctgttggaaga 1440
Db 1388 ctatgctctcttcccgacatctctggaagctcgaagcgtctgctgttggaaga 1447
QY 1441 tgtataacctggaacatccagcaagaagcagtgatgctggaagtgaacaagctcc 1500
Db 1448 tgtataacctggaacatccagcaagaagcagtgatgctggaagtgaacaagctcc 1507
QY 1501 aggaactgctgtgttccatgatctggaagcagtggaaggaactcaagcccaag 1560
Db 1508 aggaactgctgtgttccatgatctggaagcagtggaaggaactcaagcccaag 1567
QY 1561 ggaacttcatgagaacaagcagaagaatggaactgttccgaatgctgtgagcag 1620
Db 1568 ggaacttcatgagaacaagcagaagaatggaactgttccgaatgctgtgagcag 1627
QY 1621 acaatgacacatttgggaacaagcagtggaatggaatggaacccaagaatcg 1680
Db 1628 acaatgacacatttgggaacaagcagtggaatggaatggaacccaagaatcg 1687
QY 1681 tggcgttttggccaagcaccagagatgctcagatccaatgaatgctgtgtacac 1740
Db 1688 tggcgttttggccaagcaccagagatgctcagatccaatgaatgctgtgtacac 1747
QY 1741 ggaaggaagcttcaacagagactaacccagcgaatccggaactctcgctcatg 1800
Db 1748 ggaaggaagcttcaacagagactaacccagcgaatccggaactctcgctcatg 1807
QY 1801 gttcaacctgaacaagctagaacccatagacaagaagctgtgctatcaacaagtc 1860
Db 1808 gttcaacctgaacaagctagaacccatagacaagaagctgtgctatcaacaagtc 1867
QY 1861 tggagctgctgagatgagaagaagctctgagctgtgtatgtgtcaactggaatt 1920
Db 1868 tggagctgctgagatgagaagaagctctgagctgtgtatgtgtcaactggaatt 1927
QY 1921 gcaagattgagctgccccatcatgtcaagtaacagatccgaatggaattggaat 1980
Db 1928 gcaagattgagctgccccatcatgtcaagtaacagatccgaatggaattggaat 1987
QY 1981 agaggaacaataaatacaagaatggtgactggaagccctgtctcgaagctggaac 2040
Db 1988 agaggaacaataaatacaagaatggtgactggaagccctgtctcgaagctggaac 2047
QY 2041 aggaatgcggttaagctcggggggggtcctgcctcttgaggaatggtggaagc 2100
Db 2048 aggaatgcggttaagctcggggggggtcctgcctcttgaggaatggtggaagc 2107
QY 2101 tcatcaggtgtctgacggcccgagagaagaatactgtgtctatatacgacaagat 2160
Db 2108 tcatcaggtgtctgacggcccgagagaagaatactgtgtctatatacgacaagat 2167
QY 2161 atccctgttaagttgatagacatcttctgoggtgtgataagccggttaatgcct 2220
Db 2168 atccctgttaagttgatagacatcttctgoggtgtgataagccggttaatgcct 2227
QY 2221 tgaagctgctggtattacatcagtggtgtgatacacaaggagcatgtgtataga 2280
Db 2228 tgaagctgctggtattacatcagtggtgtgatacacaaggagcatgtgtataga 2287
QY 2281 agcagcgtctgaagaagacatgagatcatalggtgctggaacaacagatctgt 2340
Db 2288 agcagcgtctgaagaagacatgagatcatalggtgctggaacaacagatctgt 2347
QY 2341 gctgttcatatagtagcctaatctcttctgtgagcgtcgtgcgtgtagtgcac 2400
Db 2348 gctgttcatatagtagcctaatctcttctgtgagcgtcgtgcgtgtagtgcac 2407
QY 2401 tgaagttaggaacctgctgcctacagtgatcccaagcgtggtgtgtctctccg 2460
Db 2408 tgaagttaggaacctgctgcctacagtgatcccaagcgtggtgtgtctctccg 2467
```


QY 2461 tfttttctgttgcagacatctgcagtgcttcttgattagacacattctctccagagcca 2520
| | | | |
Db 2468 tgtttgtctgttgagaaatccgcagtgcttccgtattagacacattcttccaaagcca 2527
| | | | |
QY 2521 acctggcaagacgctgttgaggacatcatctacttcacgcttgtaacctgcctcactgtct 2580
| | | | |
Db 2528 acctggcagacgctgttgaggacatcatctacttcacgcttgtaacctgcctcactgtct 2587
| | | | |
QY 2581 gttgtgcatgagcagacatctgtggcttcaactcaagatcttgcctgaacctgtctc 2640
| | | | |
Db 2588 gttgtgcatgagcagacatctgtggcttcaactcaagatcttgcctgaacctgtctc 2647
| | | | |
QY 2641 ctgtgcttctgtgttgcctgtgagtaacttgccttcttgagagcaggagcatggag 2700
| | | | |
Db 2648 ctgtgcttctgtgttgcctgtgagtaacttgccttcttgagagcaggagcatggag 2707
| | | | |
QY 2701 tgcagtgaggacaacactgttttgagagctctgttgagagaaatggtctcaatctcaacct 2760
| | | | |
Db 2708 tgcagtgaggacaacactgttttgagagctctgttgagagaaatggtctcaatctcaacct 2767
| | | | |
QY 2761 cgaatccatgatgctgttttgacaaccttccctataggggtgatgacctgtatcatggag 2820
| | | | |
Db 2768 cggctcccatgagctgttttgacaaccttccctataggggtgatgacctgtatcatggag 2827
| | | | |
QY 2821 ctgtcttccagagcagatcaggaatcccaaggcctgtgatttctcttgacacaaagctct 2880
| | | | |
Db 2828 ctgtcttccagagcagatcaggaatcccaaggcctgtgatttctcttgacacaaagctct 2887
| | | | |
QY 2881 actggtttggcagagaaatgtatgagaaagacacacctgtgttccaaaccgaaagaaatgt 2940
| | | | |
Db 2888 actggtttggcagagaaatgtatgagaaagacacacctgtgttccaaaccgaaagaaatgt 2947
| | | | |
QY 2941 cagaatctgcatagagagagagaaacacacaccttgaaagctgtgcgttccattcagaacc 3000
| | | | |
Db 2948 cagaatctgcatagagagagagaaacacacaccttgaaagctgtgcgttccattcagaacc 3007
| | | | |
QY 3001 tggtaaaagctcaccagatagagatgaaagctgtctgcatgagcctgcagcatgaatttct 3060
| | | | |
Db 3008 tggtaaaagctcaccagatagagatgaaagctgtctgcatgagcctgcagcatgaatttct 3067
| | | | |
QY 3061 atgagggccagatcacctctctcttgggccacaatgagcggaggagaaagacacacatgt 3120
| | | | |
Db 3068 atgagggccagatcacctctctcttgggccacaatgagcggaggagaaagacacacatgt 3127
| | | | |
QY 3121 caatcctgacgggtgtgttcccccgacctcgggacacgctcactacatctggggaaagaca 3180
| | | | |
Db 3128 caatcctgacgggtgtgttcccccgacctcgggacacgctcactacatctggggaaagaca 3187
| | | | |
QY 3181 ttcgctctgagatgagacacatccgcagaaacttgggggtctgttcccaagcataacgtgc 3240
| | | | |
Db 3188 ttcgctctgagatgagacacatccgcagaaacttgggggtctgttcccaagcataacgtgc 3247
| | | | |
QY 3241 tgtttgacatgctgactgttcgaagaacacatctgtgttctatgcccgccttgaaaggctct 3300
| | | | |
Db 3248 tgtttgacatgctgactgttcgaagaacacatctgtgttctatgcccgccttgaaaggctct 3307
| | | | |
QY 3301 ctgagaaagcgtgagagcgagagatgagagagatgagcctcgagatgttgttttgcataa 3360
| | | | |
Db 3308 ctgagaaagcgtgagagcgagagatgagagagatgagcctcgagatgttgttttgcataa 3367
| | | | |
QY 3361 gcaagcgtgaaagcaaaacacagcagctgtcaggtgaaatgcagagaaatctctctgtg 3420
| | | | |
Db 3368 gcaagcgtgaaagcaaaacacagcagctgtcaggtgaaatgcagagaaatctctctgtg 3427
| | | | |
QY 3421 ccttgacctgttgcgggagatctaaagttgtcatcttgatgaacacacacagctgtgtg 3480
| | | | |
Db 3428 ccttgacctgttgcgggagatctaaagttgtcatcttgatgaacacacacagctgtgtg 3487
| | | | |
QY 3481 accttactcccgagagagagatgtgagctgtctgaaataccgacaaagcgccagaca 3540
| | | | |
Db 3488 accttactcccgagagagagatgtgagctgtctgaaataccgacaaagcgccagaca 3547
| | | | |

QY 3541 ttattctctacacacacacatggatgaagcgagctgtcttgaggagagatggcatca 3600
| | | | |
Db 3548 ttattctctacacacacacatggatgaagcgagctgtcttgaggagagatggcatca 3607
| | | | |
QY 3601 tctcccatggagagctgtgtctgtgtggcttccctcgttcttgaaagacacagctggaa 3660
| | | | |
Db 3608 tctcccatggagagctgtgtctgtgtggcttccctcgttcttgaaagacacagctggaa 3667
| | | | |
QY 3661 caggtctactacatgacctgtgttcaagaaagatgtgaaatcttccctcaatctccagaa 3720
| | | | |
Db 3668 caggtctactacatgacctgtgttcaagaaagatgtgaaatcttccctcaatctccagaa 3727
| | | | |
QY 3721 acagtagtagacatgtgtcatactgaaagaaagagagacagtgcttctcaagagcagttctg 3780
| | | | |
Db 3728 acagtagtagacatgtgtcatactgaaagaaagagagacagtgcttctcaagagcagttctg 3787
| | | | |
QY 3781 atgtgccttgaggacagacacatgagatgacagctgacacatcatgtctctcatct 3840
| | | | |
Db 3788 atgtgccttgaggacagacacatgagatgacagctgacacatcatgtctctcatct 3847
| | | | |
QY 3841 ccaactcatcaggaagacatgtcttgagagccggctgttgagagacaataggcatagc 3900
| | | | |
Db 3848 ccaactcatcaggaagacatgtcttgagagccggctgttgagagacaataggcatagc 3907
| | | | |
QY 3901 tgaactatgtctgcacatgaaagctgtcctaaagagagacacctgttgagaccttcatag 3960
| | | | |
Db 3908 tgaactatgtctgcacatgaaagctgtcctaaagagagacacctgttgagaccttcatag 3967
| | | | |
QY 3961 agatgtatgacggctctccagacctgggcatcttctagtatagatccatccaaagcagacc 4020
| | | | |
Db 3968 agatgtatgacggctctccagacctgggcatcttctagtatagatccatccaaagcagacc 4027
| | | | |
QY 4021 tggagaaatattctctcaagtggtgcgaagagatgagggtgagatgactagacacctcagatg 4080
| | | | |
Db 4028 tggagaaatattctctcaagtggtgcgaagagatgagggtgagatgactagacacctcagatg 4087
| | | | |
QY 4081 gtaaccttgccagaaagacaaacagcgcccttcggggagacagacagactgtcttcgcc 4140
| | | | |
Db 4088 gtaaccttgccagaaagacaaacagcgcccttcggggagacagacagactgtcttcgcc 4147
| | | | |
QY 4141 cgttaccagaaagatgactgtctgtatccaaatgattctgcataatgacacacaaatccagag 4200
| | | | |
Db 4148 cgttaccagaaagatgactgtctgtatccaaatgattctgcataatgacacacaaatccagag 4207
| | | | |
QY 4201 agacagactgtctcagtgatgagatggcgaagggctctaccaggttgaaagctgtgaaac 4260
| | | | |
Db 4208 agacagactgtctcagtgatgagatggcgaagggctctaccaggttgaaagctgtgaaac 4267
| | | | |
QY 4261 ttacacagcaacagttgtgtgaccttctgtgaaagacatgtaattgtccagacggagtc 4320
| | | | |
Db 4268 ttacacagcaacagttgtgtgaccttctgtgaaagacatgtaattgtccagacggagtc 4327
| | | | |
QY 4321 ggaagagatcttctcagatgtctgtccagcgtgttctgtctgcatctgccttgcct 4380
| | | | |
Db 4328 ggaagagatcttctcagatgtctgtccagcgtgttctgtctgcatctgccttgcct 4387
| | | | |
QY 4381 tcaagcttgatgtgcacaccttggcagaatgacacagcctgtgaacttcaagccttgatgt 4440
| | | | |
Db 4388 tcaagcttgatgtgcacaccttggcagaatgacacagcctgtgaacttcaagccttgatgt 4447
| | | | |
QY 4441 acaaagcaagatgacatctgtcagaatgagatgctctgagagacaaggaaccttgagac 4500
| | | | |
Db 4448 acaaagcaagatgacatctgtcagaatgagatgctctgagagacaaggaaccttgagac 4507
| | | | |
QY 4501 tcttaagcctctaccaaagacctgtcttgaggacccgctgtatggaagaaacccaa 4560
| | | | |
Db 4508 tcttaagcctctaccaaagacctgtcttgaggacccgctgtatggaagaaacccaa 4567
| | | | |
QY 4561 tcccaagacagcccttgccagagagagaaatggaacacatgcccacagcttcccca 4620
| | | | |
Db 4568 tcccaagacagcccttgccagagagagaaatggaacacatgcccacagcttcccca 4627
| | | | |
QY 4621 ccatatggaactcttccagaaatgggaactggaacatgcaagaaccttaccatgacgc 4680
| | | | |

Db 4628 ccaaccaagccctctcccaagaatggaacatgagcaatgacgaacccctccacgcatgccc 4687
Qy 4681 agtgaagcagcagaataatcaagaagatgctgctgtgtgtcccccaggcgagggggc 4740
Db 4688 agtgaagcagcagaataatcaagaagatgctgctgtgtgtcccccaggcgagggggc 4747
Qy 4741 tgcctctcccaagaagaacaaacacatgacagatccctccagacctgacagaagaa 4800
Db 4748 tgcctctcccaagaagaacaaacacatgacagatccctccagacctgacagaagaa 4807
Qy 4801 acattcgagatctgtgtaagaacatgtaagatgacatcagccaaaggttaaaaaa 4860
Db 4808 acattcgagatctgtgtaagaacatgtaagatgacatcagccaaaggttaaaaaa 4867
Qy 4861 agatctgtgtaagatgattagatgagcggttccctgggtgtcaatataactaa 4920
Db 4868 agatctgtgtaagatgattagatgagcggttccctgggtgtcaatataactaa 4927
Qy 4921 cactctccgagtcagaagatgataatgacatccaaacaaatgaaagaaacactaaagc 4980
Db 4928 cactctccgagtcagaagatgataatgacatccaaacaaatgaaagaaacactaaagc 4987
Qy 4981 tggcacaagacagttctgcagatcagatcttccacagcgttgggaagatatacagagc 5040
Db 4988 tggcacaagacagttctgcagatcagatcttccacagcgttgggaagatatacagagc 5047
Qy 5041 tggacaccagaataatgataagtggtgtcaatacaagagcgctgacatgcaatagct 5100
Db 5048 tggacaccagaataatgataagtggtgtcaatacaagagcgctgacatgcaatagct 5107
Qy 5101 cttctctgaatgtcatcaacaatgacatctccgggcacacgtccaaagggagagaaac 5160
Db 5108 cttctctgaatgtcatcaacaatgacatctccgggcacacgtccaaagggagagaaac 5167
Qy 5161 ctgagccattatggaatgactgcttcaatcatcccttgaaatccacaaagcagagctct 5220
Db 5168 ctgagccattatggaatgactgcttcaatcatcccttgaaatccacaaagcagagctct 5227
Qy 5221 cagaggtgctctgataagacacatcagtgatgtctgtgtccatctgtatcttgg 5280
Db 5228 cagaggtgctctgataagacacatcagtgatgtctgtgtccatctgtatcttgg 5287
Qy 5281 caatgtctctgtccacagcagcttgcgtatctccctgacccaagagcggttcagaa 5340
Db 5288 caatgtctctgtccacagcagcttgcgtatctccctgacccaagagcggttcagaa 5347
Qy 5341 caaaacacgtgacgttcatcagtgaggtgaagcgtgtcatctactgctctcaatttg 5400
Db 5348 caaaacacgtgacgttcatcagtgaggtgaagcgtgtcatctactgctctcaatttg 5407
Qy 5401 tctgggataatgtaacatcagttgtccctgacacagctgtaactatcatctcatctgt 5460
Db 5408 tctgggataatgtaacatcagttgtccctgacacagctgtaactatcatctcatctgt 5467
Qy 5461 tccagcagaagctctatgtgtctccacaaatctgcctgtgtgtaagcctctactttgc 5520
Db 5468 tccagcagaagctctatgtgtctccacaaatctgcctgtgtgtaagcctctactttgc 5527
Qy 5521 tgratgtgtgtcaatcacacacctctatgtaccagcctcttgggttcaagaatccca 5580
Db 5528 tgratgtgtgtcaatcacacacctctatgtaccagcctcttgggttcaagaatccca 5587
Qy 5581 gcaacgcatatgtgtgtcaccacagcgtaacctctcaatggcaatgagcagcggtg 5640
Db 5588 gcaacgcatatgtgtgtcaccacagcgtaacctctcaatggcaatgagcagcggtg 5647
Qy 5641 caaccttgtgtgagcgctgacccagcaataaagctgataataatcaatgatactctga 5700
Db 5648 caaccttgtgtgagcgctgacccagcaataaagctgataataatcaatgatactctga 5707
Qy 5701 agtcgtgtctgtgactcccaatcttgcctgtgagcagagcgctcagcagcatggtga 5760
Db 5708 agtcgtgtctgtgactcccaatcttgcctgtgagcagagcgctcagcagcatggtga 5767
Qy 5761 aaaaacagcaatgctgataatgctcctgggaaggttgggggaatcagcttctgtacacat 5820
Db 5768 aaaaacagcaatgctgataatgctcctgggaaggttgggggaatcagcttctgtacacat 5827
Qy 5821 tatcttgagcttggctgggaacgaacccctctccagcagcgttgggaaggttggcttct 5880
Db 5828 tatcttgagcttggctgggaacgaacccctctccagcagcgttgggaaggttggcttct 5887
Qy 5881 tccatatactgttctgtccagatcagatctctcaatagccacagaccttcaatcaaa 5940
Db 5888 tccatatactgttctgtccagatcagatctctcaatagccacagaccttcaatcaaa 5947
Qy 5941 agcatctcctctgaatgagaagaatgagaatgagaatgagaatgagaatgagaatctctg 6000
Db 5948 agcatctcctctgaatgagaagaatgagaatgagaatgagaatgagaatgagaatctctg 6007
Qy 6001 atgtgtgagggccagaaatgacatcttaagaatcaaggaatgacagaatataatagaaga 6060
Db 6008 atgtgtgagggccagaaatgacatcttaagaatcaaggaatgacagaatataatagaaga 6067
Qy 6061 agcgaagcctgctgtgtgacagatctgtggtgacatccctccctggtgaggtgcttggc 6120
Db 6068 agcgaagcctgctgtgtgacagatctgtggtgacatccctccctggtgaggtgcttggc 6127
Qy 6121 tccctggaggttaatgaggtggtggaataatcaacttcaagaatgtaacagagatacca 6180
Db 6128 tccctggaggttaatgaggtggtggaataatcaacttcaagaatgtaacagagatacca 6187
Qy 6181 ctgttaccagaggaatgcttcccttcaacaaatagatcttcaacaaatccatagaag 6240
Db 6188 ctgttaccagaggaatgcttcccttcaacaaatagatcttcaacaaatccatagaag 6247
Qy 6241 tacatcagaacaatggtgctactgctccctcaagtttgatgccaatcaacagagctgtgac 6300
Db 6248 tacatcagaacaatggtgctactgctccctcaagtttgatgccaatcaacagagctgtgac 6307
Qy 6301 gagaacacgtgagatgcttctcccttggagaggaatcccccaggaagaagtgtgcaag 6360
Db 6308 gagaacacgtgagatgcttctcccttggagaggaatcccccaggaagaagtgtgcaag 6367
Qy 6361 ttgtgtgagttggcgatcttcgaaacatggtgctgtgaagtatgagaagaataatgctgta 6420
Db 6368 ttgtgtgagttggcgatcttcgaaacatggtgctgtgaagtatgagaagaataatgctgta 6427
Qy 6421 actaatgtgagggacaaacaaagcgtctctcaagcagatgcttgaatcggtggcgtc 6480
Db 6428 actaatgtgagggacaaacaaagcgtctctcaagcagatgcttgaatcggtggcgtc 6487
Qy 6481 ctgtgtgttctctgatatcccaacacagcagatggtatcccaagcccggtgtctgt 6540
Db 6488 ctgtgtgttctctgatatcccaacacagcagatggtatcccaagcccggtgtctgt 6547
Qy 6541 ggaattgtgcccataagtggttgaagggagatcaagtagtgcttataatcatagta 6600
Db 6548 ggaattgtgcccataagtggttgaagggagatcaagtagtgcttataatcatagta 6607
Qy 6601 tggagaagtgtggaagccttgcacatgatatgaaatcagtgtaaatgagaagtccaagt 6660
Db 6608 tggagaagtgtggaagccttgcacatgatatgaaatcagtgtaaatgagaagtccaagt 6667
Qy 6661 gctctggcagtgctcagacatcaaaataaggttggagatggttatataatggtgtac 6720
Db 6668 gctctggcagtgctcagacatcaaaataaggttggagatggttatataatggtgtac 6727
Qy 6721 gaataagcaggttccaacccggaactggaagcctgtccaggaatctcttggactgtac 6780
Db 6728 gaataagcaggttccaacccggaactggaagcctgtccaggaatctcttggactgtac 6787
Qy 6781 ctggaagtgttcttaagaagaagaacacaggaacatgtaacataccagctcactcaat 6840
Db 6788 ctggaagtgttcttaagaagaagaacacaggaacatgtaacataccagctcactcaat 6847

QY	6841	tatcttcctgcccagagatatccagcatccctctcccaagacaaaagcgatccacaatag	6500
Db	6848	tatcttcctgcccagagatatccagcatccctctcccaagacaaaagcgatccacaatag	6507
QY	6901	aagcctactctgtttctcagcaacaaccttgcaccaagtattttgtgaactttggccaagacc	6560
Db	6908	aagcctactctgtttctcagcaacaaccttgcaccaagtattttgtgaactttggccaagacc	6567
QY	6961	aaagtgtgtatgacccacttaaaagacctctcatcaaaaaaacagacagtaatgtagcg	7020
Db	6968	aaagtgtgtatgacccacttaaaagacctctcatcaaaaaaacagacagatgtgtagcg	7027
QY	7021	ttgcagttctcacatctttcttaccagatgtgaaaagtgaaaagactatgtatgtaaagaa	7080
Db	7028	ttgcagttctcacatctttcttaccagatgtgaaaagtgaaaagactatgtatgtaaagaa	7087
QY	7081	tcctgttccatacggggtgtgctgtgaagtaaaagggaacttagactttccctttgcacatgtg	7140
Db	7088	tcctgttccatacggggtgtgctgtgaagtaaaagggaacttagactttccctttgcacatgtg	7147
QY	7141	aagctgtgtggaagaaagacccagaaagtgtgaagtgtggaagaaatgaatgtatctgtac	7200
Db	7148	aagctgtgtggaagaaagacccagaaagtgtgaagtgtggaagaaatgaatgtatctgtac	7207
QY	7201	tgatactatctcaatgtgcattgcattccatgtgcaatgtgaaaasaattccattacagggca	7260
Db	7208	tgatactatctcaatgtgcattgcattccatgtgcaatgtgaaaasaattccattacagggca	7267
QY	7261	gtgcctttgtagcctatgtcttgtatgctctcccaagtgtgaagacttgtattttttt	7320
Db	7268	gtgcctttgtagcctatgtcttgtatgctctcccaagtgtgaagacttgtattttttt	7327
QY	7321	accataacctatgtgaaacctctatcttggaacccaatgtgacatagtggtttgaaactcaaa	7380
Db	7328	accataacctatgtgaaacctctatcttggaacccaatgtgacatagtggtttgaaactcaaa	7387
QY	7381	ctttttttttttttgttctcgttgtatctccatctgtgggtgtgcacaaataatccaaag	7440
Db	7388	ctttttttttttttgttctcgttgtatctccatctgtgggtgtgcacaaataatccaaag	7447
QY	7441	taatcatgcccagagatattatgttccaataatccaaggatgatgcatactccattccactaa	7500
Db	7448	taatcatgcccagagatattatgttccaataatccaaggatgatgcatactccattccactaa	7507
QY	7501	gccatgcacatgcccaagagacgtgtttcccggtgtgacacatccatctgcgtgcgaatgaggt	7560
Db	7508	gccatgcacatgcccaagagacgtgtttcccggtgtgacacatccatctgcgtgcgaatgaggt	7567
QY	7561	gccagagttatagtgtccaaagttttccaagaatttgaagcacaatgtgtgtgcatagtctc	7620
Db	7568	gccagagttatagtgtccaaagttttccaagaatttgaagcacaatgtgtgtgcatagtctc	7627
QY	7621	acttttggaaagtgctgtcgtccagagtcataccaacatttgataatcgtttgaacgaagt	7680
Db	7628	acttttggaaagtgctgtcgtccagagtcataccaacatttgataatcgtttgaacgaagt	7687
QY	7681	gtgcacatcgtggtcctaaccctcgtcttgaatccctctgataagatgtttcgtgtgcagt	7740
Db	7688	gtgcacatcgtggtcctaaccctcgtcttgaatccctctgataagatgtttcgtgtgcagt	7747
QY	7741	aacatgtcaacaaaaatgttgggtgtctctcctagagcagggaaactgtgttccatgttatatt	7800
Db	7748	aacatgtcaacaaaaatgttgggtgtctctcctagagcagggaaactgtgttccatgttatatt	7807
QY	7801	gtcctaagtcttcgggcagatggtgttaagggtacatcccttatagactcttaataatactt	7860
Db	7808	gtcctaagtcttcgggcagatggtgtgttaagggtacatcccttatagactcttaataatactt	7867
QY	7861	agatctctgttaagagcacaagaatccaacagccaacatgctgtgggctgtcaagctgtctgaag	7920
Db	7868	agatctctgttaagagcacaagaatccaacagccaacatgctgtgggctgtcaagctgtctgaag	7927

QY	7921	ccaggcagatgggattaaagagattgctgtgcgtttcaaaccttagggagacctgtgcccattgt	7980
Db	7928	ccaggcagatgggattaaagagattgctgtgcgtttcaaaccttagggagacctgtgcccattgt	7987
QY	7991	ccctacgtctgcctaaatattgacactgtgatcccaagaattatctcgaacaagtgtat	8040
Db	7998	ccgtacgtctgcctaaacatggtacactgtgatcccaagaattatctcgaacaagtgtat	8047
QY	8041	tattctgtgcttttgatttaactctgaataactgaagaatgtaggtgttatttgacaaa	8100
Db	8048	tattctgtgcttttgatttaactctgaataactgaagaatgtaggtgttatttgacaaa	8107
QY	8101	atgttttgacttttaattgatttttggaatttaagttctatcagtagctcttaacct	8160
Db	8108	atgttttgacttttaattgatttttggaatttaagttctatcagtagctcttaacct	8167
QY	8161	tagaatgcccccttgtagaacccttggtatagaagagtagtcgcaactgtcccaattt	8220
Db	8168	tagaatgcccccttgtagaacccttggtatagaagagtagtcgcaactgtcccaattt	8227
QY	8221	tttatcttctatgttaagtttgcataatcaatgactatgctatgctccagaagaatgtgat	8280
Db	8228	tttatcttctatgttaagtttgcataatcaatgactatgctatgctccagaagaatgtgat	8287
QY	8281	gttccagatccatgacacattatattgagttcttcacagatcatttaagataactttaat	8340
Db	8288	gttccagatccatgacacattatattgagttcttcacagatcatttaagataactttaat	8347
QY	8341	ctcaattcatcaatcaaatattttttgagtgtagtcgtgtagctgaagaagtagtaacgtat	8400
Db	8348	ctcaattcatcaatcaaatattttttgagtgtagtcgtgtagctgaagaagtagtaacgtat	8407
QY	8401	cgtataaagcctaaagagatatttaagttccagtagcaccttcctgtgcagttaatacgtc	8460
Db	8408	cgtataaagcctaaagagatatttaagttccagtagcaccttcctgtgcagttaatacgtc	8467
QY	8461	actggttttaacaaatagatggtgtctgtgtgtgtgtagagcccaactgtlaacaaatttggc	8520
Db	8468	actggttttaacaaatagatggtgtctgtgtgtgtgtagagcccaactgtlaacaaatttggc	8527
QY	8521	agcccttttttttttttttttttttttaattggcaaaatgcagaagccagaagaatagaaggtcac	8580
Db	8528	agcccttttttttttttttttttttttttaattggcaaaatgcagaagaatagaagaaggtcac	8586
QY	8581	aagttctaaacaaatgaatctcttcaacagggaaaacagctagctgtgaaactgtgtgaaaaa	8640
Db	8587	aagttctaaacaaatgaatctcttcaacagggaaaacagctagctgtgaaactgtgtgaaaaa	8646
QY	8641	caacaactgtgtttatgtgcatttagatccttcaaaataatttgcttttgcgaatttggata	8700
Db	8647	caacaactgtgtttatgtgcatttagatccttcaaaataatttgcttttgcgaatttggata	8706
QY	8701	cccacattaaactgcagatcacaatttttcatcctctcaatatcactgacgaagaanaata	8760
Db	8707	cccacattaaactgcagatcacaatttttcatcctctcaatatcactgacgaagaanaata	8766
QY	8761	taaaaaacaacaatactctcatalgtgagcaattttcagaagttttcaaccagctctatt	8820
Db	8767	taaaaaacaacaatactctcatalgtgagcaattttcagaagttttcaaccagctctatt	8826
QY	8821	tttctagtcagtaaacatttgaanaaactggtttcaactatcacttaactgttcaactgtct	8880
Db	8827	tttctagtcagtaaacatttgaanaaactggtttcaactatcacttaactgttcaactgtct	8886
QY	8881	tgagagaaaagaanaataatgagagacattgtttggggaagtcaagtatcttcaat	8940
Db	8887	tgagagaaaagaanaataatgagagacattgtttggggaagtcaagtatcttcaat	8946
QY	8941	atcatattcaaatcttccacacttttccaaatattgaataaataaagctlaaaggtgtlaaga	9000
Db	8947	atcatattcaaatcttccacacttttccaaatattgaataaataaagctlaaaggtgtlaaga	9006
QY	9001	cttcagatttcaaatattcttctatattttttaaatttaacgaataattatataaacca	9060

```

Db 9007 cttcagatttcaatataccttctcatttcttaatttcaagataatatacaca 9066
QY 9061 ctgctgaagaaagaaatgattgttttagaagttaagcaataattgatttaaat 9120
Db 9067 ctgctgaagaaagaaatgattgttttagaagttaagcaataattgatttaaat 9126
QY 9121 aagtaataagagcatatttccaaatactagatagatgacatgttgcaattcaagatc 9180
Db 9127 aagtaataagagcatatttccaaatactagatagatgacatgttgcaattcaagatc 9186
QY 9181 ttcaaaaatacagaaatttataagataattcccccatttaattttcaaatcaag 9240
Db 9187 ttcaaaaatacagaaatttataagataattcccccatttaattttcaaatcaag 9246
QY 9241 ttatggttcccatatttctcctaataatcgatcttaatttccatataagtaactatga 9300
Db 9247 ttatggttcccatatttctcctaataatcgatcttaatttccatataagtaactatga 9306
QY 9301 gcaactcctacttggttccctctgatttcaaggccataatttcaaaaatacagac 9360
Db 9307 gcaactcctacttggttccctctgatttcaaggccataatttcaaaaatacagac 9366
QY 9361 tctgaactatttgaagaaacacagacatttaatacagattgaagacccctctgaa 9420
Db 9367 tctgaactatttgaagaaacacacacatttatacagattgaagacccctctgaa 9426
QY 9421 gctgaagaaacatctatagatatacatctcattcaatactggttctcctttaaataga 9480
Db 9427 gctgaagaaacatctatagatatacatctcattcaatactggttctcctttaaataga 9486
QY 9481 attttacatttccctggttaacataatgttgtagaattttaccactctatct 9540
Db 9487 attttacatttccctggttaacataatgttgtagaattttaccactctatct 9546
QY 9541 caatcaagcaaaactctgtatattccctgtggaatgttaactatgttgagattcagaat 9600
Db 9547 caatcaagcaaaactctgtatattccctgtggaatgttaactatgttgagattcagaat 9606
QY 9601 ctcaaaatacgttgcataaaatttctgcttgcatttggacactcagaactccta 9660
Db 9607 ctcaaaatacgttgcataaaatttctgcttgcatttggacactcagaactccta 9666
QY 9661 ttaacaactgtgataatgaaatacagaagaaataataaagccctctatacataatgc 9720
Db 9667 ttaacaactgtgataatgaaatacagaagaaataataaagccctctatacataatgc 9726
QY 9721 ccagcacaattcattgttaaaaaaacacacacactcacactactgtattcattatctgt 9780
Db 9727 ccagcacaattcattgtttaaaaaacacacacacactcacactactgtattcattatctgt 9786
QY 9781 actgaagaagaatgcttctgtgacttaaatgttgacatacatcatca 9830
Db 9787 actgaagaagaatgcttctgtgacttaaatgttgacatacatcatca 9836

```

RESULT 8
ID AAS06120 standard; cDNA; 9741 BP.
AAS06120;

XX 12-SEP-2001 (first entry)
XX Human ABC1 DNA sequence #1.
DE Human ABC1 DNA sequence #1.

KW Human, ABC1 gene; atherosclerosis; reverse transport; cholesterol;
KW cardiovascular; neurological; Tangier disease; LCAT deficiency;
KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
XX Homo sapiens.

XX Key Location/Qualifiers
FH

```

FT CDS 185..6967
FT /*tag= a
FT /product= "Human ABC1 protein"
Mo200130848-A2.
03-MAY-2001.
26-OCT-2000; 2000WO-EPI0886.
26-OCT-1999; 99EP-0402668.
PR 01-MAR-2000; 2000US-0186260.
XX (AVET ) AVENTIS PHARMA SA.
PA
XX Deneffe P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;
XX Lemoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
XX Dean M;
XX WPI: 2001-316327/33.
DR P-PSDB; AAU021/6.
DR
PT New human ABC1 nucleic acids and polypeptides for treating
PT atherosclerosis, malaria and diabetes -
XX
PS Claim 1: Page 204-208; 368bp; English.
XX
CC The sequence represents the coding sequence #1 of human ABC1. The
CC nucleic acid sequence, primers and probes derived from the ABC1 sequence,
CC and polypeptides and vectors are useful for the prevention of
CC atherosclerosis, in a subject affected by a dysfunction in the reverse
CC transport of cholesterol. The polypeptide encoded by the ABC1 gene is
CC useful for screening for an active ingredient for the prevention or
CC treatment of a disease resulting from dysfunction in the reverse
CC transport of cholesterol. The nucleic acids and polypeptides are also
CC useful for treating and preventing cardiovascular and neurological
CC pathologies, and other diseases e.g. Tangier disease, lecithin-
CC cholesterol (LCAT) deficiency, malaria and diabetes.
XX
SQ Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other:

```

Query Match 92.6%; Score 9672.8; DB 22; Length 9741;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 9705; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

```

QY 106 ctgtttttcccggttctgttttccctctccggaagctgtcaagggtaga 165
Db 1 ctgtttttcccggttctgttttccctctccggaagctgtcaagggtaga 60
QY 166 gaagagagcgaacacaaaggggaagtaatgacccagcggcgctcctgtc 225
Db 61 gaagagagcgaacacaaaggggaagtaatgacccagcggcgctcctgtc 119
QY 226 gtgagctctgcccgtccttccagggctcccgagcacaagctgtgctgtcga 285
Db 120 gtgagctctgcccgtccttccagggctcccgagcacaagctgtgctgtcga 179
QY 286 ggaacatgctgttggcctcagctgaggttgcgtgtggaagacccacttcaaga 345
Db 180 ggaacatgctgttggcctcagctgaggttgcgtgtggaagacccacttcaaga 239
QY 346 gaagacaacatgcatgcttacttgaagtgagccctgactatattcctccgattc 405
Db 240 gaagacaacatgcatgcttacttgaagtgagccctgactatattcctccgattc 299
QY 406 tgaactctgttgcgtgaactacacacccatgaaacaaatgaatgcaatttccaata 465
Db 300 tgaactctgttgcgtgaactacacacccatgaaacaaatgaatgcaatttccaata 359
QY 466 aagcatgcccctctgagaaacacttccctgtgttcagggtatctatcgtaatgcaaca 525
Db 360 aagcatgcccctctgagaaacacttccctgtgttcagggtatctatcgtaatgcaaca 419

```


Db	2580	agcagggattcggagtcgacgtagggaacaaacgcttttgaaagtcctcgttgaggaagaatgct	2639
QY	2746	tcaatctcaacctgcgactccatgcatgctgcttgacacctccctctatgaggtaga	2805
Db	2640	tcaatctcaacctgcgactccatgcatgctgcttgacacctccctctatgaggtaga	2699
QY	2806	cttgggtacatggagctctcttcacaggccagtagccgaattcccaagccctggatttc	2865
Db	2700	cctgttaactgtagggtctctcttcacaggccagtagccgaattcccaagccctggatttc	2759
QY	2866	cttgacccaagtctcactggtttgtagggaagtgatggaagaagccacctgttcca	2925
Db	2760	cttgacccaagctcctactggtttgtagggaagtgatggaagaagccacctgttcca	2819
QY	2926	accagaagaagaaatgcagaaatctgcgcatggaagggaaccccaacttgaagctggcg	2985
Db	2820	accagaagaagaaatgcagaaatctgcgcatggaagggaaccccaacttgaagctggcg	2879
QY	2986	tgtccatccagaaccttgtaaaagctcaacgagatggagatbaagtggtcgttcgataggc	3045
Db	2880	tgtccatccagaaccttgtaaaagctcaacgagatggagatbaagtggtcgttcgataggc	2939
QY	3046	tggcaactgaattttatgaggggccagatcacctctctctcctgggccaatggaagccggga	3105
Db	2940	tggcaactgaattttatgaggggccagatcacctctctctcctgggccaatggaagccggga	2999
QY	3106	agacagaccacatgcatcctgaccgggtgtcccccgcacccctctgggcaaccgctaca	3165
Db	3000	agacagaccacatgcatcctgaccgggtgtgtgtcccccgcacccctctgggcaaccgctaca	3059
QY	3166	tcttgggaaagagacattcgtctcgtagatgagaccatccggccagaaaccttgggggtctgc	3225
Db	3060	tcttgggaaagagacattcgtctcgtagatgagaccatccggccagaaaccttgggggtctgc	3119
QY	3226	cccaagcataaagctgctgtttgacacatgctgactgtcgaagaaacacatctggtttctatgccc	3285
Db	3120	cccaagcataaagctgctgtttgacacatgctgactgtcgaagaaacacatctggtttctatgccc	3179
QY	3286	gcttgaagaaggctctctctgtagaagacgltgaaggcgtgagatggaagacatggtccctgatatg	3345
Db	3180	gcttgaagaaggctctctctgtagaagacgltgaaggcgtgagatggaagacatggtccctgatatg	3239
QY	3346	tttggtttgccttcaagcaagctgtgaaaaagcaaaacagccagctgttcaagttggaattgcaga	3405
Db	3240	tttggtttgccttcaagcaagctgtgaaaaagcaaaacagccagctgttcaagttggaattgcaga	3299
QY	3406	gaaagctactcgttgcccttgcccttctcggggagatctaaggtttgttatcttgaatgaac	3465
Db	3300	gaaagctactcgttgcccttgcccttctcggggagatctaaggtttgttatcttgaatgaac	3359
QY	3466	ccaacagctgtgtgtggaacccctaactcccgacggggaatatavtggagctgtcgtctgaatahac	3525
Db	3360	ccaacagctgtgtgtggaacccctaactcccgacggggaatatavtggagctgtcgtctgaatahac	3419
QY	3526	gacaagggccgacattatctctctctacacacacacatgtagtggaagccgaagtcctctgggg	3585
Db	3420	gacaagggccgacattatctctctctacacacacacatgtagtggaagccgaagtcctctgggg	3479
QY	3586	acagagattgcacatctcccatggaagcgtgtgtgtgtggtggtccctccctgtttctga	3645
Db	3480	acagagattgcacatctcccatggaagcgtgtgtgtgtgtggtggtccctccctgtttctga	3539
QY	3646	agaaacagcttgagggaacgggtcactacacccctggttgcagaagaagatgttgaaatctccccc	3705
Db	3540	agaaacagcttgagggaacgggtcactacacccctggttgcagaagaagatgttgaaatctccccc	3599
QY	3706	tcaagttccttgagaaacagtagtagcacctgtgtcatctcggaaaggaaggaacagtgctt	3765
Db	3600	tcaagttccttgagaaacagtagtagcacctgtgtcatctcggaaaggaaggaacagtgctt	3659
QY	3766	ctcaggaacagttctgcatgctggtgccttggtgcagcgacatggaagtagacgctgacacatcg	3825
Db	3660	ctcaggaacagttctgcatgctggtgccttggtgcagcgacatggaagtagacgctgacacatcg	3715
QY	3826	atgtctctgtctatctccaaacctcaacgaagaatgltgtctgaagcccgctgtgtggaag	3885
Db	3720	atgtctctgtctatctccaaacctcaacgaagaatgltgtctgaagcccgctgtgtggaag	3779
QY	3886	acaatggagatgaagctgaactctatggtgcgtccatatgaagcgtgtcaagaaggaacctttg	3945
Db	3780	acaatggagatgaagctgaactctatggtgcgtccatatgaagcgtgtcaagaaggaacctttg	3839
QY	3946	tggaaacttcttcatgagatctgaacggtctctccagaccccttggtgacatltctcgttatgcca	4005
Db	3840	tggaaacttcttcatgagatctgaacggtctctccagaccccttggtgacatltctcgttatgcca	3899
QY	4006	tctcagaagacgaccttggaagaatatactcccaaggtgtgcccgaagagatgtgggttgatg	4065
Db	3900	tctcagaagacgaccttggaagaatatactcccaaggtgtgcccgaagagatgtgggttgatg	3959
QY	4066	ctgagaacctcagatgtaacctgtccagcaagaacgaagccgggacctctggggacaagc	4125
Db	3960	ctgagaacctcagatgtaacctgtccagcaagaagccgggacctctggggacaagc	4019
QY	4126	agaagctgtcttcgcccgttcaactgagaatgtagctgtcgtatccaaatgattctgacatag	4185
Db	4020	agaagctgtcttcgcccgttcaactgagaatgtagctgtcgtatccaaatgattctgacatag	4079
QY	4186	accagaataatccagaagaacagacattggtccatgtgggaatgtagtgaagaaggggtctacag	4245
Db	4080	accagaataatccagaagaacagacattggtccatgtgggaatgtagtgaagaaggggtctacag	4139
QY	4246	tgaagaagcttggaacattcacacagcaacagtttgttgcccttttgtggaagaagacatgtaa	4305
Db	4140	tgaagaagcttggaacattcacacagcaacagtttgttgcccttttgtggaagaagacatgtaa	4199
QY	4306	tggccaagacggagctcggaagaagatttttgtctcaagattgtcttcgacgctgtgttctc	4365
Db	4200	tggccaagacggagctcggaagaagatttttgtctcaagattgtcttcgacgctgtgttctc	4259
QY	4366	gcatgtcccttctgtctcaagccctgtgacgtgacaccccttggcaaataccccgccctggaac	4425
Db	4260	gcatgtcccttctgtctcaagccctgtgacgtgacgtgacaccccttggcaaataccccgccctggaac	4319
QY	4426	ttcagccctcgatgtgtaacaagaaagatcacacattgttcaagaatgtagtctctcgaaggaca	4485
Db	4320	ttcagccctcgatgtgtaacaagaaagatcacacattgttcaagaatgtagtctctcgaaggaca	4379
QY	4486	cgggaacccctgtgaactcttcaagccctccacaaagaacccgtggtcttgggaacccgctgta	4545
Db	4380	cgggaacccctgtgaactcttcaagccctccacaaagaacccgtggtcttgggaacccgctgta	4439
QY	4546	tggaaaggaaacccaatctccagaacaagccctcgtgcagggcaggggaaggaagtlgaaaccactg	4605
Db	4440	tggaaaggaaacccaatctccagaacaagccctcgtgcagggcaggggaaggaagtlgaaaccactg	4499
QY			

QY 4906 tcaagtaatactcaagcaactctctccgagtcgaagaatgaatgaatgcatacaacaatga 4965
|||||
Db 4800 tcaagtaatactcaagcaactctctccgagtcgaagaatgaatgaatgcatacaacaatga 4859
QY 4966 agaacaacactaaagcttgcccaaggaacagctctgcagatcgatcttccaacagcttgaa 5025
|||||
Db 4860 agaacaacactaaagcttgcccaaggaacagctctgcagatcgatcttccaacagcttgaa 4919
QY 5026 gattatgaacagagcttggaacacagaatgaatgaatgaatgaatgaatgaatgaatga 5085
|||||
Db 4920 gattatgaacagagcttggaacacagaatgaatgaatgaatgaatgaatgaatgaatga 4979
QY 5086 ggcagatgaatcagctctctccgagtcgaatgaatgaatgaatgaatgaatgaatgaatga 5145
|||||
Db 4980 ggcagatgaatcagctctctccgagtcgaatgaatgaatgaatgaatgaatgaatgaatga 5039
QY 5146 aaaagggagagaaacactgaacattatgaatgaatgaatgaatgaatgaatgaatgaatga 5205
|||||
Db 5040 aaaagggagagaaacactgaacattatgaatgaatgaatgaatgaatgaatgaatgaatga 5099
QY 5206 ccaagcagcagctcgaagagtgagctctgaatgaacacacatgaatgaatgaatgaatga 5265
|||||
Db 5100 ccaagcagcagctcgaagagtgagctctgaatgaacacacatgaatgaatgaatgaatga 5159
QY 5266 tctgtgtacatttgcagatctctccgagtcgaatgaatgaatgaatgaatgaatgaatga 5325
|||||
Db 5160 tctgtgtacatttgcagatctctccgagtcgaatgaatgaatgaatgaatgaatgaatga 5219
QY 5326 agcgggtcagcaaaacaaacacactgcagtcacatgaatgaatgaatgaatgaatgaatga 5385
|||||
Db 5220 agcgggtcagcaaaacaaacacactgcagtcacatgaatgaatgaatgaatgaatgaatga 5279
QY 5386 ggcctctcaatttgccttgagatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 5445
|||||
Db 5280 ggcctctcaatttgccttgagatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 5339
QY 5446 tcaatctcaatctgcctcgaagaaatgaatgaatgaatgaatgaatgaatgaatgaatga 5505
|||||
Db 5340 tcaatctcaatctgcctcgaagaaatgaatgaatgaatgaatgaatgaatgaatgaatga 5399
QY 5506 cccttcaatttgccttgagatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 5565
|||||
Db 5400 cccttcaatttgccttgagatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 5459
QY 5566 tgttcaagaatccccaagcagcctatgtgtcgaacagcgtgaacgttgcatttgga 5625
|||||
Db 5460 tgttcaagaatccccaagcagcctatgtgtcgaacagcgtgaacgttgcatttgga 5519
QY 5626 ttaatgtcagcgtgagcagccttgccttgagatgaatgaatgaatgaatgaatgaatga 5685
|||||
Db 5520 ttaatgtcagcgtgagcagccttgccttgagatgaatgaatgaatgaatgaatgaatga 5579
QY 5686 tcaatgaatctcgaatgcgtgtgttctgaatcttcccaacttcttgccctggagcagggc 5745
|||||
Db 5580 tcaatgaatctcgaatgcgtgtgttctgaatcttcccaacttcttgccctggagcagggc 5639
QY 5746 tcaatgaatctcgaatgcgtgtgttctgaatcttcccaacttcttgccctggagcagggc 5805
|||||
Db 5640 tcaatgaatctcgaatgcgtgtgttctgaatcttcccaacttcttgccctggagcagggc 5699
QY 5806 gcttctgtcaacatatacttgagatgttgagagcaaaccttccgcaatgcagctgg 5865
|||||
Db 5700 gcttctgtcaacatatacttgagatgttgagagcaaaccttccgcaatgcagctgg 5759
QY 5866 aaggggtgtgtcttccatctgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 5925
|||||
Db 5760 aaggggtgtgtcttccatctgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 5819
QY 5926 gacctgtaaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 5985
|||||
Db 5820 gacctgtaaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 5879

QY 5986 gacagagaattctctgtatggtgagccagaatgacatcttagaatacaagaatgagca 6045
|||||
Db 5880 gacagagaattctctgtatggtgagccagaatgacatcttagaatacaagaatgagca 5939
QY 6046 agatataagaagaagcaggaagcgtgtgtgaacagatgtgcgttgagcattccctcgt 6105
|||||
Db 5940 agatataagaagaagcaggaagcgtgtgtgaacagatgtgcgttgagcattccctcgt 5999
QY 6106 gtgagctcttgcctccttgagatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 6165
|||||
Db 6000 gtgagctcttgcctccttgagatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 6059
QY 6166 taacagagatacactcgttaacagagagatgcttcttcaacaaatagatctat 6225
|||||
Db 6060 taacagagatacactcgttaacagagagatgcttcttcaacaaatagatctat 6119
QY 6226 caaacatccatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 6285
|||||
Db 6120 caaacatccatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 6179
QY 6286 agctgttgagcgtgag 6345
|||||
Db 6180 agctgttgagcgtgag 6239
QY 6346 aagaatgtgcaaggtgtgtgagtgagcagatcagaaactgagcgtgagatgag 6405
|||||
Db 6240 aagaatgtgcaaggtgtgtgagtgagcagatcagaaactgagcgtgagatgag 6299
QY 6406 aaaaatagctgtgaactatgagtgagagcaaacagcaagcctcacaagcagtgct 6465
|||||
Db 6300 aaaaatagctgtgaactatgagtgagagcaaacagcaagcctcacaagcagtgct 6359
QY 6466 tgaatgcgggcctcctgt 6525
|||||
Db 6360 tgaatgcgggcctcctgt 6419
QY 6526 ccgagcgttctgtgtgaatgt 6585
|||||
Db 6420 ccgagcgttctgtgtgaatgt 6479
QY 6586 ttacatccatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 6645
|||||
Db 6480 ttacatccatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 6539
QY 6646 atggaaggttgaatgt 6705
|||||
Db 6540 atggaaggttgaatgt 6599
QY 6706 atacatagctgtgaacgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 6765
|||||
Db 6600 atacatagctgtgaacgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 6659
QY 6766 ttgagatgcatttcccttgagagtggttctaaagaagaacacgggaacatgtctaatacc 6825
|||||
Db 6660 ttgagatgcatttcccttgagagtggttctaaagaagaacacgggaacatgtctaatacc 6719
QY 6826 agcttccatcttcaatcttcttgcagagagatgaatgaatgaatgaatgaatgaatgaatga 6885
|||||
Db 6720 agcttccatcttcaatcttcttgcagagagatgaatgaatgaatgaatgaatgaatgaatga 6779
QY 6886 agcagatccacatagaactacttcttctgaacacacacttgacaagatatttga 6945
|||||
Db 6780 agcagatccacatagaactacttcttctgaacacacacttgacaagatatttga 6839
QY 6946 acttgcacagagcaaaagtgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 7005
|||||
Db 6840 acttgcacagagcaaaagtgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 6899
QY 7006 agacagtagtgagctgtgaatcttcaacatcttctcaagagagagagagagagagagag 7065
|||||
Db 6900 agacagtagtgagctgtgaatcttcaacatcttctcaagagagagagagagagagagag 6959
QY 7066 gctatgtaagaatctctgttcatagcgggtgtgtgtgaagtaagaaggaactagactt 7125

```
Db 6960 gcatgtatgaaagatcctgtcatatgaggggtgagtgaaagtaaaagagactgacatt 7019
QY 7126 cctttgacacatgtaagagttgttggaagaaagacagaagtgtgattggaagaagta 7185
Db 7020 cctttgacacatgtaagagttgttggaagaaagacagaagtgtgattggaagaagta 7079
QY 7186 aactggaactgtacgtatcctatcaatgcaatgcaatgcaatgcaatgcaatgcaat 7245
Db 7080 aactggaactgtacgtatcctatcaatgcaatgcaatgcaatgcaatgcaatgcaat 7139
QY 7246 tcaatcaaggggagtgcttctgtgacatgctgtgacatgctgtgacatgcaatgcaat 7305
Db 7140 tcaatcaaggggagtgcttctgtgacatgctgtgacatgctgtgacatgcaatgcaat 7199
QY 7306 tgaattagttttttacatcctatgtaaaactctatgatgaaacccaatggaacata 7365
Db 7200 tgaattagttttttacatcctatgtaaaactctatgatgaaacccaatggaacata 7259
QY 7366 ggggttgaactcaacttttttttttttttttttttttttttttttttttttttttt 7425
Db 7260 ggggttgaactcaacttttttttttttttttttttttttttttttttttttttttt 7319
QY 7426 caataatltcaatcaatcaatgagcagatattgatacaaaatcaaaagttaatgacac 7485
Db 7320 caataatltcaatcaatcaatgagcagatattgatacaaaatcaaaagttaatgacac 7379
QY 7486 atcctattcaatcaatcaatgagcagatattgatacaaaatcaaaagttaatgacac 7545
Db 7380 atcctattcaatcaatcaatgagcagatattgatacaaaatcaaaagttaatgacac 7439
QY 7546 gctggaatagtgctgacagatgtaattgacagatatttctggaagtttaagacaca 7605
Db 7440 gctggaatagtgctgacagatgtaattgacagatatttctggaagtttaagacaca 7499
QY 7606 tgggtgtgctgctcacttctgtgaaagcgtcgtcgtccagagttctcaacatgtaata 7665
Db 7500 tgggtgtgctgctcacttctgtgaaagcgtcgtcgtccagagttctcaacatgtaata 7559
QY 7666 tcaagttgacagaaatggtgacatgctgctgaaacatcctgtgattcctcctgataac 7725
Db 7560 tcaagttgacagaaatggtgacatgctgctgaaacatcctgtgattcctcctgataac 7619
QY 7726 tgttctgtgtgacgataacatgcaaaaaatgtgggtgtcctctagacagggaaacttg 7785
Db 7620 tgttctgtgtgacgataacatgcaaaaaatgtgggtgtcctctagacagggaaacttg 7679
QY 7786 ttcacattgtatatagttcctatgctcagcagatggtctacagggatcctcttatgaa 7845
Db 7680 ttcacattgtatatagttcctatgctcagcagatggtctacagggatcctcttatgaa 7739
QY 7846 ctcttaataatactatgatacctgttaagagcgaagaatcaacagccaactgctgggc 7905
Db 7740 ctcttaataatactatgatacctgttaagagcgaagaatcaacagccaactgctgggc 7799
QY 7906 tgaagctgtgaaagcgaagatggaattgaagagatgtgctgtcaaaacttaggaag 7965
Db 7800 tgaagctgtgaaagcgaagatggaattgaagagatgtgctgtcaaaacttaggaag 7859
QY 7966 ccgtgtccacattgtctcctacgtctgcttaacatgtaacgactcctcaagaattttat 8025
Db 7860 ccgtgtccacattgtctcctacgtctgcttaacatgtaacgactcctcaagaattttat 7919
QY 8026 ctgacaagaatgataatcttctgcttttgaatcaatcctagaanaatgaaagtgaat 8085
Db 7920 ctgacaagaatgataatcttctgcttttgaatcaatcctagaanaatgaaagtgaat 7979
QY 8086 tctatttgaacaaaatgtttgacttttaattgtatattggaatttgaattcattacag 8145
Db 7980 tctatttgaacaaaatgtttgacttttaattgtatattggaatttgaattcattacag 8039
QY 8146 tgaacttgaactccttagaatgacctctgtgagaacctgtgtatagagagatgac 8205
|||||

Db 8040 tgaacttgaactccttagaatgacctctgtgagaacctgtgtatagagagatgac 8099
QY 8206 cactgcccacattttattttcttatgtaagtttgatactgatactgactgact 8265
Db 8100 cactgcccacattttattttcttatgtaagtttgatactgatactgactgactgact 8159
QY 8266 agaaagcaatgtaatgtaagatcctcaatgacatataattgattccttcaagatcatt 8325
Db 8160 agaaagcaatgtaatgtaagatcctcaatgacatataattgattccttcaagatcatt 8219
QY 8326 taggatacttcaatcctcaatcctcaatcctcaatcctcaatcctcaatcctcaatcct 8385
Db 8220 taggatacttcaatcctcaatcctcaatcctcaatcctcaatcctcaatcctcaatcct 8279
QY 8386 aagagatgtacgtatagataagactagagataatgaatgctacgatacttctgtgc 8445
Db 8280 aagagatgtacgtatagataagactagagataatgaatgctacgatacttctgtgc 8339
QY 8446 catgtattcagctcactcaggtttacaaatagagttgtctgtgtgtgtgtgtgtgtgtgt 8505
Db 8340 catgtattcagctcactcaggtttacaaatagagttgtctgtgtgtgtgtgtgtgtgtgt 8399
QY 8506 gtaacaatattgggagccttttttttttttttttttttttttttttttttttttttttt 8565
Db 8400 gtaacaatattgggagccttttttttttttttttttttttttttttttttttttttttt 8458
QY 8566 aagataaggggtcaacagtttaaacatgaaatcctcaacaggggaaacagctagcttga 8625
Db 8459 aagataaggggtcaacagtttaaacatgaaatcctcaacaggggaaacagctagcttga 8518
QY 8626 aaactgtctgaaacacacacttgttttatgagcatttagaaccttaataattgtgctt 8685
Db 8519 aaactgtctgaaacacacacttgttttatgagcatttagaaccttaataattgtgctt 8578
QY 8686 tgcagataatggatacccatlaaatcctgacagtcacaaatttttcaatccttcaatcac 8745
Db 8579 tgcagataatggatacccatlaaatcctgacagtcacaaatttttcaatccttcaatcac 8638
QY 8746 tagtcaagaataataataataataataataataataataataataataataataataata 8805
Db 8639 tagtcaagaataataataataataataataataataataataataataataataataata 8698
QY 8806 taacagacttattttttctagtcagtaaacattgttaaaaatactgtttcaactaact 8865
Db 8699 taacagacttattttttctagtcagtaaacattgttaaaaatactgtttcaactaact 8758
QY 8866 taactgttaactgttttgaggaagaaagaaataatagagaagacattgtttgggaagttc 8925
Db 8759 taactgttaactgttttgaggaagaaagaaataatagagaagacattgtttgggaagttc 8818
QY 8926 aagtgatccttcaatatacttaactccttccacttttccaaatlttgaatataac 8985
Db 8819 aagtgatccttcaatatacttaactccttccacttttccaaatlttgaatataac 8878
QY 8986 gctaaaggtgtgaagacttcaagattcaaatattccttcaatatlttttaattacaga 9045
Db 8879 gctaaaggtgtgaagacttcaagattcaaatattccttcaatatlttttaattacaga 8938
QY 9046 atattataaacccacgtcgtgaagaaagaaagaaatgtgttttagaagttgaagccaat 9105
Db 8939 atattataaacccacgtcgtgaagaaagaaagaaatgtgttttagaagttgaagccaat 8998
QY 9106 atgattttaataataagtaagagcatatttccaaatactagatagatagatgacatgct 9165
Db 8999 atgattttaataataagtaagagcatatttccaaatactagatagatagatgacatgct 9058
QY 9166 gcaatttacagatcctcaaaaataacagaattatagaaataatttctcctcatttaaat 9225
Db 9059 gcaatttacagatcctcaaaaataacagaattatagaaataatttctcctcatttaaat 9118
QY 9226 ttctcaaaatcaaaagtattgttcccatcttcaacttaaaatctgatactcaatctcat 9285
Db 9119 ttctcaaaatcaaaagtattgttcccatcttcaacttaaaatctgatactcaatctcat 9178
```

```

RESULT      9
AAAF92835
ID    AAF92835 standard; DNA; 7860 BP.
XX
XX    AAF92835;
AC
XX
DT    17-MAY-2001 (first entry)
XX
DE    Human ABC1 cDNA.
XX
XX    High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ss
XX
XX    Homo sapiens.
OS
XX
PN    W0200115676-A2.
PM
XX
PD    08-MAR-2001.
XX
PF    01-SEP-2000; 2000MO-IB01492.
XX
XX    01-SEP-1999; 99US-0151977.
PR    15-MAR-2000; 2000US-0526193.
PR    23-JUN-2000; 2000US-0213958.
XX
XX    (UYBR-) UNIV BRITISH COLUMBIA.
PA    (XENO-) XENON GENETICS INC.
XX
XX    Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
PI    WPI; 2001-244356/25.
XX
XX

```

Qy	217	gtcctgtctgtgagctctgtgscgcgtctccctcccaagagctcccgaaacacacacgcctggagctg	276
Db	1	gtccctgcgtgtagagctctgcgcgcgcgtctcccaaggtctcccgaaacacacgcctggagctg	60
Qy	277	ctgctctgagggaaacatgagctctgtctgagctccacgtcgtgaagctgtgctgtgtgaaagaaacctca	336
Db	61	ctgctctgagggaaacatgagctctgtctgagctccacgtcgtgaagctgtgctgtgtgaaagaaacctca	120
Qy	337	cttcaagaagaagaaacacatgtaagctgttaccgtggaagatggcgcttgccctctattatct	396
Db	121	cttcaagaagaagaaacacacatgtaagctgttaccgtggaagatggcgcttgccctctattatct	180
Qy	397	tccctatccctgactctctgtttctgcgtgtagcttaccacacctatgaaacaaacatgatactgcat	456
Db	181	tccctatccctgactctctgtttctgcgtgtagcttaccacacctatgaaacaaacatgatactgcat	240
Qy	457	ttccaataaagaagcaatgcctcctctgcagaagacaactcctctgtgtctcaaggagatatctctgta	516
Db	241	ttccaataaagaagcaatgcctcctctgcagaagacaactcctctgtgtctcaaggagatatctctgta	300
Qy	517	atgccacaacaacccctgtttctcgtttaccgcgactcctctggtgaagctcccgagagtttgtgaa	576
Db	301	atgccacaacaacccctgtttctcgtttaccgcgactcctctggtgaagctcccgagagtttgtgaa	360
Qy	577	actttaacaacatccatgtgtgctgcgcgcgtttctccaagatgctcggaagcttccctttataca	636
Db	361	actttaacaacatccatgtgtgctgcgcgcgtttctccaagatgctcggaagcttccctttataca	420
Qy	637	gccagaagaacaccccgacatgtaagagacatgctgcgcgaagttctgtagaacaattacaagacata	696
Db	421	gccagaagaacaccccgacatgtaagagacatgctgcgcgaagttctgtagaacaattacaagagatca	480
Qy	697	agaacatccaagctcaaaccttgaaagcttcaagattcttcctgtgtgacacatgaaacctctctctg	756
Db	481	agaacatccaagctcaaaccttgaaagcttcaagattcttcctgtgtgacacatgaaacctctctctg	540
Qy	757	ggttccatatacacaaacctctctctccccaagaagtcaactgtgtgaacaagatgctgtgaggtcg	816
Db	541	ggttccatatacacaaacctctctctccccaagaagtcaactgtgtgaacaagatgctgtgaggtctg	600
Qy	817	atgtcaatctccacaaggatattttgtgcaagctaccacagttacatttgacaagctctgtgca	876
Db	601	atgtcaatctccacaaggatattttgtgcaagctaccacagttacatttgacaagctctgtgca	660
Qy	877	atggatcaaaatcagaagaagatgatatllcaactgtgtgaccagaagatttcgaagcttctgtg	936
Db	661	atggatcaaaatcagaagaagatgatatllcaactgtgtgaccagaagatttcgaagcttctgtg	720

QY	937	gcttaccgaaggagaacattggtcttcacgacagagcgaiacttggttccacaatgacatcc	996
Db	721	gctctcccaaggaggaacattggtcttcacgacagcgaagctacttctgttccacaatgacatcc	780
QY	997	tgaagccaattccttggaacataactctaatctccctccctcccgagcaagatctgctg	1050
Db	781	tgaagccaattccttggaacataactctaatctccctccctcccgagcaagatctgctg	840
QY	1057	aagccaacaaaacattgctctgcatactcttggaactctgcccagagacgtgttaagcatga	1116
Db	841	aagccaacaaaacattgctctgcatactcttggaactctgcccagagacgtgttaagcatga	900
QY	1117	gaagctggaagtacactggaacaggaagtgtatgtttcttgacaactgtgaaacagctccagct	1176
Db	901	gaagctggaagtacactggaacaggaagtgtatgtttcttgacaactgtgaaacagctccagct	960
QY	1177	ccttccacccaattaccaggcgtgtctctgtaattgtctgaggacatcccgagggagggg	1236
Db	961	ccttccacccaattaccaggcgtgtctctgtaattgtctgaggacatcccgagggagggg	1020
QY	1237	ggcttaagaatcaagctcttcacgtgatatagacaacaaactatacaagcccttttgag	1296
Db	1021	ggcttaagaatcaagctcttcacgtgatatagacaacaaactatacaagcccttttgag	1080
QY	1297	gcaatgacactggaagaatgctgaaaccttctatgacaactctaaactcttaactga	1356
Db	1081	gcaatgacactggaagaatgctgaaaccttctatgacaactctaaactcttaactga	1140
QY	1357	atgatttgaatgaagaattttggaagtctatgctctcttcccgcatctactgtgaagctctga	1416
Db	1141	atgatttgaatgaagaattttggaagtctatgctctcttcccgcatctactgtgaagctctga	1200
QY	1417	agccgcgtcgtgttggaagaatccctgtatacactacactccacgcacaaagacagtgta	1476
Db	1201	agccgcgtcgtgttggaagaatccctgtatacactacactccacgcacaaagacagtgta	1260
QY	1477	tgcgtgaagtgtaacaagaaccttccagaaactggtgtgttccatgtacttgaaagcatgt	1536
Db	1261	tgcgtgaagtgtaacaagaaccttccagaaactggtgtgttccatgtacttgaaagcatgt	1320
QY	1537	gggaaggaactacagccccaagaatactctgagacctctatgagaacacgaacaaatgagacctg	1596
Db	1321	gggaaggaactacagccccaagaatactctgagacctctatgagaacacgaacaaatgagacctg	1380
QY	1597	tccggaatgctgttggaacagcagggacaatgacaacttttgggaacagcagttgagatgct	1656
Db	1381	tccggaatgctgttggaacagcagggacaatgacaacttttgggaacagcagttgagatgct	1440
QY	1657	tagatttgacagcccaagaacatctgtgacgttttttggccaagcaccacagagagatgcaggt	1716
Db	1441	tagatttgacagcccaagaacatctgtgacgttttttggccaagcaccacagagagatgcaggt	1500
QY	1717	ccaagtaatggttctctgtgtacaacctggaagagaagctttcaacgaagactaaaccaagcaatcc	1776
Db	1501	ccaagtaatggttctctgtgtacaacctggaagagaagctttcaacgaagactaaaccaagcaatcc	1560
QY	1777	ggacacatactccggtttatagagatgtgtgttaaccttggaacaaagcttaagaacctaatgaacaag	1836
Db	1561	ggacacatactccggtttatagagatgtgtgttaaccttggaacaaagcttaagaacctaatgaacaag	1620
QY	1837	aagctctgctatccaacaagaatccaatgagcgtctgtgtgaatagaaggaagtcttgagcgtgtga	1896
Db	1621	aagctctgctatccaacaagaatccaatgagcgtctgtgtgaatagaaggaagtcttgagcgtgtga	1680
QY	1897	tttgtgttcaactggaattactccaagcagcaattgagctgtgcccacatcatgttcaagtacaaga	1956
Db	1681	tttgtgttcaactggaattactccaagcagcaattgagctgtgcccacatcatgttcaagtacaaga	1740
QY	1957	tccgaatggaacatggaacaatgttggaagaggaacaataaataaagaatggtactgtgagacc	2016
Db	1741	tccgaatggaacatggaacaatgttggaagaggaacaataaataaagaatggtactgtgagacc	1800
QY	2017	ctggctccctgagctgaccccttttgaagacatgcgtgtacgctcttgaggggggtcttgcctact	2076

Db	1801	ctgctcctcgagctgacccctcttgagacatgcggtacgctctggggggtcctcgctact	1861
Qy	2077	tgcaggaatctgtgctgagcgacggaacatccacgaagctgctgcagcgggacacggaataaaacg	2133
Db	1861	tgcaggaatctgtgctgagcgacggaacatccacgaagctgctgcagcgggacacggaataaaacg	1920
Qy	2137	gtgtctatactgcaacagatgccttaccctctgttaccgttgatgatactcttctgcggtgta	2196
Db	1921	gtgtctatactgcaacagatgccttaccctctgttaccgttgatgatactcttctgcggtgta	1980
Qy	2197	tgcgcgcgctgcacatgcgcctcttcacgaagctgcgccttgatttactaagctgctgcgtatca	2255
Db	1981	tgcgcgcgctgcacatgcgcctcttcacgaagctgcgccttgatttactaagctgctgcgtatca	2044
Qy	2257	tcaagggcatctgttatgagaaaggagacgcgtgcgaagaagacatgcgatatctatgcgccc	2316
Db	2041	tcaagggcatctgttatgagaaaggagacgcgtgcgaagaagacatgcgatatctatgcgccc	2100
Qy	2317	tggacaacacgacactcgtgttgtagctgtgctcatatgtagccctatctctcttctgtga	2377
Db	2101	tggacaacacgacactcgtgttgtagctgtgctcatatgtagccctatctctcttctgtga	2166
Qy	2377	gcgcctgcacgtctagctgtgttcatctcgaagcttagagaaacacgcgcctacgaagtgatccca	2436
Db	2161	gcgcctgcacgtctagctgtgttcatctcgaagcttagagaaacacgcgcctacgaagtgatccca	2220
Qy	2437	gcgtgtgtgttctctctctgtccgtgtgttctgtctgtgtgcacaatccctgcagctgtctctga	2497
Db	2221	gcgtgtgtgttctctctctgtccgtgtgttctgtctgtgtgcacaatccctgcagctgtctctga	2280
Qy	2497	ttagcacacactctctccacagacacaacacgcgcgcgcgcctctgggggcacatcaactatcca	2556
Db	2281	ttagcacacactctctccacagacacaacacgcgcgcgcgcctctgggggcacatcaactatcca	2344
Qy	2557	cgctgtacactgcgcctacgctcctctgtgtgtgtgtgcacatgcagactacgtgggtcttcaactca	2616
Db	2341	cgctgtacactgcgcctacgctcctctgtgtgtgtgtgcacatgcagactacgtgggtcttcaactca	2400
Qy	2617	agactctgcctcagctcgtctcctcctgtgcctgtggtcttcttggtcttgagcttgagacttgccc	2676
Db	2401	agactctgcctcagctcgtctcctcctgtgcctgtggtcttcttggtcttgagcttgagacttgccc	2466
Qy	2677	cttcttgaggaagcagggcatctggaagctgcgaagctgaggaacaactcgtttggaagctcctgtggaag	2736
Db	2461	cttcttgaggaagcagggcatctggaagctgcgaagctgaggaacaactcgtttggaagctcctgtggaag	2520
Qy	2737	aagatgagctctcaacttcaacacacttcogtccatcagatgcagctgtttgagacacttccctctgtg	2796
Db	2521	aagatgagctctcaacttcaacacacttcogtccatcagatgcagctgtttgagacacttccctctgtg	2580
Qy	2797	gggtgcgaacgtcctgtgatactgagagctgtcttccacagggccagtgaggaattccacagccct	2856
Db	2581	gggtgcgaacgtcctgtgatactgagagctgtcttccacagggccagtgaggaattccacagccct	2640
Qy	2857	ggatatttctcttgcaacccaagctccactacgtgttgccgaggaagaatgtatgtaggaagcacaac	2916
Db	2641	ggatatttctcttgcaacccaagctccactacgtgttgccgaggaagaatgtatgtaggaagcacaac	2700
Qy	2917	cgtggttccacaacagaagaagatgctgcagaaatctgcactgagggagggaggaacccacacacttga	2976
Db	2701	cgtggttccacaacagaagaagatgctgcagaaatctgcactgagggagggaggaacccacacacttga	2760
Qy	2977	agctgcggcgctgtccatctagaacacctgtgtaaagaatctacacgaagatggaatgaaagctgtgtg	3036
Db	2761	agctgcggcgctgtccatctagaacacctgtgtaaagaatctacacgaagatggaatgaaagctgtgtg	2820
Qy	3037	tgcgatgcgcctgcgcactgaaattttatgtagggccaagataccctctctctgggcccacaatg	3096
Db	2821	tgcgatgcgcctgcgcactgaaattttatgtagggccaagataccctctctctgggcccacaatg	2880
Qy	3097	gagcggggaagaacacaacacatgtcaactctgcagcgggtgtgttcccccgcactctgcgga	3156

Db	2881	gaacggggaagagaccaccatgtaactctgacccgggtgttccccccgacctgggca	2940
QY	3157	ccgcctacaactctgggaaaaagacatcgctcgagatgagcaacatccggcagaacctgg	3216
Db	2941	ccgcctacatactctgggaaaaagacatcgctcgagatgagcaacatccggcagaacctgg	3000
QY	3217	gggtcgtcccccagcaatacgtcgtgttgagatgtaactctgaaaaacacatctgt	3276
Db	3001	gggtcgtcccccagcaatacgtcgtgttgagatgtaactctgaaaaacacatctgt	3060
QY	3277	tcatacgcccgcttgaaaaaggtctctcgaaagcaacgttgaaagcgagatgagatgag	3336
Db	3061	tcatacgcccgcttgaaaaaggtctctcgaaagcaacgttgaaagcgagatgagatgag	3120
QY	3337	ccctggatgttggtttgcatcaagcaagctgaaaaaacaagccagctgtcaagtg	3396
Db	3121	ccctggatgttggtttgcatcaagcaagctgaaaaaacaagccagctgtcaagtg	3180
QY	3397	gaatgcagaagaagctatctgtgaccttgacctgttcgggggagatcaagttgtcatc	3456
Db	3181	gaatgcagaagaagctatctgtgaccttgacctgttcgggggagatcaagttgtcatc	3240
QY	3457	tgagtgaacccaacagctggtgtggaaccttactccgcaggggaaatagtgagctgtgc	3516
Db	3241	tgagtgaacccaacagctggtgtggaaccttactccgcaggggaaatagtgagctgtgc	3300
QY	3517	tgaatataccgaagaagcgccgcacatattctctcaacacacacatggaatgaagcgagc	3576
Db	3301	tgaatataccgaagaagcgccgcacatattctctcaacacacacatggaatgaagcgagc	3360
QY	3577	tccttgggggaacagatgcatcatctccatctcgaaagctgtgctgtgtgggctctccc	3636
Db	3361	tccttgggggaacagatgcatcatctccatctcgaaagctgtgctgtgtgggctctccc	3420
QY	3637	tgttctctgaagaacacagctgaggaaacagctactacccttgctcaagaagaatgtg	3696
Db	3421	tgttctctgaagaacacagctgaggaaacagctactacccttgctcaagaagaatgtg	3480
QY	3697	aatctccctcaagttccctcgcaagaacagtagaacctgttcaacacctgaaaaagggg	3756
Db	3481	aatctccctcaagttccctcgcaagaacagtagaacctgttcaacacctgaaaaagggg	3540
QY	3757	acagtgttctcaagaacagttctgaatgctggccttggcagcgacaatgaggtgacaacg	3816
Db	3541	acagtgttctcaagaacagttctgaatgctggccttggcagcgacaatgaggtgacaacg	3600
QY	3817	tgaacatgagtgctctgctatcttccaaacctcataggaacatgtgtctgaagccggc	3876
Db	3601	tgaacatgagtgctctgctatcttccaaacctcataggaacatgtgtctgaagccggc	3660
QY	3877	tggtagaagacataagggcatagctgacctaagtgtcgtccatatgaagctcttaaggg	3936
Db	3661	tggtagaagacataagggcatagctgacctaagtgtcgtccatatgaagctcttaaggg	3720
QY	3937	gagccttgttggaactcttcaatgagatgtagcagcgctctcagaacctgggcatctca	3996
Db	3721	gagccttgttggaactcttcaatgagatgtagcagcgctctcagaacctgggcatctca	3780
QY	3997	gttatggcatctcagagacgagccctggagaagaatatctctaaagttggccgaagaagtg	4056
Db	3781	gttatggcatctcagagacgagccctggagaagaatatctctaaagttggccgaagaagtg	3840
QY	4057	gggtggaatgctgagacctaagatgtaactgtgcagcagaacgaaaacggcgccctcg	4116
Db	3841	gggtggaatgctgagacctaagatgtaactgtgcagcagaacgaaaacggcgccctcg	3900
QY	4117	gggaacaacagagctgttcttgcgcgttccactgaaagatgagtgtcgtcgtatccaaatgatt	4176
Db	3901	gggaacaacagagctgttcttgcgcgttccactgaaagatgagtgtcgtcgtatccaaatgatt	3960
QY	4177	ctgacatagaccagaacatccagagagacagactgctcagtgagatgagatgcaaaaggt	4236
Db	3961	ctgacatagaccagaacatccagagagacagactgctcagtgagatgagatgcaaaaggt	4020
QY	4237	ccatacaggtgaaagagctggaacacttaacagcaacagttgtgaccttgttggaaga	4296
Db	4021	ccatacaggtgaaagagctggaacacttaacagcaacagttgtgaccttgttggaaga	4080
QY	4297	gactgctaattgccaagacggagcttggaagaagatttttgcataagatgtcttcagctg	4356
Db	4081	gactgctaattgccaagacggagcttggaagaagatttttgcataagatgtcttcagctg	4140
QY	4357	tgttgcctgcatgacctgtgtgttcagcctgtaacgtgcagcccttggcaatccccca	4416
Db	4141	tgttgcctgcatgacctgtgtgttcagcctgtaacgtgcagcccttggcaatccccca	4200
QY	4417	gctctggaactcagccctgtagtatacagaacagatgacacattgtcaagcaatgtctc	4476
Db	4201	gctctggaactcagccctgtagtatacagaacagatgacacattgtcaagcaatgtctc	4260
QY	4477	ctgagagacagggaaaccttggaactttaaagccctcaccaagaccctggttcggga	4536
Db	4261	ctgagagacagggaaaccttggaactttaaagccctcaccaagaccctggttcggga	4320
QY	4537	cccgctgataaggaagaaacccaatcccaagaacgacctgcagcgagggaggaagagt	4596
Db	4321	cccgctgataaggaagaaacccaatcccaagaacgacctgcagcgagggaggaagagt	4380
QY	4597	ggaccacatgcccagcttccccaagacatacatggaactcttcacgaalgggaactgacaa	4656
Db	4381	ggaccacatgcccagcttccccaagacatacatggaactcttcacgaalgggaactgacaa	4440
QY	4657	tgcagaacccctcaacctgcatgtagctgtagcagcgacgaacaaatcaagaagaatgctcgtg	4716
Db	4441	tgcagaacccctcaacctgcatgtagctgtagcagcgacgaacaaatcaagaagaatgctcgtg	4500
QY	4717	tgtgtcccccagggcgagggggtgctgctctccacaaaagaaaacaacaacatgacagata	4776
Db	4501	tgtgtcccccagggcgagggggtgctgctctccacaaaagaaaacaacaacatgacagata	4560
QY	4777	tccttcagagacctggaacgagaagaacaattcggatattctcgtggaagagctagtgacaga	4836
Db	4561	tccttcagagacctggaacgagaagaacaattcggatattctcgtggaagagctagtgacaga	4620
QY	4837	tcataagccaagaagcttlaaagaacaagaatcgggtgtaatgagtttaagtagcgctctt	4896
Db	4621	tcataagccaagaagcttlaaagaacaagaatcgggtgtaatgagtttaagtagcgctctt	4680
QY	4897	ccctgggtgtcagtaatactcaagcaactctcccgagctcaagaagttaatgatagcatac	4956
Db	4681	ccctgggtgtcagtaatactcaagcaactctcccgagctcaagaagttaatgatagcatac	4740
QY	4957	aacaaatgaaagaacaactaaagctggccgaagacagttctgacatgcatcttcaaca	5016
Db	4741	aacaaatgaaagaacaactaaagctggccgaagacagttctgacatgcatcttcaaca	4800
QY	5017	gcttgggaagatttatagcagagctggaacccaagaaataatgtcaagagtgtgttcaata	5076
Db	4801	gcttgggaagatttatagcagagctggaacccaagaaataatgtcaagagtgtgttcaata	4860
QY	5077	acaaaggtgtgcatgcaatcaagctcttctctgaaatgtcatcaacaatgcatcttccggg	5136
Db	4861	acaaaggtgtgcatgcaatcaagctcttctctgaaatgtcatcaacaatgcatcttccggg	4920
QY	5137	ccaacctgcaaaaagggaagaacccctagccattatggaatttaattgcttccaatcccc	5196
Db	4921	ccaacctgcaaaaagggaagaacccctagccattatggaatttaattgcttccaatcccc	4980
QY	5197	tgaatctcaacaaagcagctcttcagaggttgctctgataagaccacatcagtgagatgctc	5256
Db	4981	tgaatctcaacaaagcagctcttcagaggttgctctgataagaccacatcagtgagatgctc	5040
QY	5257	tgtgtccatctgtgtcatctcttgcagatgacctgtgtccagccagcttgtccgatctcc	5316
Db	5041	tgtgtccatctgtgtcatctcttgcagatgacctgtgtgtccagccagcttgtgtgatctcc	5100

QY	5317	tgatccagagcgcggtgccagcaagaacaaacactgcaattcatcaagtgagggtgaagcctg	5370
Db	5101	tgatccagagcgcggtgccagcaagaacaaacactgcaattcatcaagtgagggtgaagcctg	5160
QY	5377	tcaatcaactgacctataattgtctggtgacatgtgaactaacgtgtgacctgcccacac	5436
Db	5161	tcaatcaactgacctataattgtctggtgacatgtgaactaacgtgtgacctgcccacac	5220
QY	5437	tggtcatatcatctcatctgtcttccagcaagaatctctatggtgttccccaactctgc	5496
Db	5221	tggtcatatcatctcatctgtcttccagcaagaatctctatggtgttccccaactctgc	5280
QY	5497	ctgtgcacgacctctactcttctgtctgtatgggttgcaatcacacctctcatgtaccag	5556
Db	5281	ctgtgcacgacctctactcttctgtctgtatgggttgcaatcacacctctcatgtaccag	5340
QY	5557	ccctccttgtgttcaagaaluccccagcacagcctatgvtgtctacacgctgaacctct	5616
Db	5341	ccctccttgtgttcaagaaluccccagcacagcctatgvtgtctacacgctgaacctct	5400
QY	5617	tcatctgcatatgacgagctggtgcacaccttctgtgctgagctgtttacacgaataagc	5676
Db	5401	tcatctgcatatgacgagctggtgcacaccttctgtgctgagctgtttacacgaataagc	5460
QY	5677	tgaaataatcaatgatatctgaatctgaatctccgtgttcttgatcttcccaactttgtcctg	5736
Db	5461	tgaaataatcaatgatatctgaatctgaatctccgtgttcttgatcttcccaactttgtcctg	5520
QY	5737	gacgaagggcctcatcgcacatctgtgtgaanaaacgacatgctctgtacgaccttgaaagtcttgc	5796
Db	5521	gacgaagggcctcatcgcacatctgtgtgaanaaacgacatgctctgtacgaccttgaaagtcttgc	5580
QY	5797	ggaggaatcgcttctgtctcaacattactctgtgaccttgggtggagcaaacctcttgcca	5856
Db	5581	ggaggaatcgcttctgtctcaacattactctgtgaccttgggtggagcaaacctcttgcca	5640
QY	5857	tgcccggtggaaagggtgtgtcttctccatcactgtcttgatccaagtaacagattcttca	5916
Db	5641	tgcccggtggaaagggtgtgtcttctccatcactgtcttgatccaagtaacagattcttca	5700
QY	5917	tcaagcccaagaccctgtaaatgcaaaagcctatctccctctgaatgatagaagataagatgtga	5976
Db	5701	tcaagcccaagaccctgtaaatgcaaaagcctatctccctctgaatgatagaagataagatgtga	5760
QY	5977	ggcgggaaagacagagaatctctgtatgtgtgagccagaaatgaaactcttaagaatcaag	6036
Db	5761	ggcgggaaagacagagaatctctgtatgtgtgagccagaaatgaaactcttaagaatcaag	5820
QY	6037	agttgacgaagaatatagaagaagaacgagaaagccctgtcttacaagatcttgctgggca	6096
Db	5821	agttgacgaagaatatagaagaagaacgagaaagccctgtcttacaagatcttgctgggca	5880
QY	6097	tctcctcctgtgtgagtgctcttgggctccctgtgagatlttaatggggcttgagaaatcatcaact	6156
Db	5881	tctcctcctgtgtgagtgctcttgggctccctgtgagatlttaatggggcttgagaaatcatcaact	5940
QY	6157	tcaagatgtttaaaccgagatacaacactgttaccagagaaatgacttcccttaacaaata	6216
Db	5941	tcaagatgtttaaaccgagatacaacactgttaccagagaaatgacttcccttaacaaata	6000
QY	6217	gtatcttatacaaaatcatcgaagtcatcatcaagaacaatgggctctactgacctctgtatg	6276
Db	6001	gtatcttatacaaaatcatcgaagtcatcatcaagaacaatgggctctactgacctctgtatg	6060
QY	6277	ccatcacagagctgtctgactctggagagaaacgttgaggttcttctgaccttttgaaagag	6336
Db	6061	ccatcacagagctgtctgactctggagagaaacgttgaggttcttctgaccttttgaaagag	6120
QY	6337	tcccaagaaagaagctgtggcaagctgtgtgtatgtgtggctggatcttccgaaacatggccctgga	6396
Db	6121	tcccaagaaagaagctgtggcaagctgtgtgtatgtgtggctggatcttccgaaacatggccctgga	6180
QY	6397	agtatggagaaatatatctgtgtactatagtgtgaggaacaaacgcaagctctctacag	6456

Db	6181	agcatgagagaaaaataatgctcgtgnaactatagcggagcaacaaacgcgaagctctctcaag	6240
Qy	6457	ccatgagctcttgatccgcgcggcctctcgtggtgttctctggaatgaacccacccgaagcctg	6516
Db	6241	ccatgagctcttgatccgcgcggcctctcgtggtgttctctggaatgaacccacccgaagcctg	6300
Qy	6517	atcccaagaacccgcgcgttctctctgtgnaatctgtcccaagctgtctcaaggagagggagat	6576
Db	6301	atcccaagaacccgcgcgttctctctgtgnaatctgtcccaagctgtctcaaggagagggagat	6360
Qy	6577	cagtaagtgtctacatccatcctatgatacgtgaagaatgtgaagcctcttgacatcgtatgacaa	6636
Db	6361	cagtaagtgtctacatccatcctatgatacgtgaagaatgtgaagcctcttgacatcgtatgacaa	6420
Qy	6637	tcatagtgcatactggaagttcaagctgtccttcggcgcgcgtcccaagatcctaaaaataagcttg	6696
Db	6421	tcatagtgcatactggaagttcaagctgtccttcggcgcgcgtcccaagatcctaaaaataagcttg	6480
Qy	6697	gagaatgttctacacatagttgttacaataagcagaggtctcaaccccgagactgaagcctgtcc	6756
Db	6481	gagaatgttctacacatagttgttacaataagcagaggtctcaaccccgagactgaagcctgtcc	6540
Qy	6757	aggatctctcttgtagactgtgcatcttccctcggaagtggtctcttaaaagaagaacccggaacatgc	6816
Db	6541	aggatctctcttgtagactgtgcatcttccctcggaagtggtctcttaaaagaagaacccggaacatgc	6600
Qy	6817	tacataaccagctctccatctctcatctctctctcgcgcgaagctatctcaagcactccctcc	6876
Db	6601	tacataaccagctctccatctctcatctctctctcgcgcgaagctatctcaagcactccctcc	6660
Qy	6877	agagcaaaaagcgagctccacatacgaagaactactcgttctctcagacacacattgaccag	6936
Db	6661	agagcaaaaagcgagctccacatacgaagaactactcgttctctcagacacacattgaccag	6720
Qy	6937	tatttctggaactcttgccaagaagaccagaatgtatgatacacccttaaaagaagcctctatcac	6996
Db	6721	tatttctggaactcttgccaagaagaccagaatgtatgatacacccttaaaagaagcctctatcac	6780
Qy	6997	acaaaacccagacagatgagctgagctgtgcagttctccacatcttctctacagatacgaataag	7056
Db	6781	acaaaacccagacagatgagctgagctgtgcagttctccacatcttctctacagatacgaataag	6840
Qy	7057	tgaaaagaagctatgatacgaagaatcctcgtctcaacaggggtgcctggaagaataaagaagaa	7116
Db	6841	tgaaaagaagctatgatacgaagaatcctcgtctcaacaggggtgcctggaagaataaagaagaa	6900
Qy	7117	ctagaactctctctgcacccctgtgaagctgtctgtggaagaagaagccagaagctgtatgtg	7176
Db	6901	ctagaactctctctgcacccctgtgaagctgtctgtggaagaagaagccagaagctgtatgtg	6960
Qy	7177	gaagaagtaaaactgagatacgttactgatactatctaatcgaatgcaatctcaatgcaatga	7236
Db	6961	gaagaagtaaaactgagatacgttactgatactatctaatcgaatgcaatctcaatgcaatga	7020
Qy	7237	aaacaaaattccattacaaggcgagtcctcttgtaacctatgctcgtgtatacgtgctcccaag	7296
Db	7021	aaacaaaattccattacaaggcgagtcctcttgtaacctatgctcgtgtatacgtgctcccaag	7080
Qy	7297	tgaaaagacttgaaattgatttttaacctatacctatgtgaacactctatacgtgaacccaa	7356
Db	7081	tgaaaagacttgaaattgatttttaacctatacctatgtgaacactctatacgtgaacccaa	7140
Qy	7357	tggaacatactggtcttgagaccgaacgcttttttttttttttttttttttttttttttttttttt	7415
Db	7141	tggaacatactggtcttgagaccgaacgcttttttttttttttttttttttttttttttttttttt	7200
Qy	7416	ggagcttgcaaaaactatcacaagtaatacgtccatgcccagcgatattatgatacaaatcaaaa	7475
Db	7201	ggagcttgcaaaaactatcacaagtaatacgtccatgcccagcgatattatgatacaaatcaaaa	7260
Qy	7476	ggtaatgcacatcctcatcctaagccatgccaatgcccagggagatggtttcccggtga	7536

XX		PF	01-NOV-2000; 2000MD-US30109.
XX		PR	01-NOV-1999; 990US-0162803.
XX		PR	30-JUN-2000; 2000US-0215564.
XX		PA	(MISC) WISCONSIN ALUMNI RES FOUND.
PI		PI	Attie AD, Cook M, Gray-Keller MP, Hayden MR, Pimstone S;
XX		PI	Brooks-Wilson A;
DR		DR	MPI; 2001-335779/35.
XX		PT	P-PsDB; AAB62691.
PT		PT	New method for inhibiting cholesterol uptake in the gut comprises
XX		XX	administration of an inhibitor of an ABC1 protein -
PS		PS	disclosure; Page 34-36; 41pp; English.
XX		CC	The invention relates to a new method for inhibiting cholesterol uptake
CC		CC	in the gut that comprises administration of an inhibitor of an ABC1
CC		CC	protein. The method is useful for: lowering levels of LDL (low density
CC		CC	lipoprotein) cholesterol by reducing the activity of ABC1 protein in the
CC		CC	intestinal cells and the abundance of the ABC1 protein in the individual
CC		CC	by inhibiting the activity of the protein; identifying drugs that can
CC		CC	lower serum cholesterol and LDL levels comprising assaying the drug to
CC		CC	test if it can bind to an ABC1 protein; testing LDL cholesterol lowering
CC		CC	agents; and for modulation of ABC1 biological activity. The present
XX		XX	sequence represents a human ABC1 nucleotide sequence.
SQ			Sequence 7860 BP; 2013 A; 1861 C; 2009 G; 1977 T; 0 other;
			Query Match 74.9%; Score 7822.6; DB 22; Length 7860;
			Best Local Similarity 99.9%; Pred. No. 0;
			Matches 7850; Conservative 0; Mismatches 9; Indels 2; Gaps 2.
OY	217	gaccctgtctgaagctctgcgcgcgtcccttcagaaggctcccgacacacgctgggcgtg	276
Db	1	gtcccctcgtttagctctgcgcgcgtcccttcagaaggctcccgacacacgctgggcgtg	60
OY	277	cctgcctgaaggagacatgctcttgctgcctcacgtacaggttgtctgttggaagaacctca	336
Db	61	ctgcgtctgaaggagacatgctcttgctgcctcacgtacaggttgtctgttggaagaacctca	120
OY	337	cttcagaagaagacaacaatgctcagctgttaacttggaagtgcgcctgcctcattatct	396
Db	121	cttcagaagaagacaacaatgctcagctgttgctgttggaagtgcgcctgcctcattatct	180
OY	397	tccitactcgtctctctgttcgtcgtcagctataccacacctatgaacaacatgaatgccatt	456
Db	181	tccitactcgtctctctgttcgtcgtcagctataccacacctatgaacaacatgaatgccatt	240
OY	457	ttccaataaaaccaatgcctctgcctcgaagaaaccttccttggtttaagggaattactcta	516
Db	241	ttccaataaaaccaatgcctctgcctcgaagaaaccttccttggtttaagggaattactcta	300
OY	517	atgccacaacccccgttltcogtiaaccgactcctggggaggtlcccgagttgttgaa	576
Db	301	atgccacaacccccgttltcogtiaaccgactcctggggaggtlcccgagttgttgaa	360
OY	577	acttaacaacaatcctgttgctgcgcctgttcagatgcgcgcggaggtcttttataca	636
Db	361	acttaacaacaatcctgttgctgcgcctgttcagatgcgcgcggaggtcttttataca	420
OY	637	gccagaagaacacacgacatgaagacatgcgcgcaaatctctagaaacattacagacatca	696
Db	421	gccagaagaacacacgacatgaagacatgcgcgcaaatctctagaaacattacagacatca	480
OY	697	agaaatcacgctcaaaccttgaagcttcaaagatttcctcgtgtgacaaatgaaaaccttctctg	756
Db	481	agaaatcacgctcaaaccttgaagcttcaaagatttcctcgtgtgacaaatgaaaaccttctctg	540

QY	757	ggtctctatataccaacactctctctcccaagctactgttggacaagatgctgaaggtctg	816
Db	541	ggttctctgtataccaacactctctcccaagctactgttggacaagatgctgaaggtctg	600
QY	817	atgttcattctcccaaggtatttttggaaaggtcccaagttacatttgaagaagctgttga	876
Db	601	atgtcatctccccaaggtatttttggaaaggtcccaagttacatttgaagaagctgttga	660
QY	877	atggtatcaaatcaagaagagatgattcacttgtgtgacaagaaggttctgaagcttgtg	936
Db	661	atggtatcaaatcaagaagagatgatttcaacttgtgtgacaagaaggttctgaagcttgtg	720
QY	937	gctctaccaaaagagaaactgctgctgcagcagcagtgtaactcgttcccaaatgatcc	996
Db	721	gctctaccaaaagagaaactgctgctgcagcagcagtgtaactcgttcccaaatgatcc	780
QY	997	tgaagccaatccctggaataaacttaaacctacactcccttcccgagaaagagctgtgtg	1056
Db	781	tgaagccaatccctggaataaacttaaacctacactcccttcccgagaaagagctgtgtg	840
QY	1057	aagccacaanaaacatgtctgtcatagtccttggactctgtgcccagagagcttcaagcatg	1116
Db	841	aagccacaanaaacatgtctgtcatagtccttggactctgtgcccagagagcttcaagcatg	900
QY	1117	gaagcttggagttgacatgacgacaggaagtatgtttcttcaacaatgtaaacgctccagct	1176
Db	901	gaagcttggagttgacatgacgacaggaagtatgtttcttcaacaatgtaaacgctccagct	960
QY	1177	ctctccacaacatctacacagctgtgtctgtatgtctgtggtggtcaltccgagggaggg	1236
Db	961	ctctccacaacatctacacagctgtgtctgtatgtctgtggtggtcaltccgagggaggg	1020
QY	1237	ggctgaagaatcaagttctctcaactgtgtatgagaacaacaactcaaaagccctcttggag	1296
Db	1021	ggctgaagaatcaagttctctcaactgtgtatgagaacaacaactcaaaagccctcttggag	1080
QY	1297	gcaabtgacatctgaggaagatgtgtgaaacctctatagacaactctacaactccttactgca	1356
Db	1081	gcaabtgacatctgaggaagatgtgtgaaacctctatagacaactctacaactccttactgca	1140
QY	1357	atgatttgaataaagaatttggagttcagtcctcttcccgactatctcggaaagctctga	1416
Db	1141	atgatttgaataaagaatttggagttcagtcctcttcccgactatctcggaaagctctga	1200
QY	1417	agccgctgtctgttggggaagaatccctgtatatacaactgtgacaactccacgacaagcagtgca	1476
Db	1201	agccgctgtctgttggggaagaatccctgtatatacaactgtgacaactccacgacaagcagtgca	1260
QY	1477	tggctggaagtgaacaagaacttccaagaatgtgcgtgtgtccatbatcttggaaagcatgt	1536
Db	1261	tggctggaagtgaacaagaacttccaagaatgtgcgtgtgtccatbatcttggaaagcatgt	1320
QY	1537	gggaaggaactcaagccccaagaatctcgtgaccttcatggaagacagcccaagaatvgaaacttg	1596
Db	1321	gggaaggaactcaagccccaagaatctcgtgaccttcatggaagacagcccaagaatvgaaacttg	1380
QY	1597	tccggatgtctgttggacaagcagggacaatatcaaacatttgggaaacagcagttgtgagct	1656
Db	1381	tccggatgtctgttggacaagcagggacaatatcaaacatttgggaaacagcagttgtgagct	1440
QY	1657	tagaatttgacagccccaagacatctgttggcgttlttggccaagacccaagagatgtccagtt	1716
Db	1441	tagaatttgacagccccaagacatctgttggcgttlttggccaagacccaagagatgtccagtt	1500
QY	1717	ccagttaaatgttctgtgtacacccctggagaaagcttcaagagagacttaacaggaatcc	1776
Db	1501	ccagttaaatgttctgtgtacacccctggagaaagcttcaagagagacttaacaggaatcc	1560
QY	1777	ggacaatatctgcgttcatggaagtgttcaacctgtgaacaagctatgaaacccaatagaacaag	1836
Db	1561	ggacaatatctgcgttcatggaagtgttcaacctgtgaacaagctatgaaacccaatagaacaag	1620
QY	1837	aagctgtgctacatcaacaagtccatvgagcgtgctgtgatatgaggaaggttctgtgctgtga	1896

Db	1621	aagtcggtctcaacaagatccaagagccgctgcggtgaggaagttcctggtctgta	1680
QY	1897	tttgttcaactggaattactcccaagcagcatctgagctgcgcccatacgtlcaagtacaaga	1956
Db	1681	tttgttcaactggaattactcccaagcagcatctgagctgcgcccatacgtlcaagtacaaga	1740
QY	1957	tcggaatvgacatctgacaatgtgagagagacaataataatcaagatggtgttacttggacc	2016
Db	1741	tcggaatvgacatctgacaatgtgagagagacaataataatcaagatggtgttacttggacc	1800
QY	2017	ctgtgcttcgagctgagccctcttgagagacacgctgcgtctcgtgaggggtcttgcctact	2076
Db	1801	ctgtgcttcgagctgagccctcttgagagacacgctgcgtctcgtgaggggtcttgcctact	1860
QY	2077	tgacagagctgtgtgtagcagcagcgaatcatcaaggtgtctgacggtgcacccgagaagaacatg	2136
Db	1861	tgacagagctgtgtgtagcagcagcgaatcatcaaggtgtctgacggtgcacccgagaagaacatg	1920
QY	2137	gtgtgtctatagcaacagatgagccctcttcctgttaagtttgaatgagacatcttctcgggtga	2196
Db	1921	gtgtgtctatagcaacagatgagccctcttcctgttaagtttgaatgagacatcttctcgggtga	1980
QY	2197	tgaaaccggtcaaaagccctcttcatgacgctgagccctggaattactcaagtggtctgtatca	2256
Db	1981	tgaaaccggtcaaaagccctcttcatgacgctgagccctggaattactcaagtggtctgtatca	2040
QY	2257	lcaagggcatcgtgtatgtaggaagggagcaagcgtgaagaagacaabgcgatacatctggcc	2316
Db	2041	lcaagggcatcgtgtatgtaggaagggagcaagcgtgaagaagacaabgcgatacatctggcc	2100
QY	2317	tgagcaacagcatcacactctgatttaagctgtgtltaactagtagccatcatcctctctgtga	2376
Db	2101	tgagcaacagcatcacactctgatttaagctgtgtltaactagtagccatcatcctctctgtga	2160
QY	2377	gctgcgtgcctcgtctaggtgtgtatcatcctcgtgaagttagagaaacctctctccatacgtatccca	2436
Db	2161	gctgcgtgcctcgtctaggtgtgtatcatcctcgtgaagttagagaaacctctctccatacgtatccca	2220
QY	2437	gctgcgtgtgtgtcttccctcctccgtcttgctgcgtgtgtagacatccctgcagtgcttccctga	2496
Db	2221	gctgcgtgtgtgtcttccctcctccgtcttgctgcgtgtgtagacatccctgcagtgcttccctga	2280
QY	2497	ttagacaactctcttcacagagccaacctgtgcagcagctgtggtgggtgcataactactactca	2556
Db	2281	ttagacaactctcttcacagagccaacctgtgcagcagctgtggtgggtgcataactactactca	2340
QY	2557	cgctgttaacctccctacagctcgtgtgtgtgtagcaltgtagaagatcaagctgagctctcaactca	2616
Db	2341	cgctgttaacctccctacagctcgtgtgtgtgtagcaltgtagaagatcaagctgagctctcaactca	2400
QY	2617	agatcttcgtctagcctgtctgtctcctgtgagcttcttggtcttggtctgtgagatcttggccc	2676
Db	2401	agatcttcgtctagcctgtctgtctcctgtgagcttcttggtcttggtctgtgagatcttggccc	2460
QY	2677	tttttgagagacaaggatcagtgagagtgtagagagacaacctgttttagaggtcctgttgagg	2736
Db	2461	tttttgagagacaaggatcagtgagagtgtagagagacaacctgttttagaggtcctgttgagg	2520
QY	2737	aagatvggtcttaaatctcaaccaacttcgactcgaatcgaatcgtgtttgacaaccttctctatg	2796
Db	2521	aagatvggtcttaaatctcaaccaacttcgactcgaatcgaatcgtgtttgacaaccttctctatg	2580
QY	2797	gggtgtatgaacctgttataattgagagcgtctcttccaagccagtaggaatctccagagccct	2856
Db	2581	gggtgtatgaacctgttataattgagagcgtctcttccaagccagtaggaatctccagagccct	2640
QY	2857	gggtatttctcttgcacaagaatctcactgtgttttgtagaagaaagtgaagaaagagcaacc	2916
Db	2641	gggtatttctcttgcacaagaatctcactgtgttttgtagaagaaagtgaagaaagagcaacc	2700
QY	2917	ctgtgttccaacagaagaagtgttcagaaatctgcaltgtaggaaggaaccacacacttga	2976

Db 2701 ctggtccaccagaagaatatacaagaatctgcatgagaggaagccaccacttga 2760
QY 2977 agctggcgctgtccattcagaacctgtgtaaaagtctacagagatgagatgaagtgctg 3036
Db 2761 agctggcgctgtccattcagaacctgtgtaaaagtctacagagatgagatgaagtgctg 2820
QY 3037 tcnatgacctgagcactgtaattttatagaaggcgacatcaacctctctctggccacaatg 3096
Db 2821 tcnatgacctgagcactgtaattttatagaaggcgacatcaacctctctctggccacaatg 2880
QY 3097 gggcgaggagaagaagccaccatgccaatccctgagccgggtgttcccccagacctgggca 3156
Db 2881 gggcgaggagaagaagccaccatgccaatccctgagccgggtgttcccccagacctgggca 2940
QY 3157 ccgcatcaatccctgaggaagaacatctcgctctgagatgagagacccatccgggacaacctg 3216
Db 2941 ccgcatcaatccctgaggaagaacatctcgctctgagatgagagacccatccgggacaacctg 3000
QY 3217 gggctgtccaccagataacgtgtgtgttggacatgctgacgtctgaagaacacatctgtg 3276
Db 3001 gggctgtccaccagataacgtgtgtgttggacatgctgacgtctgaagaacacatctgtg 3060
QY 3277 tctatgcccgtctgaaagggctctctgagagacagctgaagcgagatgagatgagatgag 3336
Db 3061 tctatgcccgtctgaaagggctctctgagagacagctgaagcgagatgagatgagatgag 3120
QY 3337 cccctgagatgttggtctgccaatcaagcaagctgnaaaagcaaaacaagccagctgccaagt 3396
Db 3121 cccctgagatgttggtctgccaatcaagcaagctgnaaaagcaaaacaagccagctgccaagt 3180
QY 3397 gaattgagagaaagctatctgtgctgctgctgctgctgctgggggagcttaaggttttcaatc 3456
Db 3181 gaattgagagaaagctatctgtgctgctgctgctgctgctgggggagcttaaggttttcaatc 3240
QY 3457 tggatgaaccaccaagctggtgtgagaccccttaccgccgaggggaaatagtgagagctgtg 3516
Db 3241 tggatgaaccaccaagctggtgtgagaccccttaccgccgaggggaaatagtgagagctgtg 3300
QY 3517 tgaataaccgaagaagcgagaccatatactctctacaacacacatggaatgaagcgagag 3576
Db 3301 tgaataaccgaagaagcgagaccatatactctctacaacacacatggaatgaagcgagag 3360
QY 3577 tccctggggagacagatgtgcatcatctcccatgggagagctgtgctgtgtggtctctccc 3636
Db 3361 tccctggggagacagatgtgcatcatctcccatgggagagctgtgctgtgtggtctctccc 3420
QY 3637 tgttcttgaagaacagctgaggaacagagctactactgagacctgtg lcaagaagaatgtg 3696
Db 3421 tgttcttgaagaacagctgaggaacagagctactactgagacctgtg lcaagaagaatgtg 3480
QY 3697 aatctctccctagttccctgcaagaacagtagtagaactgtgtcatcaactgaaaaagagag 3756
Db 3481 aatctctccctagttccctgcaagaacagtagtagaactgtgtcatcaactgaaaaagagag 3540
QY 3757 acaggtgttctcagagacagcttctgagctgagctgagctggagcgagacatgagatgacagc 3816
Db 3541 acaggtgttctcagagacagcttctgagctgagctgagctggagcgagacatgagatgacagc 3600
QY 3817 tgaaccatcgaatgtctctgctatctccaacctcatcgaagaagatgtgtctgaagccggc 3876
Db 3601 tgaaccatcgaatgtctctgctatctccaacctcatcgaagaagatgtgtctgaagccggc 3660
QY 3877 tgggtggaagacatagggcatgagctgagctgactatgtgtgccaatgagctgttaaggagag 3936
Db 3661 tgggtggaagacatagggcatgagctgagctgactatgtgtgccaatgagctgttaaggagag 3720
QY 3937 gaggcttggggaacctcttcatgagatgagatgagccggtctcagaagccgggcatcttca 3996
Db 3721 gaggcttggggaacctcttcatgagatgagatgagccggtctcagaagccgggcatcttca 3780
QY 3997 gttatggcatctcagagacagacctggaagaataatctcctcaaggtggccggaagagatg 4056
Db 3781 gttatggcatctcagagacagacctggaagaataatctcctcaaggtggccggaagagatg 3840

QY 4057 ggggtgagatgctgagacactcagatgtgtactcttgcagagcaagcgaaacagcggggcttgc 4116
Db 3841 ggggtgagatgctgagacactcagatgtgtactcttgcagagcaagcgaaacagcggggcttgc 3900
QY 4117 gggacaagcagagctgtctctgcgcttcaactgagaatgagtgctgtgctgtaaccatgatt 4176
Db 3901 gggacaagcagagctgtctctgcgcttcaactgagaatgagtgctgtgctgtaaccatgatt 3960
QY 4177 ctgacatagaccagaatccagagagacagactgtctcagtgaggatgagatgagcaagaggt 4236
Db 3961 ctgacatagaccagaatccagagagacagactgtctcagtgaggatgagatgagcaagaggt 4020
QY 4237 cctaccaggtgaagaagcgctgggaacttacaacagcaacaggttggggcccttcttggaaga 4296
Db 4021 cctaccaggtgaagaagcgctgggaacttacaacagcaacaggttggggcccttcttggaaga 4080
QY 4297 gactgtaattgccaagcagagctcggaagagatttttgcacagatgtctgtccagctg 4356
Db 4081 gactgtaattgccaagcagagctcggaagagatttttgcacagatgtctgtccagctg 4140
QY 4357 tgttgtctgcatgtcccttgtgttcaagctgcatcggtgcaaccccttggcaagatgacca 4416
Db 4141 tgttgtctgcatgtcccttgtgttcaagctgcatcggtgcaaccccttggcaagatgacca 4200
QY 4417 gcttgaacttcaagccctgagatgtatacaacgaatgatacatctgttcaagcatgtgtc 4476
Db 4201 gcttgaacttcaagccctgagatgtatacaacgaatgatacatctgttcaagcatgtgtc 4260
QY 4477 ctgagagacagggaaacctgtgaactcttaacgacctcaaccaagacctgtgtcgga 4536
Db 4261 ctgagagacagggaaacctgtgaactcttaacgacctcaaccaagacctgtgtcgga 4320
QY 4537 cccgctgtatlggaaggaacccatccagacagcccttgcagagcgaggagaaagt 4596
Db 4321 cccgctgtatlggaaggaacccatccagacagcccttgcagagcgaggagaaagt 4380
QY 4597 ggaaccactgcccagcttcccagacatcatggaactcttccagaatggaactgtgaca 4656
Db 4381 ggaaccactgcccagcttcccagacatcatggaactcttccagaatggaactgtgaca 4440
QY 4657 tgcagaaccttcaactcagctgacgtgtgagcagcgacaataatgaagaagtgtgtcgt 4716
Db 4441 tgcagaaccttcaactcagctgacgtgtgagcagcgacaataatgaagaagtgtgtcgt 4500
QY 4717 tgggtcccccagggagagggggtgtgctctctccacaagaagaacaaacctgcagata 4776
Db 4501 tgggtcccccagggagagggggtgtgctctctccacaagaagaacaaacctgcagata 4560
QY 4777 tccctcagacctgacaggaagaacatctcgatattctggtgagaagcgtatgtgaca 4836
Db 4561 tccctcagacctgacaggaagaacatctcgatattctggtgagaagcgtatgtgaca 4620
QY 4837 tcatagccaagaagcttaagaacaagatcttggtgtgagtgagtttgaatgagtgagcgctt 4896
Db 4621 tcatagccaagaagcttaagaacaagatcttggtgtgagtgagtttgaatgagtgagcgctt 4680
QY 4897 cccctgggtgtcaataactcaagcacttcccccaggtcaagaagttaagtgtgacatca 4956
Db 4681 cccctgggtgtcaataactcaagcacttcccccaggtcaagaagttaagtgtgacatca 4740
QY 4957 aacaatgagaagaacacctaagaactgagcaagagacagctgtcagatgcgattctcaaca 5016
Db 4741 aacaatgagaagaacacctaagaactgagcaagagacagctgtcagatgcgattctcaaca 4800
QY 5017 gcttgggaagatttatagacagagctgagacccaagaataatgtaaggtgtgtgtaata 5076
Db 4801 gcttgggaagatttatagacagagctgagacccaagaataatgtaaggtgtgtgtaata 4860
QY 5077 acaaggtctgagcatgacatagctcttccctgagatgtcaacaatgcatctcccg 5136
Db 4861 acaaggtctgagcatgacatagctcttccctgagatgtcaacaatgcatctcccg 4920

QY 5137 ccaacctcgcaaaaggagagaaacccctagccatlatgaaatctactgtcttccatcatccccc 5196
 Db 4921 ccaaccccgcaaaaggagagaaacccctagccatlatgaaatctactgtcttccatcatccccc 4980
 QY 5197 tgaatccaccagagcagcagcctctcagaggtgctctgatagacacatcagtgagatgccc 5256
 Db 4981 tgaatccaccagagcagcagcctctcagaggtgctctgatagacacatcagtgagatgccc 5040
 QY 5257 ttgtgtaacatctgtgtaacatcttctgtaacatcttctgtaacatcttctgtaacatcttcc 5316
 Db 5041 ttgtgtaacatctgtgtaacatcttctgtaacatcttctgtaacatcttctgtaacatcttcc 5100
 QY 5317 tgaatccagagcggtgtaacagcaagcaaacacacccctgtaacatcttctgtaacatcttcc 5376
 Db 5101 tgaatccagagcggtgtaacagcaagcaaacacacccctgtaacatcttctgtaacatcttcc 5160
 QY 5377 tcaatccatctgctctcctaatcttctgtaacatcttctgtaacatcttctgtaacatcttcc 5436
 Db 5161 tcaatccatctgctctcctaatcttctgtaacatcttctgtaacatcttctgtaacatcttcc 5220
 QY 5437 tgaatccatctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5496
 Db 5221 tgaatccatctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5280
 QY 5497 ctgtgtaacagcctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5556
 Db 5281 ctgtgtaacagcctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5340
 QY 5557 cctcctctgtgtcgaagaccccgagacagcctcctcctcctcctcctcctcctcctcctc 5616
 Db 5341 cctcctctgtgtcgaagaccccgagacagcctcctcctcctcctcctcctcctcctcctc 5400
 QY 5617 tgaatccatctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5676
 Db 5401 tgaatccatctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5460
 QY 5677 tgaatccatctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5736
 Db 5461 tgaatccatctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5520
 QY 5737 gacagagcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5796
 Db 5521 gacagagcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5580
 QY 5797 gggagagcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5856
 Db 5581 gggagagcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5640
 QY 5857 tggcgcgtggaaggggtggtgtctcctcctcctcctcctcctcctcctcctcctcctc 5916
 Db 5641 tggcgcgtggaaggggtggtgtctcctcctcctcctcctcctcctcctcctcctcctc 5700
 QY 5917 tgaagccagagcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5976
 Db 5701 tgaagccagagcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 5760
 QY 5977 ggcgggaaagacagagaaatctctgagtggtgagggcagagacatctctgaaagacag 6036
 Db 5761 ggcgggaaagacagagaaatctctgagtggtgagggcagagacatctctgaaagacag 5820
 QY 6037 agttgagcagagataatataagagagagcggaagcctgctgtgtaagagattggtgagca 6096
 Db 5821 agttgagcagagataatataagagagagcggaagcctgctgtgtaagagattggtgagca 5880
 QY 6097 ttcctcccggtgagtgctgt 6156
 Db 5881 ttcctcccggtgagtgctgt 5940
 QY 6157 tcaagatgtaacagagagataccactgttaccagagagagtgctgttcccttaacaaata 6216
 Db 5941 tcaagatgtaacagagagataccactgttaccagagagagtgctgttcccttaacaaata 6000
 QY 6217 gtatctatacaacatcagatgaagtaacatcagaaacatggtcctcagtggtgag 6276

Db 6001 gtatctatacaacatcagatgaagtaacatcagaaacatggtcctcagtggtgag 6060
 QY 6277 ccatcacagagcgtgtgacatgagagagacacgtggaagttctctgtgaccttctgagagag 6336
 Db 6061 ccatcacagagcgtgtgacatgagagagacacgtggaagttctctgtgaccttctgagagag 6120
 QY 6337 tcccaagagaaagagtggtgcaaggttgggtgagtggtgagtggtgagtggtgagtggtgag 6396
 Db 6121 tcccaagagaaagagtggtgcaaggttgggtgagtggtgagtggtgagtggtgagtggtgag 6180
 QY 6397 agtatggaagaaatatactgtgtaactatagtggaagcaacaaacagcaagcctctcagag 6456
 Db 6181 agtatggaagaaatatactgtgtaactatagtggaagcaacaaacagcaagcctctcagag 6240
 QY 6457 ccatggtctgtatcgtgagcggtcctcctggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6516
 Db 6241 ccatggtctgtatcgtgagcggtcctcctggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6300
 QY 6517 atcccaagcgccggtcctcctggtgagtggtgagtggtgagtggtgagtggtgagtggtgag 6576
 Db 6301 atcccaagcgccggtcctcctggtgagtggtgagtggtgagtggtgagtggtgagtggtgag 6360
 QY 6577 cagtaagtgtaacatcctcctatagataggaagaaatggaagccttctgactatagatgca 6636
 Db 6361 cagtaagtgtaacatcctcctatagataggaagaaatggaagccttctgactatagatgca 6420
 QY 6637 tcatggtgtaacagagtggtgagtggtgagtggtgagtggtgagtggtgagtggtgagtggtg 6696
 Db 6421 tcatggtgtaacagagtggtgagtggtgagtggtgagtggtgagtggtgagtggtgagtggtg 6480
 QY 6697 gagaatggtatatacatatagtgtaacagaaatggaagtggtgagtggtgagtggtgagtggtg 6756
 Db 6481 gagaatggtatatacatatagtgtaacagaaatggaagtggtgagtggtgagtggtgagtggtg 6540
 QY 6757 aggaatctcttggagccttggaatctcctggaagtggttcttaaaagagaaacacggaaacatgc 6816
 Db 6541 aggaatctcttggagccttggaatctcctggaagtggttcttaaaagagaaacacggaaacatgc 6600
 QY 6817 tacaatccagcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 6876
 Db 6601 tacaatccagcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 6660
 QY 6877 agagcaaaagagcactcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 6936
 Db 6661 agagcaaaagagcactcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 6720
 QY 6937 tatttggaacttgccaagagacaaagtgaatgaatgaatgaatgaatgaatgaatgaatgaatga 6996
 Db 6721 tatttggaacttgccaagagacaaagtgaatgaatgaatgaatgaatgaatgaatgaatga 6780
 QY 6997 acaaaaacagacagtagtgagcgtgcaagttctcctcctcctcctcctcctcctcctcctcctc 7056
 Db 6781 acaaaaacagacagtagtgagcgtgcaagttctcctcctcctcctcctcctcctcctcctc 6840
 QY 7057 tgaagagaaagctatgtaataagaaatcctgttaataaggggtggtcgtgaagtaagagaa 7116
 Db 6841 tgaagagaaagctatgtaataagaaatcctgttaataaggggtggtcgtgaagtaagagaa 6900
 QY 7117 ctgagcttctccttgcaacatgtaagtggttggaagaaagccaaagagtggtgtg 7176
 Db 6901 ctgagcttctccttgcaacatgtaagtggttggaagaaagccaaagagtggtgtg 6960
 QY 7177 gaagagtaaacctgtaactgtactgtatatactltaaatgcaatgcaatgcaatgcaatgca 7236
 Db 6961 gaagagtaaacctgtaactgtactgtatatactltaaatgcaatgcaatgcaatgcaatgca 7020
 QY 7237 aaacaaatccattacagagggcgagtgccctgtgagcctatgtctgtatgagtgctcag 7296
 Db 7021 aaacaaatccattacagagggcgagtgccctgtgagcctatgtctgtatgagtgctcag 7080
 QY 7297 tgaagagctggaattagtttttaactatacctatggaactatataaggaaccaa 7356

Dh 1 gtccctgtctgtgagctctgcccgtccctcccaaggctcccgagccacacgctggggtg 60
QY 277 ctgctctgagggagaaatggtctgtgtgtccctcagctcgtgaagctgtctgtgtgaagaactta 336
Db 61 ctgctctgagggagaaatggtctgtgtgtccctcagctcgtgaagctgtctgtgtgaagaactta 120
QY 337 ctcttcagaagaagaacaaacatgtcagctgttactgtgaagtgtgccttgcccttattatct 396
Db 121 ctcttcagaagaagaacaaacatgtcagctgttactgtgaagtgtgccttgcccttattatct 180
QY 397 tccgtatccgtatctctgtcttcgtcgtgagctacccaacctatgtgaacacatgtgacatt 456
Db 181 tccgtatccgtatctctgtcttcgtcgtgagctacccaacctatgtgaacacatgtgacatt 240
QY 457 ttccaataaaggcctatgctcctctgcagagaaacctccttggtgtcaggggattatctgta 516
Db 241 ttccaataaaggcctatgctcctctgcagagaaacctccttggtgtcaggggattatctgta 300
QY 517 atgccaacaaacccctgttccgttaccgactcctgtggagaggtcccggaagtgtttgtgaa 576
Db 301 atgccaacaaacccctgttccgttaccgactcctgtggagaggtcccggaagtgtttgtgaa 360
QY 577 actttaaacaatccatctgtgtcgtccgtcttctcagaatgctcggaggtctcttattaca 636
Db 361 actttaaacaatccatctgtgtcgtccgtcttctcagaatgctcggaggtctcttattaca 420
QY 637 gccagaagaacacacagatgaaagacatgcacagctcgaagtcttgagaacatatacagcagatca 696
Db 421 gccagaagaacacacagatgaaagacatgcacagctcgaagtcttgagaacatatacagcagatca 480
QY 697 agaaatccagctcaaaactgtgaagctcgaagattccctgtgtggaacaaatgaacctctctg 756
Db 481 agaaatccagctcaaaactgtgaagctcgaagattccctgtgtggaacaaatgaacctctctg 540
QY 757 gttctctatctcaaacacctctctctcccaaggcttctactgtggaacaaatgctcggaggtctg 816
Db 541 gttctctgtatctcaaacacctctctctcccaaggcttctactgtggaacaaatgctcggaggtctg 600
QY 817 atgtcatctctcaacaaggatattttgtcaaggctacacagttacattgtgcaaatgctctgtgca 876
Db 601 atgtcatctctcaacaaggatattttgtcaaggctacacagttacattgtgcaaatgctctgtgca 660
QY 877 atggtatcaaaatcagaagaagatgatttcaactgtgtgacccaagaagttctcgaagctttgtg 936
Db 661 atggtatcaaaatcagaagaagatgatttcaactgtgtgacccaagaagttctcgaagctttgtg 720
QY 937 gccctacaaaggagaactgtcgtcagcagagcgagtaacttcgtttccaaactggaactc 996
Db 721 gccctacaaaggagaactgtcgtcagcagagcgagtaacttcgtttccaaactggaactc 780
QY 997 tgaagccaatctctgtgaagaacactaaactatactccctcccgagcaaggagctgtgctg 1056
Db 781 tgaagccaatctctgtgaagaacactaaactatactccctcccgagcaaggagctgtgctg 840
QY 1057 aagccaacaaacatctgtctgcaatgcttctgagctctgcccagaagctgttcaagcattga 1116
Db 841 aagccaacaaacatctgtctgcaatgcttctgagctctgcccagaagctgttcaagcattga 900
QY 1117 gaaagctggaagtgtacatgcgacaggaagtgtatgtttctgtacaaagtgtgaacagctcagct 1176
Db 901 gaaagctggaagtgtacatgcgacaggaagtgtatgtttctgtacaaagtgtgaacagctcagct 960
QY 1177 cctccaccaaatctacacagagctgtgtctgttatgtctcgtgggcatcccgaggaggagg 1236
Db 961 cctccaccaaatctacacagagctgtgtctgttatgtctcgtgggcatcccgaggaggagg 1020
QY 1237 ggtctgaagatcaatctctcactacgtgtatgaggaacaaactacaagagccctcttgagg 1296
Db 1021 ggtctgaagatcaatctctcactacgtgtatgaggaacaaactacaagagccctcttgagg 1080
QY 1297 gcaatgagcactgaggaagatgtctgaacactctatgacaactctacaactccttactgca 1356
Db 1081 gcaatgagcactgaggaagatgtctgaacactctatgacaactctacaactccttactgca 1140

QY 1357 atgatttgatgaagaatatttgagctagctccctctcccgcaattatctggaagactctgta 1416
Db 1141 atgatttgatgaagaatatttgagctagctccctctcccgcaattatctggaagactctgta 1200
QY 1417 agccgctgcctgtgtggaagaatccctgtatacaactgtgaacactccagccaagaagcaggtgca 1476
Db 1201 agccgctgcctgtgtggaagaatccctgtatacaactgtgaacactccagccaagaagcaggtgca 1260
QY 1477 tggctgtggtgtgacaagaactccccaagaaactgtgtgttccatgatctgtgaagcattgt 1536
Db 1261 tggctgtggtgtgacaagaactccccaagaaactgtgtgttccatgatctgtgaagcattgt 1320
QY 1537 gggaggaacccaagccccaagaatctggaactctatgtgagaagaacccaagaatggaactgt 1596
Db 1321 gggaggaacccaagccccaagaatctggaactctatgtgagaagaacccaagaatggaactgt 1380
QY 1597 tccggtatgtctgtgtgaaagcagggacaatgtgaccacttttggaagaagcagatltgtgact 1656
Db 1381 tccggtatgtctgtgtgaaagcagggacaatgtgaccacttttggaagaagcagatltgtgact 1440
QY 1657 taagattggaagcccaagacatcgtgtggttttgccaagcaccagaagatltccaact 1716
Db 1441 taagattggaagcccaagacatcgtgtggttttgccaagcaccagaagatltccaact 1500
QY 1717 ccaagtaatgtctgtgtgtacacactgtgagaagacttccaagagatatacagaagcaatcc 1776
Db 1501 ccaagtaatgtctgtgtgtgtacacactgtgagaagacttccaagagatatacagaagcaatcc 1560
QY 1777 ggaaccaatctcgtctcatgaggtgtgtgtacaaactgtgaacactgtgaacccaatgacaag 1836
Db 1561 ggaaccaatctcgtctcatgaggtgtgtgtacaaactgtgaacactgtgaacccaatgacaag 1620
QY 1837 aagctgtgctatctcaacaagaagctcagtgagactgtgtgaacgaagaagttctcgtgtgta 1896
Db 1621 aagctgtgctatctcaacaagaagctcagtgagactgtgtgaacgaagaagttctcgtgtgta 1680
QY 1897 ttgtgttccctgtgaattactccagagcagacttgagctgtgcccacatgtcaagtatacaaga 1956
Db 1681 ttgtgttccctgtgaattactccagagcagacttgagctgtgcccacatgtcaagtatacaaga 1740
QY 1957 tccgaatgagacattacaaatgtgagagagacaataaataaagatgggttactggagacc 2016
Db 1741 tccgaatgagacattacaaatgtgagagagacaataaataaagatgggttactggagacc 1800
QY 2017 ctggtctccctcagactgaaccccttgagagacatgcggtactcgtgtggggggtctgcact 2076
Db 1801 ctggtctccctcagactgaaccccttgagagacatgcggtactcgtgtggggggtctgcact 1860
QY 2077 tgcagagatgtgtgtgagagcagacatcatcaggtgtgtgacggtgacccggaagaagaactg 2136
Db 1861 tgcagagatgtgtgtgagagcagacatcatcaggtgtgtgacggtgacccggaagaagaactg 1920
QY 2137 --gtgtctatatgtcaacagatgtccctatccctgttactcgtgtgacatctctctgggt 2194
Db 1921 gdtgtctctatatgtcaacagatgtccctatccctgttactcgtgtgacatctctctgggt 1980
QY 2195 gatgagccggtcgaatgtccctctctcatgacgctgtgctgtgattactcaagtgtgctgtg 2254
Db 1981 gatgagccggtcgaatgtccctctctcatgacgctgtgctgtgattactcaagtgtgctgtg 2040
QY 2255 catcaagggtcgtgtgtatgagaagagcagcgtgtgaagaagacatctcggaatactgtg 2314
Db 2041 catcaagggtcgtgtgtatgagaagagcagcgtgtgaagaagacatctcggaatactgtg 2100
QY 2315 cctgtgacaacagcactactcgtgtttagctgttcatatgagcctcatctctcttctgt 2374
Db 2101 cctgtgacaacagcactactcgtgtttagctgttcatatgagcctcatctctcttctgt 2160
QY 2375 gagcgtggtcgtgtgtgtgtgtctcctggaagttagaagaacctgtgcccataagatgacc 2434
Db 2161 gagcgtggtcgt 2220

QY 2435 cagcgtggttcttctcctcgtctgttctgtgtgtaacatccctcagcttccct 2494
|||||
Db 2221 cagcgtggttcttctcctcctcctcgttctgttctgtgtgtaacatccctcagcttccct 2280
|||||
QY 2495 gattagacaactctctccagagccaacttggcaagccttctgttggggcatalctact 2554
|||||
Db 2281 gattagacaactctctccagagccaacttggcagcagccttctgttggggcatalctact 2340
|||||
QY 2555 cagcgtgtacctgtccctacgttccctgtgtgtgcatgtgcaggaactaagtggttcaact 2614
|||||
Db 2341 cagcgtgtacctgtccctacgttccctgtgtgtgcatgtgcaggaactaagtggttcaact 2400
|||||
QY 2615 caagatctcgttgaactcctgtctcctcgttggcttttggttggcttgaacttctgc 2674
|||||
Db 2401 caagatctcgttgaactcctgtctcctcgttggcttttggttggcttgaacttctgc 2460
|||||
QY 2675 ccttttggagagcagggagcatgtgagtgagtgaggaacaactctgttgaagctctgtga 2734
|||||
Db 2461 ccttttggagagcagggagcatgtgagtgagtgaggaacaactctgttgaagctctgtga 2520
|||||
QY 2735 ggaagatgcttccatctcaacttccatctccatgtatgctgttgaaccttccctta 2794
|||||
Db 2521 ggaagatgcttccatctcaacttccatctccatgtatgctgttgaaccttccctta 2580
|||||
QY 2795 tgggtgtatgacctgtatcatctgagcgtctcttccagagcagtaacccaagcc 2854
|||||
Db 2581 tgggtgtatgacctgtgtatcatctgagcgtctcttccagagcagtaacccaagcc 2640
|||||
QY 2855 ctgtatcttctctgtacccaagtcctactgttctgtgcagaggaagtgtatgagaagcca 2914
|||||
Db 2641 ctgtatcttctctgtacccaagtcctactgttctgtgcagaggaagtgtatgagaagcca 2700
|||||
QY 2915 cctcgttcccaacccaagaaagtgtcagaatcttgcagtgagggaggaacccaact 2974
|||||
Db 2701 cctcgttcccaacccaagaaagtgtcagaatcttgcagtgagggaggaacccaact 2760
|||||
QY 2975 gaaagctggagctgttccatctcagaaccttgaataagtctacccaagatgtgaagtgtgc 3034
|||||
Db 2761 gaaagctggagctgttccatctcagaaccttgaataagtctacccaagatgtgaagtgtgc 2820
|||||
QY 3035 tgtcgtatgctgtgcactgtgaattttaaagggccagatccactcctctctgtggccaaca 3094
|||||
Db 2821 tgtcgtatgctgtgcactgtgaattttaaagggccagatccactcctctctgtggccaaca 2880
|||||
QY 3095 tggagggggggaagacacacacatctcctgacccggtgttcccccagaccccgag 3154
|||||
Db 2881 tggagggggggaagacacacacatctcctgacccggtgttcccccagaccccgag 2940
|||||
QY 3155 caccgactacatcctgtggaagaagacattcgtctctgtatgtgagcacatcccgacagact 3214
|||||
Db 2941 caccgactacatcctgtggaagaagacattcgtctctgtatgtgagcacatcccgacagact 3000
|||||
QY 3215 ggggtgtcttcccgacataaagctgtctgttgaacatgtcgtatgtcgaagaacacatctg 3274
|||||
Db 3001 ggggtgtcttcccgacataaagctgtctgttgaacatgtcgtatgtcgaagaacacatctg 3060
|||||
QY 3275 gtctctgtcccgctgtgaagggctctctgaagaagcagtggaagggcggaatgtgaagat 3334
|||||
Db 3061 gtctctgtcccgctgtgaagggctctctgaagaagcagtggaagggcggaatgtgaagat 3120
|||||
QY 3335 ggcctgtgagtgtgttctgtccatcaagcaagctgaaagcaaaacagccagctgtcag 3394
|||||
Db 3121 ggcctgtgagtgtgttctgtccatcaagcaagctgaaagcaaaacagccagctgtcag 3180
|||||
QY 3395 tggaaatgcagaaagaaatctatctgtgtccttgccttgccttgcggggggtctaaagtctat 3454
|||||
Db 3181 tggaaatgcagaaagaaatctatctgtgtccttgccttgccttgcggggggtctaaagtctat 3240
|||||
QY 3455 tctgtgataacccaacagctgtgtgtgaccccttaccocgagggagatgtgagactgtct 3514
|||||
Db 3241 tctgtgataacccaacagctgtgtgtgaccccttaccocgagggagatgtgagactgtct 3300
|||||
QY 3515 gctgaataacccaagagccgcacatctatctctctacacacacatgtgataagcgga 3574
|||||

Db 3301 gctgaataacccaagagccgcacatctatctctctacacacacatgtatgaagcgga 3360
|||||
QY 3575 cgtcctgtgggagacaggaattgcatactccatctcgaagaaactgtgtctgtgtgtccctc 3634
|||||
Db 3361 cgtcctgtgggagacaggaattgcatactccatctcgaagaaactgtgtctgtgtgtccctc 3420
|||||
QY 3635 cctgttctgaagaacagagcctgggaacagctactacttgaacttggctgaagaagtgt 3694
|||||
Db 3421 cctgttctgaagaacagagcctgggaacagctactacttgaacttggctgaagaagtgt 3480
|||||
QY 3695 ggaatccctccctcagcttccctgtcagaagaaacagtagtagcactgtgtcatalactgaagaaagga 3754
|||||
Db 3481 ggaatccctccctcagcttccctgtcagaagaaacagtagtagcactgtgtcatalactgaagaaagga 3540
|||||
QY 3755 ggaacagtgttctcagaagcagcttctgtatgtctgtgcctgtgcagcagacatgaagtgacac 3814
|||||
Db 3601 gctgaacatcgaatgtctcctgtctatctccaaactcaatgaagaagcatgtgtctgaagcccg 3660
|||||
QY 3875 gctgtgtgaagacaatgaagcatalgaagctgaactatgtctgtccatalgaagctgtctaaagga 3934
|||||
Db 3661 gctgtgtgaagacaatgaagcatalgaagctgaactatgtctgtccatalgaagctgtctaaagga 3720
|||||
QY 3935 gggagccttctgtgaactcttcaatgaatgtatgtgagccgcttccaaacttggacattc 3994
|||||
Db 3721 gggagccttctgtgaactcttcaatgaatgtatgtgagccgcttccaaacttggacattc 3780
|||||
QY 3995 tagtatgtgcatctcagaagcagccctgtgaagaatattctccaaagtgtgcgaagagag 4054
|||||
Db 3781 tagtatgtgcatctcagaagcagccctgtgaagaatattctccaaagtgtgcgaagagag 3840
|||||
QY 4055 tgggtgtgatactgtgagactcctaagatgtgtaccttgcagcaagacgaagcggtcct 4114
|||||
Db 3841 tgggtgtgatactgtgagactcctaagatgtgtaccttgcagcaagacgaagcggtcct 3900
|||||
QY 4115 cgggagcaagacagagctgtcttgcgcttcaactgaagaatgtatgtctgtatccaaatga 4174
|||||
Db 3901 cgggagcaagacagagctgtcttgcgcttcaactgaagaatgtatgtctgtatccaaatga 3960
|||||
QY 4175 tt-ctgacatagaccacaatccagagagacagactgtgtcgaatgtgagatgtgcaag 4233
|||||
Db 3961 ttgctgacatagaccacaatccagagagacagactgtgtcgaatgtgagatgtgcaag 4020
|||||
QY 4234 gttcctacaggtgaagagctgtgaacttaccagacacagcttctgtgtgtga 4293
|||||
Db 4021 gttcctacaggtgaagagctgtgaacttaccagacacagcttctgtgtgtga 4080
|||||
QY 4294 agaagctgtctaattgcagagcagagctgtggaagaatttctgtccagatgtcttgcag 4353
|||||
Db 4081 agaagctgtctaattgcagagcagagctgtggaagaatttctgtccagatgtcttgcag 4140
|||||
QY 4354 ctgtgttctgtcgtacatgtccctgtgttcaagcctgtatgtgtccaccccttggcaagtaac 4413
|||||
Db 4141 ctgtgttctgtcgtacatgtccctgtgttcaagcctgtatgtgtgtccaccccttggcaagtaac 4200
|||||
QY 4414 ccaagcctggaacttaagccctgtgagatgtacacgaagataacattgttcaagcaatgt 4473
|||||
Db 4201 ccaagcctggaacttaagccctgtgagatgtacacgaagataacattgttcaagcaatgt 4260
|||||
QY 4474 ctccctgaaggaacaggaacccctgtgaactcttaaaagccctaccaaagacccctgtctcg 4533
|||||
Db 4261 ctccctgaaggaacaggaacccctgtgaactcttaaaagccctaccaaagacccctgtctcg 4320
|||||
QY 4534 ggaacccgtgtatgtgaagaaacccaatccagacagccctgtccagcgagggaggaag 4593
|||||
Db 4321 ggaacccgtgtatgtgaagaaacccaatccagacagccctgtccagcgagggaggaag 4380
|||||
QY 4594 agtgaacacatgtcccaagcttcccaagacacatcaggaacttccagatgtgaagcgga 4653
|||||

Db 4381 agtggaccactggcccagtlccccaagacatcgtacctctccagaatgggaactgga 4440
QY 4654 caatgcaagaaccttcacctgcatgccaagttagcagcagcaaaatcaagaagatgctgc 4713
Db 4441 caatgcaagaaccttcacctgcatgccaagttagcagcagcaaaatcaagaagatgctgc 4500
QY 4714 ctggtgttccccaggggagggggtgctgcctcccaagaagaacaaacactgagcag 4773
Db 4501 ctgtgtgtccccaggggagggggtgctgcctcccaagaagaacaaacactgagcag 4560
QY 4774 atatccttcaggaccttacaggaagaacatttcggatattctgtgttaagaactatgtgc 4833
Db 4561 atatccttcaggaccttacaggaagaacatttcggatattctgtgttaagaactatgtgc 4620
QY 4834 agatcatagccaaagaacttaagaagaaga tctgtgtgaatgtatgttaggtatgtgcgct 4893
Db 4621 agatcatagccaaagaacttaagaagaaga tctgtgtgaatgtatgttaggtatgtgcgct 4680
QY 4894 ttcccttggtgtgtcatgaataactaagaaccttccctcgaatcaagaatgaatgtgcga 4953
Db 4681 ttcccttggtgtgtcatgaataactaagaaccttccctcgaatcaagaatgaatgtgcga 4740
QY 4954 tcaacaataatgaagaacacactaaagctggccaagaacatttcgagatcgatttctca 5013
Db 4741 tcaacaataatgaagaacacactaaagctggccaagaacatttcgagatcgatttctca 4800
QY 5014 acagcttgggaagaattatgtacaggaactgtgacacccaataatgtlcaaggtgtgttca 5073
Db 4801 acagcttgggaagaattatgtacaggaactgtgacacccaataatgtlcaaggtgtgttca 4860
QY 5074 ataacaagggtctgtgcatatgaatacagctcttccctgaatgtlcaataatgtccatctcc 5133
Db 4861 ataacaagggtctgtgcatatgaatacagctcttccctgaatgtlcaataatgtccatctcc 4920
QY 5134 gggccaacccggccaagaaggaggaacccctagccatattatgaattactgtcttcaatcacc 5193
Db 4921 gggccaacccggccaagaaggaggaacccctagccatattatgaattactgtcttcaatcacc 4980
QY 5194 cccctgaattccacccaagcagcagctctcagaaggtgtgctgtatgacacacatcagtgatg 5253
Db 4981 cccctgaattccacccaagcagcagctctcagaaggtgtgctgtatgacacacatcagtgatg 5040
QY 5254 tccctgtgtcatctgtgtgtatcttttggcaatgtcttccctgtgtcccaagcattgtcgtat 5313
Db 5041 tccctgtgtcatctgtgtgtatcttttggcaatgtcttccctgtgtcccaagcattgtcgtat 5100
QY 5314 tccctgtatccagagcggttcaagaagaacacactgtccatcagtgaggtgaagc 5373
Db 5101 tccctgtatccagagcggttcaagaagaacacactgtccatcagtgaggtgaagc 5160
QY 5374 ctgtcatctactgtgtcttaatttgtctggagatagtgtcaattacgttgcctgtgca 5433
Db 5161 ctgtcatctactgtgtcttaatttgtctggagatagtgtcaattacgttgcctgtgca 5220
QY 5434 cactgtgtatcatcatcttatctgttccagcagaagaatgtctatgttccctccacaatc 5493
Db 5221 cactgtgtatcatcatcttatctgttccagcagaagaatgtctatgttccctccacaatc 5280
QY 5494 tggctgtgtagcccttctacttctgtgtatgtgtgtlcaatcacaacctccatgtacc 5553
Db 5281 tggctgtgtagcccttctacttctgtgtatgtgtgtlcaatcacaacctccatgtacc 5340
QY 5554 cagcctccttgtgttcaagaatccccaagcagcctaigtgtgtcaccagcggtgaacc 5613
Db 5341 cagcctccttgtgttcaagaatccccaagcagcctaigtgtgtcaccagcggtgaacc 5400
QY 5614 tcttcatgttgatataatgtgcaaggtgtgccaacctgtgtgtgagcgtgttccacccaata 5673
Db 5401 tcttcatgttgatataatgtgcaaggtgtgccaacctgtgtgtgagcgtgttccacccaata 5460
QY 5674 agctgaataataatcaatgtatctcgtgaagtcgtgttctgtatcttccacaatttggc 5733
Db 5461 agctgaataataatcaatgtatctcgtgaagtcgtgttctgtatcttccacaatttggc 5520

QY 5734 tgggaagaggtctcatcgaatgtgtgaataaaccaagcaatgtgtatgctccctggaaggt 5793
Db 5521 tgggaagaggtctcatcgaatgtgtgaataaaccaagcaatgtgtatgctccctggaaggt 5580
QY 5794 ttggggagaatctgcttgtgtcatcactatcttggagctgtgtgtggacgaacctctgcg 5853
Db 5581 ttggggagaatctgcttgtgtcatcactatcttggagctgtgtgtggacgaacctctgcg 5640
QY 5854 ccattggcggtgaagaagggtgtgtctccctcattacagttctgtatccatgaagattct 5913
Db 5641 ccattggcggtgaagaagggtgtgtctccctcattacagttctgtatccatgaagattct 5700
QY 5914 tcatcagggcccaagacctgttaaatgtcaaaactatcctccttgaatgtatgaatgaatga 5973
Db 5701 tcatcagggcccaagacctgttaaatgtcaaaactatcctccttgaatgtatgaatgaatga 5760
QY 5974 tgaagcggtgaagaagcagaagaatcttgaatgtgtgagggccaagaatgtacatcttaagaatca 6033
Db 5761 tgaagcggtgaagaagcagaagaatcttgaatgtgtgagggccaagaatgtacatcttaagaatca 5820
QY 6034 aggaattgacgaagaatataagaagaagcggaagcctgtctgttgaacagattgtgtgg 6093
Db 5821 aggaattgacgaagaatataagaagaagcggaagcctgtctgttgaacagattgtgtgg 5880
QY 6094 gcatcctcctgtgtgagcttgtggtcctcctggaggttaatgtgggtctggaataatcatca 6153
Db 5881 gcatcctcctgtgtgagcttgtggtcctcctggaggttaatgtgggtctggaataatcatca 5940
QY 6154 ctttcaagaatgttcaacaggaatatacactgttcaacagaagagatgtcttcccttaacaaa 6213
Db 5941 ctttcaagaatgttcaacaggaatatacactgttcaacagaagagatgtcttcccttaacaaa 6000
QY 6214 ata-gtatcttatacaaatccatcatgaagaatgaatgaatgaatgaatgaatgaatga 6272
Db 6001 ataagttatcttatacaaatccatcatgaagaatgaatgaatgaatgaatgaatgaatga 6060
QY 6273 gatgtccatcaacagaagctgtgtgacttggagagaacacgtgtggtcttcccttcttga 6332
Db 6061 gatgtccatcaacagaagctgtgtgacttggagagaacacgtgtggtcttcccttcttga 6120
QY 6333 ggaatcccaagaaagaagttgtgcaaggtgtgtgaggtggcagatcttggaaactgtgcctc 6392
Db 6121 ggaatcccaagaaagaagttgtgcaaggtgtgtgaggtggcagatcttggaaactgtgcctc 6180
QY 6393 gtyaaggtatggagaataatgctgtgtaactatgtgtgaagccaacaaagcaagctctct 6452
Db 6181 gtyaaggtatggagaataatgctgtgtaactatgtgtgaagccaacaaagcaagctctct 6240
QY 6453 acaagcattgtgcttgaatcggcggtcctcctgtgtgttcttgaatgaaccacacagc 6512
Db 6241 acaagcattgtgcttgaatcggcggtcctcctgtgtgttcttgaatgaaccacacagc 6300
QY 6513 atggtatcccaagacccggcggttcttgtgtgaatgtgtgcctaaagtgtgttcaagaagg 6572
Db 6301 atggtatcccaagacccggcggttcttgtgtgaatgtgtgcctaaagtgtgttcaagaagg 6360
QY 6573 agatcagtagtgttactatcctcatagtaatgtgaagaatgtgaagcttcttcaacagatg 6632
Db 6361 agatcagtagtgttactatcctcatagtaatgtgaagaatgtgaagcttcttcaacagatg 6420
QY 6633 gcaatcatgttcaatgtgaagttcaaggtccttggcaggtgtccagcatcttaaaaaatag 6692
Db 6421 gcaatcatgttcaatgtgaagttcaaggtccttggcaggtgtccagcatcttaaaaaatag 6480
QY 6693 ttggagagatgttataataatgtgtatcgaatagcaggttccaaacccggagcttgaagcct 6752
Db 6481 ttggagagatgttataataatgtgtatcgaatagcaggttccaaacccggagcttgaagcct 6540
QY 6753 gtccaagatcttcttgaactgtcatctccctgtgaaggttcttcaaaagaagaacccggaac 6812
Db 6541 gtccaagatcttcttgaactgtcatctccctgtgaaggttcttcaaaagaagaacccggaac 6600

QY 6813 atgtacataaccagcttcacattcattatcttctctgcccagatatcaacacctc 6872
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 6601 atgtacataaccagcttcacattcattatcttctctgcccagatatcaacacctc 6660
 QY 6873 tcccagagcaaaaacgactccacatagagaactactgtttcccaacaacacttac 6932
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 6661 tcccagagcaaaaacgactccacatagagaactactgtttcccaacaacacttac 6720
 QY 6933 caagtaattgtgaactctgccaaggaaccaagtgatgacacttaaaagactctca 6992
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 6721 caagtaattgtgaactctgccaaggaaccaagtgatgacacttaaaagactctca 6780
 QY 6993 ttacccaaaaacccagcagtaagtgagctgtgacgttccacactcttcttaagatatag 7052
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 6781 ttacccaaaaacccagcagtaagtgagctgtgacgttccacactcttcttaagatatag 6840
 QY 7053 aaagtgaagaagaactatgatgaagaatccctgttcatacaggggtgctgtaagaaga 7112
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 6841 aaagtgaagaagaactatgatgaagaatccctgttcatacaggggtgctgtaagaaga 6900
 QY 7113 ggaactagaactctctctgcccacatgtagatgtgtgtggaagaagaagccagaattgat 7172
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 6901 ggaactagaactctctctgcccacatgtagatgtgtgtggaagaagaagccagaattgat 6960
 QY 7173 gtgggaagaagaactaaactgtactgtactgtactgtactgtactgtactgtactgtactgt 7232
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 6961 gtgggaagaagaactaaactgtactgtactgtactgtactgtactgtactgtactgtactgt 7020
 QY 7233 atgaacaacaaatccattacacaggggagtgccctgtgtagcctatgtctgtatagctct 7292
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7021 atgaacaacaaatccattacacaggggagtgccctgtgtagcctatgtctgtatagctct 7080
 QY 7293 caagtgaagaagaactgtatgtatgttttctccatacactatggaactatataaggaac 7352
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7081 caagtgaagaagaactgtatgtatgttttctccatacactatggaactatataaggaac 7140
 QY 7353 ccaatgacatatgggtgtggaactcacac-tttttttttttttttttctctgtatct 7411
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7141 ccaatgacatatgggtgtggaactcacac-tttttttttttttttttctctgtatct 7200
 QY 7412 cattggggtgtgcaacaataatcatcaagtaacatgagccagcagattatgatacaaac 7471
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7201 cattggggtgtgcaacaataatcatcaagtaacatgagccagcagattatgatacaaac 7260
 QY 7472 aaaagtaatgacatccatccatccatccatccatccatccatccatccatccatccatcc 7531
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7261 aaaagtaatgacatccatccatccatccatccatccatccatccatccatccatccatcc 7320
 QY 7532 gtgacacatccatctgtgcaatgagtgtagcagagttatgtagccaagttttcacaga 7591
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7321 gtgacacatccatctgtgcaatgagtgtagcagagttatgtagccaagttttcacaga 7380
 QY 7592 agtttgaagcacaatggtgtgtcagtcacactttgtgaaagctgctctgcacagctc 7651
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7381 agtttgaagcacaatggtgtgtcagtcacactttgtgaaagctgctctgcacagctc 7440
 QY 7652 ataaacttgaataatgaatgtagagaatgtagcagcgtggtgtaacatccctgtttag 7711
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7441 ataaacttgaataatgaatgtagagaatgtagcagcgtggtgtaacatccctgtttag 7500
 QY 7712 tccctctgaataagctgttctgtgtagcagtaacatgcaacaaaatgtgggtgctctag 7771
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7501 tccctctgaataagctgttctgtgtagcagtaacatgcaacaaaatgtgggtgctctag 7560
 QY 7772 caagggaactgtgtccattgttatattgtcctatgtctgagcagcatgggtctacaggg 7831
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7561 caagggaactgtgtccattgttatattgtcctatgtctgagcagcatgggtctacaggg 7620
 QY 7832 tcatcctatgagactttataataataataataataataataataataataataataataata 7891
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7621 tcatcctatgagactttataataataataataataataataataataataataataataata 7680
 QY 7892 caactgtctgggctgcaagctgtgcaagcagcagtgagattaaagagattgttcgct 7951

Db 7681 caactgtctgggctgcaagctgtgcaagcagcagtgagattaaagagattgttcgct 7739
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 7952 caacttagaggaagcctgtgcccattgtccctgactgtctgtaacatgtaactgcat 8011
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7740 caacttagaggaagcctgtgcccattgtccctgactgtctgtaacatgtaactgcat 7799
 QY 8012 ctcaagatgttatctgacacaaagtgatattattctgtgcttttgaataactagaaga 8071
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7800 ctcaagatgttatctgacacaaagtgatattattctgtgcttttgaataactagaaga 7859
 QY 8072 tgaag 8076
 ||||||
 Db 7860 tgaag 7864

RESULT 12
 AAC69385
 ID AAC69385 standard; cDNA; 7864 BP.
 XX
 AC AAC69385;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human ABC1 cholesterol transporter TD-1 mutant cDNA (74503C).
 XX
 KW Human ABC1 cholesterol transporter; chromosome 9q31;
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
 KW Tangier disease; TD; familial HDL deficiency; FHL; polymorphism;
 KW cardiovascular disease; coronary artery disease; coronary restenosis;
 KW cerebrovascular disease; peripheral vascular disease;
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
 KW prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO20005318-A2.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-IB00532.
 XX
 PR 15-MAR-1999; 99US-0124702.
 XX 08-JUN-1999; 99US-0138048.
 PR 17-JUN-1999; 99US-0139600.
 PR 01-SEP-1999; 99US-0151977.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON BIORESEARCH INC.
 XX
 PI Hayden MR, Wilson AR, Plimstone SN;
 XX
 DR WPI: 2000-587528/55.
 XX P-PSDB: AAB38104.
 XX
 PT New ABC1 polypeptide is useful for treating diseases associated with
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
 PT disease and cancer -
 XX
 PS Examples; Page -: 229pp; English.
 CC The invention relates to the human ABC1 cholesterol transporter protein
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of
 CC proteins, and plays a crucial role in cholesterol transport, particularly
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
 CC located on chromosome 9q31, and mutations in this gene are associated
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,
 CC Tangier disease (TD) and familial HDL deficiency (FHL). These diseases
 CC are distinguishable in that TD is an autosomal recessive disorder, while
 CC FHL is inherited as an autosomal dominant trait. Low levels of HDL ('good

CC cholesterol¹ in the blood correlate with a high risk of cardiovascular
CC disease, particularly coronary artery disease, but also cerebrovascular
CC disease, coronary restenosis, and peripheral vascular disease.
CC Conversely, a high level of HDL has protective effects against
CC cardiovascular disease. The invention provides genetic constructs and
CC transgenic cells and non-human animals comprising human ABC1 nucleic
CC acids, and methods of gene therapy for the treatment or prevention of
CC cardiovascular disease comprising the administration of an expression
CC vector encoding ABC1 or an active fragment thereof. The invention also
CC encompasses compounds which mimic ABC1 activity, compounds which
CC stimulate ABC1 expression and methods of screening for such compounds.
CC It further relates to methods for determining whether a patient has an
CC increased risk for cardiovascular disease due to polymorphisms in the
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
CC or prevent cardiovascular disease, especially coronary artery disease,
CC cerebrovascular disease, coronary restenosis or peripheral vascular
CC disease. They may also be used in the treatment of disease associated
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC The invention specifically excludes proteins with the exact amino acid
CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC present sequence represents cDNA encoding a mutant human ABC1 cholesterol
CC transporter associated with an altered cholesterol level and therefore an
CC altered risk of cardiovascular disease.
CC Note: The present sequence is not shown in the specification, but is
CC derived from the native human ABC1 cDNA shown on pages 157-160.
CC XX
SQ Sequence 7864 BP; 2014 A; 1861 C; 2011 G; 1977 T; 1 other;

Query Match 74.6%; Score 7790.2; DB 21; Length 7864;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7851; Conservative 0; Mismatches 8; Indels 6; Gaps 5;

QY 217 gtccctgtgtgagcttgcgcgtgcctccagggctcccgagcacacgtgtggcgtg 276
DB 1 gtccctgtgtgagcttgcgcgtgcctccagggctcccgagcacacgtgtggcgtg 60
QY 277 ctggctgaggaagcaatgagcttgcgtcccaagctgaggtgtgcgtgtgtgaagaacctta 336
DB 61 ctggctgaggaagcaatgagcttgcgtcccaagctgaggtgtgcgtgtgtgaagaacctta 120
QY 337 ctctcagaagaacaacaatgcaagctgttactgtgaagtggtcgtgctctattatct 396
DB 121 ctctcagaagaacaacaatgcaagctgttactgtgaagtggtcgtgctctattatct 180
QY 397 tccctgaccgactctgttctgtgagctacccaccctatgaacaacatgaatgcatt 456
DB 181 tccctgaccgactctgttctgtgagctacccaccctatgaacaacatgaatgcatt 240
QY 457 ttccaataaagcagctcctcgcaggaacaactccttgggtttcaggagattatctga 516
DB 241 ttccaataaagcagctcctcgcaggaacaactccttgggtttcaggagattatctga 300
QY 517 atgcacaacaacccctgttccgtttaccgacctcccgaggagctcccgagttgttgaa 576
DB 301 atgcacaacaacccctgttccgtttaccgacctcccgaggagctcccgagttgttgaa 360
QY 577 actttaacaatccatgtgtgctgcgtgttccagaatgtcggagagcttctttataga 636
DB 361 actttaacaatccatgtgtgctgcgtgttccagaatgtcggagagcttctttataga 420
QY 637 gccagaagaacacagcatgaaagacatgacgaagtcttgagaacatatacagcagatca 696
DB 421 gccagaagaacacacagcatgaaagacatgacgaagtcttgagaacatatacagcagatca 480
QY 697 agaaatccagctcaaatgtgaagcttcaagattctcgtgtggaacaatgaacctctctg 756
DB 481 agaaatccagctcaaatgtgaagcttcaagattctcgtgtggaacaatgaacctctctg 540
QY 757 ggttcctatatacaacactctctcccaaatctactgtgacaagaatgctggaagctg 816
DB 1621 ggttcctatatacaacactctctcccaaatctactgtgacaagaatgctggaagctg 1680

DB 541 ggttcctatatacaacactctctcccaaatctactgtgacaagaatgctggaagctg 600
QY 817 atgtatcttccacaagaatgttcttgcgaagctaccagattacattgaacagctgtgca 876
DB 601 atgtatcttccacaagaatgttcttgcgaagctaccagattacattgaacagctgtgca 660
QY 877 atgtatcaaatcaagaagatgattcactgtgtgacacaagaattcttgaagctgtg 936
DB 661 atgtatcaaatcaagaagatgattcactgtgtgacacaagaattcttgaagctgtg 720
QY 937 gcttaccacaagaagaactgtgtgcagcagagcgaagacttcgttccacaatgacatcc 996
DB 721 gcttaccacaagaagaactgtgtgcagcagagcgaagacttcgttccacaatgacatcc 780
QY 997 taaagccaactcttggaacacactaaacttaactccctcccgagcagaagagctgtg 1036
DB 781 taaagccaactcttggaacacactaaacttaactccctcccgagcagaagagctgtg 840
QY 1057 aagccacaanaaacattgtctgcatagcttcttggaactctgcccagaagagctgtgca 1116
DB 841 aagccacaanaaacattgtctgcatagcttcttggaactctgcccagaagagctgtgca 900
QY 1117 gaagctgagtgagcatgagcagaagagagtgatgttctgaccaaagtgaacagctccagct 1176
DB 901 gaagctgagtgagcatgagcagaagagagtgatgttctgaccaaagtgaacagctccagct 960
QY 1177 cctccacaacaaatccacagagctgtctcgttatgtctgtcgggcatcccgaggagagg 1236
DB 961 cctccacaacaaatccacagagctgtctcgttatgtctgtcgggcatcccgaggagagg 1020
QY 1237 ggtctgaagaatcaatgcttcaactgtgtatgagagacaacataaagccctcttgag 1296
DB 1021 ggtctgaagaatcaatgcttcaactgtgtatgagagacaacataaagccctcttgag 1080
QY 1297 gcaatgagcactgaggaagaatctgaaaactctctatgaacactcaacactcttactga 1356
DB 1081 gcaatgagcactgaggaagaatctgaaaactctctatgaacactcaacactcttactga 1140
QY 1357 atgatttgatgaagaatttgagctcctctcttcccgattatcttgaagaactctga 1416
DB 1141 atgatttgatgaagaatttgagctcctctcttcccgattatcttgaagaactctga 1200
QY 1417 agccgctgctgtgtggaagatctctgtatatacctgtgacacccagcacaaggaagtga 1476
DB 1201 agccgctgctgtgtggaagatctctgtatatacctgtgacacccagcacaaggaagtga 1260
QY 1477 tgcgtgaggtgaacaagaacttccaggaactgctgtgttccatgaltctggaagcagtg 1536
DB 1261 tgcgtgaggtgaacaagaacttccaggaactgctgtgttccatgaltctggaagcagtg 1320
QY 1537 gggaggaactcagccccaagaatctggaactctcatgaggaacagccaagtgtgacctg 1596
DB 1321 gggaggaactcagccccaagaatctggaactctcatgaggaacagccaagtgtgacctg 1380
QY 1597 tccggaatgctgttgagacagcaggacaatgacacatttgggaacagcagttgagtgct 1656
DB 1381 tccggaatgctgttgagacagcaggacaatgacacatttgggaacagcagttgagtgct 1440
QY 1657 taagtgtgacagcccaagaatctggtgtgttctggccaagacccaggaagatgctcag 1716
DB 1441 taagtgtgacagcccaagaatctggtgtgttctggccaagacccaggaagatgctcag 1500
QY 1717 ccaatgaatgtctgtgttataccttgagagagaagcttccaacaggaactcaacagcaatcc 1776
DB 1501 ccaatgaatgtctgtgttataccttgagagagaagcttccaacaggaactcaacagcaatcc 1560
QY 1777 ggaacatatctgcttcatatgagtggtgtcaactggaacagcagtagaaccatagaacag 1836
DB 1561 ggaacatatctgcttcatatgagtggtgtgtcaactggaacagcagtagaaccatagaacag 1620
QY 1837 aagctgtgcatcaacaagaatctgagctgtcgtgagtgaggaaggttctgtgctgtga 1896
DB 1621 aagctgtgcatcaacaagaatctgagctgtcgtgagtgaggaaggttctgtgctgtga 1680

QY 1897 tttgttcaatggaattatccaaagcagattgagctgccccatcatgtacaataaga 1956
|||||
Db 1681 ttgtttcaatggaattatccaaagcagattgagctgccccatcatgtacaataaga 1740
QY 1957 tccgaatggaattatgacaatgttgagaggaacaataataaagatgagtgagacc 2016
|||||
Db 1741 tccgaatggaattatgacaatgttgagaggaacaataataaagatgagtgagacc 1800
QY 2017 ctgtctcccgagctgacccctttgagacatgctgtaactgtgggggcttcgctact 2076
|||||
Db 1801 ctgtctcccgagctgacccctttgagacatgctgtaactgtgggggcttcgctact 1860
QY 2077 tgcagagatgtgtgagagcaggaatcatcagagtgctgacgagcccgagagaataatg 2136
|||||
Db 1861 tgcagagatgtgtgagagcaggaatcatcagagtgctgacgagcccgagagaataatg 1920
QY 2137 - -gttctataatgcaacaagatgcccataccctgtacgttgaatgacatcttctgaggt 2194
|||||
Db 1921 gdtgtctataatgcaacaagatgcccataccctgtacgttgaatgacatcttctgaggt 1980
QY 2195 gatgagccggttaatgcccccttcttataagctggtcgtgatttactaagtggctgtat 2254
|||||
Db 1981 gatgagccggttaatgcccccttcttataagctggtcgtgatttactaagtggctgtat 2040
QY 2255 catcaagggcatcgtgtatgagaagagcaagctgtaagaagacatgctgagatgag 2314
|||||
Db 2041 catcaagggcatcgtgtatgagaagagcaagctgtaagaagacatgctgagatgag 2100
QY 2315 ccttggaacaacagacatactctgtttagctgtgtcataatgtagccatcttctctgt 2374
|||||
Db 2101 ccttggaacaacagacatactctgtttagctgtgtcataatgtagccatcttctctgt 2160
QY 2375 gagcgtctgagctgctgagtggtcatctctgaagttaagaaacctgctcccttaagtgatcc 2434
|||||
Db 2161 gagcgtctgagctgctgagtggtcatctctgaagttaagaaacctgctcccttaagtgatcc 2220
QY 2435 cagcgtggtgttgccttccctgctgctgtgttctgttgagacaatcccgagctgtctct 2494
|||||
Db 2221 cagcgtggtgttgccttccctgctgctgtgttctgttgagacaatcccgagctgtctct 2280
QY 2495 gattagacacactcttctccagagccaacctggaagcagctgttgagggcatcatact 2554
|||||
Db 2281 gattagacacactcttctccagagccaacctggaagcagctgttgagggcatcatact 2340
QY 2555 cagcgtgtaacctgacctgaactgtgtgttgagcaatgagcagctacgttggttcaacct 2614
|||||
Db 2341 cagcgtgtaacctgacctgaactgtgtgttgagcaatgagcagctacgttggttcaacct 2400
QY 2615 caagatcttcgctgaagcctgcttccctgttgagcttggcttggctgagtaactgtgac 2674
|||||
Db 2401 caagatcttcgctgaagcctgcttccctgttgagcttggcttggctgagtaactgtgac 2460
QY 2675 cctttttgagagcagaggaatgagatgagatgaggaacaacctgtttgagagctcgttga 2734
|||||
Db 2461 cctttttgagagcagaggaatgagatgagatgaggaacaacctgtttgagagctcgttga 2520
QY 2735 ggaagatgcttcaatctcaaccttgaatcccatgagtgctgtttgaaaccttctctca 2794
|||||
Db 2521 ggaagatgcttcaatctcaaccttgaatcccatgagtgctgtttgaaaccttctctca 2580
QY 2795 tggagtgagatgagctgttatactgagagcgttcttccagagccagatccagagctccagagcc 2854
|||||
Db 2581 tggagtgagatgagctgttatactgagagcgttcttccagagccagatccagagctccagagcc 2640
QY 2855 ctgtaatttctccttgacaacaagtctcactgagtttgagcaggaagaatgtaagaaagcca 2914
|||||
Db 2641 ctgtaatttctccttgacaacaagtctcactgagtttgagcaggaagaatgtaagaaagcca 2700
QY 2915 cctgtgttccaacagagaagaatgtcagaataatctgcatggaagaggaacccacact 2974
|||||
Db 2701 cctgtgttccaacagagaagaatgtcagaataatctgcatggaagaggaacccacact 2760

QY 2975 gaagctggcgctgtccatctcaagaacctgtgtaaagtctacccgaatgagatgaagtgagc 3034
|||||
Db 2761 gaagctggcgctgtccatctcaagaacctgtgtaaagtctacccgaatgagatgaagtgagc 2820
QY 3035 tgtcgaatgctgtgcaactgaaattttatgagggccagatcaactcttctgtggccacaa 3094
|||||
Db 2821 tgtcgaatgctgtgcaactgaaattttatgagggccagatcaactcttctgtggccacaa 2880
QY 3095 tggagcgagggaagagccacccatgtcaatccctgaacgggtgtgtcccccagaccccgag 3154
|||||
Db 2881 tggagcgagggaagagccacccatgtcaatccctgaacgggtgtgtcccccagaccccgag 2940
QY 3155 caccgcttaacatccctgggaagaagacatctgctctgagatgagacacatcccgagaacct 3214
|||||
Db 2941 caccgcttaacatccctgggaagaagacatctgctctgagatgagacacatcccgagaacct 3000
QY 3215 gggggtctgtcccccagacataatgctgtctgttgaatgtcactgttgaagaataacatctg 3274
|||||
Db 3001 gggggtctgtcccccagacataatgctgtctgttgaatgtcactgttgaagaataacatctg 3060
QY 3275 gtctatgccccgtttgaaagagcctctctgagaaagcaagtgaaagcgagatgagacagat 3334
|||||
Db 3061 gtctatgccccgtttgaaagagcctctctgagaaagcaagtgaaagcgagatgagacagat 3120
QY 3335 ggccttgagatgtgttgtccatcaagcaagctgaaagaacaaacaaagcagctgtcaag 3394
|||||
Db 3121 ggccttgagatgtgttgtccatcaagcaagctgaaagaacaaacaaagcagctgtcaag 3180
QY 3395 tggaaatgagaagaagctatctgtgtgcttggccttggcttgggggagatgaattgtcat 3454
|||||
Db 3181 tggaaatgagaagaagctatctgtgtgcttggccttggcttgggggagatgaattgtcat 3240
QY 3455 tcttgagaaccccaacagctgtgtgtgaccccttaactcccgcaagggaaataagagctgtc 3514
|||||
Db 3241 tcttgagaaccccaacagctgtgtgtgaccccttaactcccgcaagggaaataagagctgtc 3300
QY 3515 gctgaataacccaagaagcgccacacatctctcttatacacacacataatgaaagcgga 3574
|||||
Db 3301 gctgaataacccaagaagcgccacacatctctcttatacacacacataatgaaagcgga 3360
QY 3575 gctcctgggggaacagatgtgcatcatctcccatgggaagctgtgtcgtgttggtctctc 3634
|||||
Db 3361 gctcctgggggaacagatgtgcatcatctcccatgggaagctgtgtcgtgttggtctctc 3420
QY 3635 cctgttcttgagaagaacagcctgggaacaggttaactactgagcttggccaagaagaatgt 3694
|||||
Db 3421 cctgttcttgagaagaacagcctgggaacaggttaactactgagcttggccaagaagaatgt 3480
QY 3695 ggaatcctccctcagtttctctgcaagaacagtagtagcactgtgtcatactgtaaaaaaga 3754
|||||
Db 3481 ggaatcctccctcagtttctctgcaagaacagtagtagcactgtgtcatactgtaaaaaaga 3540
QY 3755 ggaagatgttctcaagagcagttctgagtgctgtgcttggcgagcgacatagagatgagcac 3814
|||||
Db 3541 ggaagatgttctcaagagcagttctgagtgctgtgcttggcgagcgacatagagatgagcac 3600
QY 3815 gctgaacatgagatgtctctgtatctccaacctatcataggaagatgtgtctgaagccg 3874
|||||
Db 3601 gctgaacatgagatgtctctgtatctccaacctatcataggaagatgtgtctgaagccg 3660
QY 3875 gctgttgagaagacatagagcctgagctgacatagtgtcgcacatagaaagctgtctaaga 3934
|||||
Db 3661 gctgttgagaagacatagagcctgagctgagctgacatagtgtcgcacatagaaagctgtctaaga 3720
QY 3935 gggagccttgttgaaactcttcaatgagatgagatgagcagctcctcaacctgtggcatctc 3994
|||||
Db 3721 gggagccttgttgaaactcttcaatgagatgagatgagcagctcctcaacctgtggcatctc 3780
QY 3995 taagtatgacatctcagaagagcagccttgaagaagaatcttctcaaggtggccgaagag 4054
|||||
Db 3781 taagtatgacatctcagaagagcagccttgaagaagaatcttctcaaggtggccgaagag 3840
QY 4055 tgggttgatgtctgagacatcagatgtgtaccttgcagcaagaacgaagcgagcctt 4114

QY	6273	gagtgccatccacagactgtgtgacctgggagagaacacgttgagctctctgtcccttttgaga	6332
Db	6061	gatgcctacacagactgtgtgactggagagaaacccgtggagctctctgtcccttttgaga	6120
QY	6333	ggagtgcccaagaaaagaattggcgaaggttggtagtgccgatttcggaaactggcgctc	6392
Db	6121	ggagtgcccaagaaaagaattggcgaaggttggtagtgccgatttcggaaactggcgctc	6180
QY	6393	gtgaaagcatgtgagaaaataatctgtcgtaaactaagtggagggcaacagaaagctctct	6452
Db	6181	gtgaaagcatgtgagaaaataatctgtcgtaaactaagtggagggcaacagaaagctctct	6240
QY	6453	acagacatggtcttgatcggcgcgcgctcctgtgtgtcttcgtagtgaacccacaaagcg	6512
Db	6241	acagacatggtcttgatcggcgcgcgctcctgtgtgtcttcgtagtgaacccacaaagcg	6300
QY	6513	atgtagtcccaagcccgcgcggtctctgtgtgaaatttgccccaagtgtgtctaaagaaagg	6572
Db	6301	atgtagtcccaagcccgcgcggtctctgtgtgaaatttgccccaagtgtgtctaaagaaagg	6360
QY	6573	agatcagtagtgcttaacatcctacatagtaatggaagaatgtgaaagctctttgacatagatg	6632
Db	6361	agatcagtagtgcttaacatcctacatagtaatggaagaatgtgaaagctctttgacatagatg	6420
QY	6633	gcaatctatgttcaatgtgaagaagcttcaggtgcttcgtgccttgccagtgctacatctaaataatag	6692
Db	6421	gcaatctatgttcaatgtgaagaagcttcaggtgcttcgtgccttgccagtgctacatctaaataatag	6480
QY	6693	tttggaatctgttaataacatagtttgaacatagacaaggtctccaaacccggaacctaaagct	6752
Db	6481	tttggaatctgttaataacatagtttgaacatagacaaggtctccaaacccggaacctaaagct	6540
QY	6733	gtccaggaattcttggagcttgcatcttcctgtgaaagtgtctaaagaagaacacccgaac	6812
Db	6541	gtccaggaattcttggagcttgcatcttcctgtgaaagtgtctaaagaagaacacccgaac	6600
QY	6813	atgtcacacaataccagcgttccatcttcatactctctctcgtgcagagatatccaagctctc	6872
Db	6601	atgtcacacaataccagcgttccatcttcatactctctctcgtgcagagatatccaagctctc	6660
QY	6873	tcocagagcaaaaagcgactccacalagaaagactactcgtttctccagacaacactggac	6932
Db	6661	tcocagagcaaaaagcgactccacalagaaagactactcgtttctccagacaacactggac	6720
QY	6933	caagatatttggaaactttgccaagggccaaagtgtgataagcaccatttaaagaactctca	6992
Db	6721	caagatatttggaaactttgccaagggccaaagtgtgataagcaccatttaaagaactctca	6780
QY	6993	ttacacaaaacccagacagtagtggaacgtgtgcagttctcaacactttctcaacagatagag	7052
Db	6781	ttacacaaaacccagacagtagtggaacgtgtgcagttctcaacactttctcaacagatagag	6840
QY	7053	aaagtgtgaagaagaacctatgtatgaagaatccgtttcataccgggggtgcctgaaagtgaaga	7112
Db	6841	aaagtgtgaagaagaacctatgtatgaagaatccgtttcataccgggggtgcctgaaagtgaaga	6900
QY	7113	ggaaactagaacttctcctttgcacacatgtggaagttcttgtagaagaagagccagaagttag	7172
Db	6901	ggaaactagaacttctcctttgcacacatgtggaagttcttgtagaagaagagccagaagttag	6960
QY	7173	gtgggaagaagtaaacctggaatacgtgaatacctatcaatgtgaatgtcaattcaatgtga	7232
Db	6961	gtgggaagaagtaaacctggaatacgtgaatacctatcaatgtgaatgtcaattcaatgtga	7020
QY	7233	atgaaacaacaatctccattaaacgggggaaggtcctttgtagccataatgtctgtatgtgcct	7292
Db	7021	atgaaacaacaatctccattaaacgggggaaggtcctttgtagccataatgtctgtatgtgcct	7080
QY	7293	caagtgaaagaactgtgaatttagttttttacctaatacctatgtgaaactctatatgtgaac	7352
Db	7081	caagtgaaagaactgtgaatttagttttttacctaatacctatgtgaaactctatatgtgaac	7140

QY	7333	ccaaaggacata	tggtttggaactcaac-	tttttttttttttttttctgttgatct	7411
Db	7141	ccaaatggacata	tggtttgaactcaacttttttttttttctgttgatct		7200
QY	7412	cattggattc	caacaataatcaacgaatcaatgatgacgatattatgatacaalc		7471
Db	7201	cattggattc	caacaataatcaatcaatgaatcaatgatgacgatattatgatacaalc		7260
QY	7472	aaaagfta	atgcacatctcatcctaagaagcatatgcacatgcacagagacttgttccg		7531
Db	7261	aaaagfta	atgcacatctcatcctaagaagcatatgcacatgcacagagacttgttccg		7320
QY	7532	gtgacacatc	cattgctggtgcaatgaatgctccaaagtattatgtccaaagtttttcaaga		7591
Db	7321	gtgacacatc	cattgctggtgcaatgaatgctccaaagtattatgtccaaagtttttcaaga		7380
QY	7592	agtttgaagc	acacatggtgtgtcattgtctacatttctgtgaagctgtctcagaagct		7651
Db	7381	agtttgaagc	acacatggtgtgtgtcattgtctacatttctgtgaagctgtctcagaagct		7440
QY	7652	atcaacattga	atatacagttgacagaatggtgcacatgctgtgcttaaatcttccttgat		7711
Db	7441	atcaacattga	atatacagttgacagaatggtgcacatgctgtgcttaaatcttccttgat		7500
QY	7712	tccctctgata	agctgttctgtgtgtgacgaatcaatgcacacaaaatgtgtgtctctag		7771
Db	7501	tccctctgata	agctgttctgtgtgtgacgaatcaatgcacacaaaatgtgtgtctctag		7560
QY	7772	cacgggaact	gtgtctcatgtatattgtcctatgcttcctgacatgggtcctacagg		7831
Db	7561	cacgggaact	gtgtctcatgtatattgtcctatgcttcctgacatgggtcctacagg		7620
QY	7832	tcatccttat	gagactcttaataatcacttaactctgtgtaagagcgaagaatcaacag		7891
Db	7621	tcatccttat	gagactcttaataatcacttaactctgtgtaagagcgaagaatcaacag		7880
QY	7892	caaacgtctg	gtgtcgcacagctgtctgaagccagggcaltgagatlaaagaaatgtgtcgt		7951
Db	7681	caaacgtctg	gtgtcgcacagctgtctgaagccagggcaltgagatlaaagaaatgtgtcgt		7739
QY	7952	caaacctagg	gaagcgtgtgccatttgtcctgactgtctgtcctaacttgtaaacctgcat		8011
Db	7740	caaacctagg	gaagcgtgtgccatttgtcctgactgtctgtcctaacttgtaaacctgcat		7799
QY	8012	cctcaagatc	tcttatctgcacacagtgattattcttgctgtcttttgaattaatctagaaa		8071
Db	7800	cctcaagatc	tcttatctgcacacagtgattattcttgctgtcttttgaattaatctagaaa		7859
QY	8072	tgaaa	8076		
Db	7860	tgaaa	7864		
RESULT 13					
ID	AAC69386	standard; cDNA: 7864 BP.			
XX	AAC69386;				
XX	29-JAN-2001	(first entry)			
DE	Human ABC1	cholesterol transporter TD-2 mutant cDNA (A1864c).			
XX	Human ABC1	cholesterol transporter; chromosome 9q31;			
KW	ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;				
KW	cardiovascular disease; familial HDL deficiency; FHL; polymorphism;				
KW	cardiovascular disease; coronary artery disease; coronary restenosis;				
KW	Alzheimer's disease; Niemann-Pick disease; Huntington's disease;				
KW	X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;				
OS	Homo sapiens.				

XX XX WO20005318-A2.
 XX PM
 XX PD 21-SEP-2000.
 XX PF 15-MAR-2000; 2000MO-IB00532.
 XX PR 15-MAR-1999; 9905-0124702.
 XX PR 08-JUN-1999; 9905-0138048.
 XX PR 17-JUN-1999; 9905-0139600.
 XX PR 01-SEP-1999; 9905-0151977.
 XX
 PA (UYBR-) UNIV. BRITISH COLUMBIA.
 XX (XENO-) XENON BIORESEARCH INC.
 PI Hayden MR, Wilson AR, Pimstone SN;
 DR WPI; 2000-587528/55.
 DR P-PDB; AAB38105.
 XX
 PT New ABC1 polypeptide is useful for treating diseases associated with
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
 PT disease and cancer -
 PS
 PS Examples: Page -: 229pp; English.
 XX
 CC The invention relates to the human ABC1 cholesterol transporter protein
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of
 CC proteins, and plays a crucial role in cholesterol transport, particularly
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
 CC located on chromosome 9q31, and mutations in this gene are associated
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,
 CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
 CC are distinguishable in that TD is an autosomal recessive disorder, while
 CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
 CC cholesterol") in the blood correlate with a high risk of cardiovascular
 CC disease, particularly coronary artery disease, but also cerebrovascular
 CC disease, coronary restenosis, and peripheral vascular disease.
 CC Conversely, a high level of HDL has protective effects against
 CC cardiovascular disease. The invention provides genetic constructs and
 CC transgenic cells and non-human animals comprising human ABC1 nucleic
 CC acids, and methods of gene therapy for the treatment or prevention of
 CC cardiovascular disease comprising the administration of an expression
 CC vector encoding ABC1 or an active fragment thereof. The invention also
 CC encompasses compounds which mimic ABC1 activity, compounds which
 CC stimulate ABC1 expression and methods of screening for such compounds.
 CC It further relates to methods for determining whether a patient has an
 CC increased risk for cardiovascular disease due to polymorphisms in the
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
 CC or prevent cardiovascular disease, especially coronary artery disease,
 CC cerebrovascular disease, coronary restenosis or peripheral vascular
 CC disease. They may also be used in the treatment of diseases associated
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
 CC The invention specifically excludes proteins with the exact amino acid
 CC sequences of Genbank Accession No: CAA10005.1 and X75926, and the nucleic
 CC acid with the exact sequence as Genbank Accession No: A01012376.1. The
 CC present sequence represents a cDNA encoding a mutant human ABC1 cholesterol
 CC transporter associated with an altered cholesterol level and therefore an
 CC altered risk of cardiovascular disease.
 CC Note: The present sequence is not shown in the specification, but is
 CC derived from the native human ABC1 cDNA shown on pages 157-160.
 CC
 XX
 SQ Sequence 7864 BP: 2013 A; 1860 C; 2012 G; 1978 T; 1 other;

Db 1 gtccctgtgtgagctctgcccgtccttcacaggtcccccagacacacgtctgggtg 60
 QY 277 ctggtctgaggaacatggtctgttggcctcaagctgaggtgtgtgtgaaagacctca 336
 Db 61 ctggtctgaggaacatggtctgttggcctcaagctgaggtgtgtgtgaaagacctca 120
 QY 337 ctccaagaagaagaacacatgcaagctgttaccgtgaagtggtcgtccctattatct 396
 Db 121 ctccaagaagaagaacacatgcaagctgttaccgtgaagtggtcgtccctattatct 180
 QY 397 tccgtatccctgctgttgcgtgtgagctaccaccctatgaacacatgaatgcatc 456
 Db 181 tccgtatccctgctgttgcgtgtgagctaccaccctatgaacacatgaatgcatc 240
 QY 457 tccaataaagaacatgcccctcaggaacacttctgttgggttcaaggagattatcgt 516
 Db 241 tccaataaagaacatgcccctcaggaacacttctgttgggttcaaggagattatcgt 300
 QY 517 atgccaacaacccctgttccgttaccggaactcctgtggagagctcccgagttgtgaa 576
 Db 301 atgccaacaacccctgttccgttaccggaactcctgtggagagctcccgagttgtgaa 360
 QY 577 acttaacaataatcattgt 636
 Db 361 acttaacaataatcattgt 420
 QY 637 gccagaagaacacacagatgagagacatgcgcaagttctgagacattacaagatca 696
 Db 421 gccagaagaacacacagatgagagacatgcgcaagttctgagacattacaagatca 480
 QY 697 agaattcagttcaacttgaagtttaagatttccgtgtgagaaatgaacttctctg 756
 Db 481 agaattcagttcaacttgaagtttaagatttccgtgtgagaaatgaacttctctg 540
 QY 757 gttcctataatcaaacctctctcccaagttactgtggaacagatctgaggtg 816
 Db 541 gttcctataatcaaacctctctcccaagttactgtggaacagatctgaggtg 600
 QY 817 atgtcatctccacagatattttgcaaggtctacagttacattgacaaagtctgtga 876
 Db 601 atgtcatctccacagatattttgcaaggtctacagttacattgacaaagtctgtga 660
 QY 877 atgataataatcagaagatgatttaacttgttgacccaagaattctgagattgtg 936
 Db 661 atgataataatcagaagatgatttaacttgttgacccaagaattctgagattgtg 720
 QY 937 gccaccaagaagaaactgtgtcaagcagagcagactgttccaaatgagacatcc 996
 Db 721 gccaccaagaagaaactgtgtcaagcagagcagactgttccaaatgagacatcc 780
 QY 997 tgaagccaatctctgagacacataactctacatccctcccgagcaagagctgtg 1056
 Db 781 tgaagccaatctctgagacacataactctacatccctcccgagcaagagctgtg 840
 QY 1057 aagccacaataaactgtgtcatagttctgtgagctctgcccagggaggttgaagata 1116
 Db 841 aagccacaataaactgtgtcatagttctgtgagctctgcccagggaggttgaagata 900
 QY 1117 gaagctgagatgacatgacagagagtgatgttcttgacaaatggaacagctcagct 1176
 Db 901 gaagctgagatgacatgacagagagtgatgttcttgacaaatggaacagctcagct 960
 QY 1177 cctccacccaatctacacagctgtgtctctgtgtgtgtgtgtgtgtgtgtgtgtgt 1236
 Db 961 cctccacccaatctacacagctgtgtctctgtgtgtgtgtgtgtgtgtgtgtgtgt 1020
 QY 1237 ggtcgaagatcaagctctcaactgtgtatgaggaacaactacaagccctcttgag 1296
 Db 1021 ggtcgaagatcaagctctcaactgtgtatgaggaacaactacaagccctcttgag 1080
 QY 1297 gcaatgagcattgaggaagatgtctgaacctctatgacaaactacaactcttactga 1356

Query Match 74.6%; Score 7790.2; DB 21; Length 7864;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 7851; Conservative 0; Mismatches 8; Indels 6; Gaps 5;

Dh	1081	gcaatgagactgtgagaaagtgtcgtbaaacctctatagacaactctacaactcttaactgtca	1140
Qy	1357	atgatttgaaagaaatttgagagctagtcctcttcccgattatctvgaaagcttga	1416
Dh	1141	atgatttgaaagaaatttgagagctagtcctcttcccgattatctvgaaagcttga	1200
Qy	1417	agccgcgtcgtcttvggaaagatcctgtataaccttgacactccagcccaagcaggtca	1476
Dh	1201	agccgcgtcgtcttvggaaagatcctgtataaccttgacactccagcccaagcaggtca	1260
Qy	1477	tgcgtcgggtgaaacaaagaccttccaggaactctgctgtgttccatgaltctgaagcagt	1536
Dh	1261	tgcgtcgggtgaaacaaagacccctccaggaactctgctgtgttccatgaltctgaagcagt	1320
Qy	1537	ggagaggaactccagccccaagatctvgaaacttcaatvgaaagacaagccaagaaatvgaccttg	1596
Dh	1321	ggagaggaactccagccccaagatctvgaaacttcaatvgaaagacaagccaagaaatvgaccttg	1380
Qy	1597	tcggatagctgtttgggacagggacaaatgacccatttttgggaacagagtgtgattgct	1656
Dh	1381	tcggatagctgtttgggacagggacaaatgacccatttttgggaacagagtgtgattgct	1440
Qy	1657	taagatttgaaagcccaagacatctgctgtgttttttggccaagaccccaagagatttccagt	1716
Dh	1441	taagatttgaaagcccaagacatctgctgtgtgttttttggccaagaccccaagagatttccagt	1500
Qy	1717	ccagtaatgtctctgtataacactctggagagaagcttccaacgagataccaaggaatcc	1776
Dh	1501	ccagtaatgtctctgtataacactctggagagaagcttccaacgagataccaaggaatcc	1560
Qy	1777	ggacacatctctgtccaatvgaggtgtgtcaaccttgaaacagctaaagccaatgaacaag	1836
Dh	1561	ggacacatctctgtccaatvgaggtgtgtcaaccttgaaacagctaaagccaatgaacaag	1620
Qy	1837	aagctcgtcatccaacaagtcocatvgagctgtcgtgaatgaagagaaagttctggtcgtga	1896
Dh	1621	aagctcgtcatccaacaagtcocatvgagctgtcgtgaatgaagagaaagttctggtcgtga	1680
Qy	1887	tctgttccattctgaaatataacccagagacgatctgagctccccaatattctaaagtacaaga	1956
Dh	1681	tctgttccattctgaaatataacccagagacgatctgagctctgccccaatattctaaagtacaaga	1740
Qy	1957	tcggaaatvgacatttgacaatvtgagagagagacaataaatacaagaaatggttactvggacc	2016
Dh	1741	tcggaaatvgacatttgacaatvtgagagagagacaataaatacaagaaatggttactvggacc	1800
Qy	2017	ctggtctctgagactgacccctttggagaaatagtcgttagctctgggggggactcttgccact	2076
Dh	1801	ctggtctctgagactgacccctttggagaaatagtcgttagctctgggggggactcttgccact	1860
Qy	2077	tgcagagatgtgtgtgagagacagacatcatcaaggtctgtcagcgggacccgagaagaagaaatg	2136
Dh	1861	tgcagagatgtgtgtgagagacagacatcatcaaggtctgtcagcgggacccgagaagaagaaatg	1920
Qy	2137	--gtctatatatgaaagaagtgtgcccatatcccggttaactgttatgtacacttcttcggcggt	2194
Dh	1921	gdtgtctatatatgaaagaagtgtgcccatatcccggttaactgttatgtacacttcttcggcggt	1960
Qy	2195	gatagacccggtccaatgtccctcttcaatgacgcgtgcgtgacttactcaagtgtgcgtgat	2254
Dh	1981	gatagacccggtccaatgtccctcttcaatgacgcgtgcgtgacttactcaagtgtgcgtgat	2040
Qy	2255	catcaagggcatcgtgtataatgaagaaggacaggtctgaagaagacccatgtcgatcataggg	2314
Dh	2041	catcaagggcatcgtgtataatgaagaaggacaggtctgaagaagacccatgtcgatcataggg	2100
Qy	2315	cccttgaaacaaagcaatactctgtgttttagcgtgttcaatttagcctccaatctccctctgt	2374
Dh	2101	cccttgaaacaaagcaatactctctgtgttttagcgtgttcaatttagcctccaatctccctctgt	2160
Qy	2375	gagcgtctgctgttagtgtcatcctgaagattagaanaactgtgcctactagatgacc	2434
Dh	2161	gagcgtctgctgttagtgtcatcctgaagattagaanaactgtgcctactagatgacc	2220

[illegible]

[illegible]

Db	4381	agtggaacacactgccagcttcccgagacacacatgagaccccttcacgaatggaactgga	4440
Qy	4654	caatgcagaaccccttcacctcactgcacgagtgtaacacgaacatccaagaatgctgc	4715
Db	4441	caatgcagaaccccttcacctcactgcacgagtgtaacacgaacatccaagaatgctgc	4500
Qy	4714	ctgtgtgtcccccaggggcaggggggctgcctccctccacaagaacaaacactgcag	4773
Db	4621	agatcatagcccaaaagcttaagaacaaagctctgggtgaaatggttaagtgcgcgt	4680
Qy	4894	tttccctgggtgtcagatcatatctcaaacacttccctccggatccaagaagttaatgtcca	4955
Db	4681	tttccctgggtgtcagatcatatctcaaacacttccctccggatccaagaagttaatgtcca	4740
Qy	4954	tcaaacacaataagaacaacacctaaagcttggccagaaggaacagttctgaaagctatctcca	5013
Db	4741	tcaaacacaataagaacaacacctaaagcttggccagaaggaacagttctgaaagctatctcca	4800
Qy	5014	acagcttvggaagattatgacagagcttgacacccaagaataatgtcaagtgtgtgtcca	5073
Db	4801	acagcttvggaagattatgacagagcttgacacccaagaataatgtcaagtgtgtgtcca	4860
Qy	5074	atcaacaagggtcgtgcagatgcaatgaagctcttccttcgattgtcatcaacaatgcatctccc	5133
Db	4861	atcaacaagggtcgtgcagatgcaatgaagctcttccttcgattgtcatcaacaatgcatctccc	4922
Qy	5134	ggggccaacctgcgaagaaggagagaacctcagcatatagaaattactgtcttccaatcac	5193
Db	4921	ggggccaacctgcgaagaaggagagaacctcagcatatagaaattactgtcttccaatcac	4980
Qy	5194	ccctgaatctcaaccaagaagagctcaccaggttggtctcgtatgagacacaataaagtgggtg	5255
Db	4981	ccctgaatctcaaccaagaagagctcaccaggttggtctcgtatgagacacaataaagtgggtg	5040
Qy	5254	tccctgtgtccatctgtgtcaatctcttgcgaatgtcccttgcacagccagcttgcgat	5313
Db	5041	tccctgtgtccatctgtgtcaatctcttgcgaatgtcccttgcacagccagcttgcgat	5100
Qy	5314	tccctgaatccagaagcgggtgaagaagaacaaacaactcgcagtctcatcagtagtggaagc	5373
Db	5101	tccctgaatccagaagcgggtgaagaagaacaaacaactcgcagtctcatcagtagtggaagc	5160
Qy	5374	ctgtcatcatcagctgcctcctaatttcttcgcggatattgtcgaattacgcttgcctctgcca	5433
Db	5161	ctgtcatcatcagctgcctcctaatttcttcgcggatattgtcgaattacgcttgcctctgcca	5220
Qy	5434	caactggtcatatcatatcttcaatctgtcttcacagagaagctcctaattgtctccccaactc	5493
Db	5221	caactggtcatatcatatcttcaatctgtcttcacagagaagctcctaattgtctccccaactc	5280
Qy	5494	tgcctgtgtcagccctcctaacttctgtgtatggtgtgtgtgtgcaataaacctctccatgtacc	5553
Db	5281	tgcctgtgtcagccctcctaacttctgtgtatggtgtgtgtgtgcaataaacctctccatgtacc	5340
Qy	5554	cagcctccttgtgttcaagaatccccaagacagactatgtgtgtcaccagcgttgaacc	5613
Db	5341	cagcctccttgtgttcaagaatccccaagacagactatgtgtgtcaccagcgttgaacc	5400
Qy	5614	tcttcattggtgattaaaggaaggtgtgcacaccttgggtgtgtaagctgtttccacgaacata	5673
Db	5401	tcttcattggtgattaaaggaaggtgtgcacaccttgggtgtgtaagctgtttccacgaacata	5460
Qy	5674	agctgaataatataagatatccttgaagctcagctgttcttgcattcttccacattttgc	5733

Db 5461 agctgaataatcaatgatatacttcctgaagtcggttcttgatcttcccaattttgccc 5520
QY 5734 ttggacagaggtctcatcgatcgtgtgtaaaaaacaggcaatgctga tggccctggaaaaagtt 5793
Db 5521 ttggacagaggtctcatcgatcgtgtgtaaaaaacaggcaatgctga tggccctggaaaaagtt 5580
QY 5794 ttggagagaatcgtcttctgttccacattatcttggacttgtgtggagcaagaactcttcg 5853
Db 5581 ttggagagaatcgtcttctgttccacattatcttggacttgtgtggagcaagaactcttcg 5640
QY 5854 ccatggccgtggagaggtgtgttcttctctcaattactgttctgacccaagtataagttctc 5913
Db 5641 ccatggccgtggagaggtgtgttcttctctcaattactgttctgacccaagtataagttctc 5700
QY 5914 tcatcaagccccagacctgttaaatgtcaaaagctatctctcctgtaaatgtatgaagtgaagatg 5973
Db 5701 tcatcaagccccagacctgttaaatgtcaaaagctatctctcctgtaaatgtatgaagatg 5760
QY 5974 ttgagcgaggaaagacagagatcttctgtatgtgtgagggccagaaatgacatttgaagaaatca 6033
Db 5761 ttgagcgaggaaagacagagatcttctgtatgtgtgagggccagaaatgacatttgaagaaatca 5820
QY 6034 agaggttgacgaagataatagaaagagcgagagcctgtctgttgaacaggatttgcgtgg 6093
Db 5821 agaggttgacgaagataatagaaagagcgagagcctgtctgttgaacaggatttgcgtgg 5880
QY 6094 gcatctcctctgttgaagtgcttgggctcctggaggttaattggggctgtgaataatcatcaa 6153
Db 5881 gcatctcctctgttgaagtgcttgggctcctggaggttaattggggctgtgaataatcatcaa 5940
QY 6154 ctttcaagagtgttaacagagagataccactgtttccagagagagatgcttcttcaacaaaa 6213
Db 5941 ctttcaagagtgttaacagagagataccactgtttccagagagagatgcttcttcaacaaaa 6000
QY 6214 ata-gtatctatcaaacatccatcgtaaatgatacatcaagaacatggggtactgtccctcaagtt 6272
Db 6001 atagttatcttcatcaaacatccatcgtaaatgatacatcaagaacatggggtactgtccctcaagtt 6060
QY 6273 gatgtccatcaacagagctgttggactcgtggagagaaacgttgaagtcttcttggccctttgaga 6332
Db 6061 gatgtccatcaacagagctgttggactcgtggagagaaacgttgaagtcttcttggccctttgaga 6120
QY 6333 ggaatcccaagaaagaaatgtgcaaggttctgttgaagtgagcgatctcgaaacttgagcctc 6392
Db 6121 ggaatcccaagaaagaaatgtgcaaggttctgttgaagtgagcgatctcgaaacttgagcctc 6180
QY 6393 gtgaagatagagaataaataatgtctgttaactatagtgagagcgcaaaacgcaagctctctc 6452
Db 6181 gtgaagatagagaataaataatgtctgttaactatagtgagagcgcaaaacgcaagctctctc 6240
QY 6453 acaacgaatgtgttgcattcgcggcgccctcctgtgtgtttctcgtgataaaccacacagcgc 6512
Db 6241 acaacgaatgtgttgcattcgcggcgccctcctgtgtgtttctcgtgataaaccacacagcgc 6300
QY 6513 atgtgataccaaagccggcggttctctgtgaaatgttgccttaaatgttgcataaagagggg 6572
Db 6301 atgtgataccaaagccggcggttctctgtgaaatgttgccttaaatgttgcataaagagggg 6300
QY 6573 agatcaagtagtgcatacatcctatagatagaaagaaatgtgaagctcttgcataagatg 6632
Db 6361 agatcaagtagtgcatacatcctatagatagaaagaaatgtgaagctcttgcataagatg 6420
QY 6633 gcaatcaatgtcgaatgtgaaggtttcaagttgccttgcaggttgcagcatcttaaaaaatag 6692
Db 6421 gcaatcaatgtcgaatgtgaaggtttcaagttgccttgcaggttgcagcatcttaaaaaatag 6480
QY 6693 ttgtgagatgtttatatacatatgttgaagaaatagcaaggtcccaacccggacttaagcct 6752
Db 6481 ttgtgagatgtttatatacatatgttgaagaaatagcaaggtcccaacccggacttaagcct 6540
QY 6753 gtccagagattctcttgagcttgcatcttccgtgaaggtgttcttaaaagaaacacccggagc 6812
Db 6541 gtccagagattctcttgagcttgcatcttccgtgaaggtgttcttaaaagaaacacccggagc 6600
QY 6813 atgtcaataatcacagctcccatcttcatatcttctcgtgcagagataatgaacatctc 6872
Db 6601 atgtcaataatcacagctcccatcttcatatcttctcgtgcagagataatgaacatctc 6660
QY 6873 tcccgagcaaaaagcgactccacataagaactactctgttcttccagacaacttgac 6932
Db 6661 tcccgagcaaaaagcgactccacataagaactactctgttcttccagacaacttgac 6720
QY 6933 caagtaattgtgaacttgcagagccaagtgatgtatgaacacttaaaagactctca 6992
Db 6721 caagtaattgtgaacttgcagagccaagtgatgtatgaacacttaaaagactctca 6780
QY 6993 ttacacaaaacacagacagtagtgaagttcgaatccctgtcatcaggggtgtcgtgaagtaaaga 7052
Db 6781 ttacacaaaacacagacagtagtgaagttcgaatccctgtcatcaggggtgtcgtgaagtaaaga 6840
QY 7053 aaagtgaagaagatgtatgtgaagaatccctgtcatcaggggtgtcgtgaagtaaaga 7112
Db 6841 aaagtgaagaagatgtatgtgaagaatccctgtcatcaggggtgtcgtgaagtaaaga 6900
QY 7113 ggaactagacttctccttgcacacatgtgaagtggtgtgagaaagagccagaaatgtat 7172
Db 6901 ggaactagacttctccttgcacacatgtgaagtggtgtgagaaagagccagaaatgtat 6960
QY 7173 gtggagagagatgaagaatgtatgtatcttactgtactatccatcaatgaatgaatgaatga 7232
Db 6961 gtggagagagatgaagaatgtatgtatcttactgtactatccatcaatgaatgaatgaatga 7020
QY 7233 atgaaacaaaatccatcattacagggcgagtgcccttgaacatgtctgtatgagctct 7292
Db 7021 atgaaacaaaatccatcattacagggcgagtgcccttgaacatgtctgtatgagctct 7080
QY 7293 caagtgaagaacttgaatttttttaccatatacctatgtgaacactatagagac 7352
Db 7081 caagtgaagaacttgaatttttttaccatatacctatgtgaacactatagagac 7140
QY 7353 ccaatgacatagtggttgaactcacac-ttttttttttttcttctgttctgtatctc 7411
Db 7141 ccaatgacatagtggttgaactcacac-ttttttttttttcttctgttctgtatctc 7200
QY 7412 catlgtgtgtgcaacaataatccatcaagaatgaatgaatgaatgaatgaatgaatgaatga 7471
Db 7201 catlgtgtgtgcaacaataatccatcaagaatgaatgaatgaatgaatgaatgaatgaatga 7260
QY 7472 aaaaagtaatgcacatcccatccatccatcaagaatgaatgaatgaatgaatgaatgaatga 7531
Db 7261 aaaaagtaatgcacatcccatccatccatcaagaatgaatgaatgaatgaatgaatgaatga 7320
QY 7532 gtgacacatccatctgtcgcgaatgtgtgcagagttatagtgccaagtcttccagaa 7591
Db 7321 gtgacacatccatctgtcgcgaatgtgtgcagagttatagtgccaagtcttccagaa 7380
QY 7592 agtttgaagcaacatgtgtgtcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7651
Db 7381 agtttgaagcaacatgtgtgtcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7440
QY 7652 atcaacatgtgaatgaatgaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7711
Db 7441 atcaacatgtgaatgaatgaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 7500
QY 7712 tccctgtgaatgaatgt 7771
Db 7501 tccctgtgaatgaatgt 7560
QY 7772 caagggaaactgtgtccatgttcatatgttccatgttccatgttccatgttccatgttccatgt 7831
Db 7561 caagggaaactgtgtccatgttcatatgttccatgttccatgttccatgttccatgttccatgt 7620
QY 7832 tcaatccttaagaaccttaataatataatcttagatccctgtgaagaggaaggaatgaacagc 7891
Db 7621 tcaatccttaagaaccttaataatataatcttagatccctgtgaagaggaaggaatgaacagc 7680

Db	541	ggtcttcgtatcaaacctctctccccaagaagctcgtgagcaagctgctgagggctg	600
Qy	817	atgtatctctccacaaggtatttttgcagaagctacacagttacatttgacaggtctgtca	876
Db	601	atgtatctctccacaaggtatttttgcagaagctacacagttacatttgacaggtctgtca	660
Qy	877	atgtatcaaatcagaagagatgatctcaactgtgtgacccaagaagttctgagcttgtg	936
Db	661	atgtatcaaatcagaagagatgatctcaactgtgtgacccaagaagttctgagcttgtg	720
Qy	937	gctctcccaagaagaactgtgctgcagagagcgagttacattctgttccaaacttgacaatcc	996
Db	721	gctctcccaagaagaactgtgctgcagagagcgagttacattctgttccaaacttgacaatcc	780
Qy	997	tgaagccaatcctctgagaaacactaaactctacatctccctcccgagcaaggagctgctg	1056
Db	781	tgaagccaatcctctgagaaacactaaactctacatctccctcccgagcaaggagctgctg	840
Qy	1057	aagccacaataaactgtgtgcatagttcttgagactctgcccagagagctgtctcagatga	1116
Db	841	aagccacaataaactgtgtgcatagttcttgagactctgcccagagagctgtgtcagatga	900
Qy	1117	gaagcttgagtgacatgctgcagagaggtgagtgattcttgacaacatgtgacaagctccagct	1176
Db	901	gaagcttgagtgacatgctgcagagaggtgagtgattcttgacaacatgtgacaagctccagct	960
Qy	1177	cctccacaacaaactacacagagctgtgtctcgtatgtctgcggagatcccgagagaggg	1236
Db	961	cctccacaacaaactacacagagctgtgtctcgtatgtctgcggagatcccgagagaggg	1020
Qy	1237	ggctgaagatcagttctctcaactgtgtatgagagacaacactacaagaagctctttgag	1296
Db	1021	ggctgaagatcagttctctcaactgtgtatgagagacaacactacaagaagctctttgag	1080
Qy	1297	gcaatggcactgaggaagatgtctgaaacctctatgacaactctacaactctctactca	1356
Db	1081	gcaatggcactgaggaagatgtctgaaacctctatgacaactctacaactctctactca	1140
Qy	1357	atgatttgaatgaagaatttgaagctagtcctcttcccgacatctctgaaagactctga	1416
Db	1141	atgatttgaatgaagaatttgaagctagtcctcttcccgacatctctgaaagactctga	1200
Qy	1417	agccgctgtctgttggagaatcctgtatataccctgcgaactctccacacaaagcgctga	1476
Db	1201	agccgctgtctgttggagaatcctgtatataccctgcgaactctccacacaaagcgctga	1260
Qy	1477	tggctgaagtgaacaagacctcccaaggaactgtgctgttcatatctcgaagcgatgt	1536
Db	1261	tggctgaagtgaacaagacctcccaaggaactgtgctgttcatatctcgaagcgatgt	1320
Qy	1537	gggaggaactcagccccaagatctggaactctcaatggaagacagccaagaatctgagctg	1596
Db	1321	gggaggaactcagccccaagatctggaactctcaatggaagacagccaagaatctgagctg	1380
Qy	1597	tccgagatgtctgttggacagcagggacaatgatccaacttttgggaaacagcagttgagtgct	1656
Db	1381	tccgagatgtctgttggacagcagggacaatgatccaacttttgggaaacagcagttgagtgct	1440
Qy	1657	tgaattggacaagcccaagacatcgtggttttggccaagacccaagagagtgcccat	1716
Db	1441	tgaattggacaagcccaagacatcgtggttttggccaagacccaagagagtgcccat	1500
Qy	1717	ccagtaaatgttctgttgaacacttgagagaagcttccaacagagataccagcgcaatcc	1776
Db	1501	ccagtaaatgttctgttgaacacttgagagaagcttccaacagagataccagcgcaatcc	1560
Qy	1777	ggacataatctcgtctcagtgaggtgtgtcaacttgacaagagcttagaaccataagcaacg	1836
Db	1561	ggacataatctcgtctcagtgaggtgtgtcaacttgacaagagcttagaaccataagcaacg	1620
Qy	1837	aaatcctgctcatcaacaagctccatgagagctgctgatatagaggaagttctggtctgta	1896

Db	1621	aagtctgctcatcaacaagaagctccatgagctgctgtagatgagagaagttcttggctgtga	1680
Qy	1897	tgtgttactatggaattactccagcgacgaatctgagctgcccacatctgcaagtacaaga	1956
Db	1681	tgtgttactatggaattactccagcgacgaatctgagctgcccacatctgcaagtacaaga	1740
Qy	1957	tccgaatgagcatttgacaagtgtgagagagagcaataaatacaagagatggttacttgacc	2016
Db	1741	tccgaatgagcatttgacaagtgtgagagagagcaataaatacaagagatggttacttgacc	1800
Qy	2017	ctgtctcctcagctgacccctcttgagagacatgctgtactgttgcgttgagagagcttccgctact	2076
Db	1801	ctgtctcctcagctgacccctcttgagagacatgctgtactgttgcgttgagagagcttccgctact	1860
Qy	2077	tgcagagatgtgttggagcagagcaatcaacagagtgctgcagcgagcaaccgagaagaaactg	2136
Db	1861	tgcagagatgtgttggagcagagcaatcaacagagtgctgcagcgagcaaccgagaagaaactg	1920
Qy	2137	--gtgtctataatgacaagaatgccccttcccttcttactgttgcgttgagacatcttctgcgggt	2194
Db	1921	gdtgtctataatgacaagaatgccccttcccttcttactgttgcgttgagacatcttctgcgggt	1980
Qy	2195	gatgagccggttcaatgtccctcttcaatgacgctgagcctgagattactcagtgagctgagat	2254
Db	1981	gatgagccggttcaatgtccctcttcaatgacgctgagcctgagattactcagtgagctgagat	2040
Qy	2255	catcaagagcactgctgatatagaagaagagcagcgctgtgaaagaagacatctgagatcatggg	2314
Db	2041	catcaagagcactgctgatatagaagaagagcagcgctgtgaaagaagacatctgagatcatggg	2100
Qy	2315	ccttgacaacagacatctcctgctgtttagctgttcatatagtagctcatctcctctctgt	2374
Db	2101	ccttgacaacagacatctcctgctgtttagctgttcatatagtagctcatctcctctctgt	2160
Qy	2375	gagcgctgagcctgtctagtgatcctcctgaagtttagaagaacctgctgcctacagtgatcc	2434
Db	2161	gagcgctgagcctgtctagtgatcctcctgaagtttagaagaacctgctgcctacagtgatcc	2220
Qy	2435	cagcgctgctgttcttctcctgctgctgttgcgtgtgtgagaaatcctctgaaagtgctcct	2494
Db	2221	cagcgctgctgttcttctcctgctgctgttgcgtgtgtgagaaatcctctgaaagtgctcct	2280
Qy	2495	gattagcaactcttctccagagccaacctggagagcgagcctgttgaggacatctactact	2554
Db	2281	gattagcaactcttctccagagccaacctggagagcgagcctgttgaggacatctactact	2340
Qy	2555	cagcgtgacactgacctgaactgctctgtgtgtgacatggaagactacgttgagcttcaact	2614
Db	2341	cagcgtgacactgacctgaactgctctgtgtgtgacatggaagactacgttgagcttcaact	2400
Qy	2615	caagatctcgtacgctgctgtctcctgtgagcttttgggttttggcgttgagtaacttgc	2674
Db	2401	caagatctcgtacgctgctgtctcctgtgagcttttgggttttggcgttgagtaacttgc	2460
Qy	2675	ccttttggagagcagggacatctgagagtgagcaatgggacaacctgtttgagagctcgtgga	2734
Db	2461	ccttttggagagcagggacatctgagagtgagcaatgggacaacctgtttgagagctcgtgga	2520
Qy	2735	ggaagatgcttcaatctcaacactctcgatctccatgatgctgtttgacacactctctca	2794
Db	2521	ggaagatgcttcaatctcaacactctcgatctccatgatgctgtttgacacactctctca	2580
Qy	2795	tggggtgatacctgtgatacatatgaggtgtcttctccagagcagtaaggaattcccaagcc	2854
Db	2581	tggggtgatacctgtgatacatatgaggtgtcttctccagagcagtaaggaattcccaagcc	2640
Qy	2855	ctggtatcttctctgacccaagctcctactgtgttggcgagagaagtgatatagaagaacca	2914
Db	2641	ctggtatcttctctgacccaagctcctactgtgttggcgagagaagtgatatagaagaacca	2700
Qy	2915	ccctgtgttccaacagagaagatgtcagaatctctgcatggaagaggaaccaccaact	2974
Db	2701	ccctgtgttccaacagagaagatgtcagaatctctgcatggaagaggaaccaccaact	2760


```
Db 4921 gggccaactcgtcaaaaggagagaaacccctagccattatgaaattactgcttccaatcacc 4980
Qy 5194 cccctgaatcccaagcagcagcctctcagaggctgctctgataccacatacagtgatg 5253
Db 4981 cccctgatactcaacagcagcagcctctcagaggctgctctgataccacatacagtgatg 5040
Qy 5254 tccctgtgcaactctgtgcatctcttgcaatgtccctgtgcccacagccttctgctat 5313
Db 5041 tccctgtgcaactctgtgcatctcttgcaatgtccctgtgcccacagccttctgctat 5100
Qy 5314 tccctgtgcaactctgtgcatctcttgcaatgtccctgtgcccacagccttctgctat 5373
Db 5101 tccctgtgcaactctgtgcatctcttgcaatgtccctgtgcccacagccttctgctat 5160
Qy 5374 ctgtcaactactgtgctctcaatcttctgtcgggatactgcaatcagttctccctgcca 5433
Db 5161 ctgtcaactactgtgctctcaatcttctgtcgggatactgcaatcagttctccctgcca 5220
Qy 5434 caactgtcaactatcatctctctctgtctccagcagaagctcctatgtctctccaacac 5493
Db 5221 caactgtcaactatcatctctctctgtctccagcagaagctcctatgtctctccaacac 5280
Qy 5494 tgcctgtgtagccctctctctctctctgtctgtatggtgtgcaatccaactcctcatgacc 5553
Db 5281 tgcctgtgtagccctctctctctctctgtgtatggtgtgcaatccaactcctcatgacc 5340
Qy 5554 cagcctccttctgtctcaagatcccaagcagcctaagtgtgtctaccagcgtgaacc 5613
Db 5341 cagcctccttctgtctcaagatcccaagcagcctaagtgtgtctaccagcgtgaacc 5400
Qy 5614 tctctctgtgcatatagtcagcgtgtgccaactgtgtctgtgagcctgttccacagcaata 5673
Db 5401 tctctctgtgcatatagtcagcgtgtgccaactgtgtctgtgagcctgttccacagcaata 5460
Qy 5674 agctggaataataatcaatgatactctcctgaagtcctgtctctgatactccacattctgac 5733
Db 5461 agctggaataataatcaatgatactctcctgaagtcctgtctctgatactccacattctgac 5520
Qy 5734 tgggacgagggctcatcgatcgtatgtaaaacccaagcaatgtgctgacctggaagaagt 5793
Db 5521 tgggacgagggctcatcgatcgtatgtaaaacccaagcaatgtgctgacctggaagaagt 5580
Qy 5794 tttgggaggaatcgtctgtgtccactatctctggagactgtgtgggacgaacactcttg 5853
Db 5581 tttgggaggaatcgtctgtgtccactatctctggagactgtgtgggacgaacactcttg 5640
Qy 5854 ccatggtcgtggaagggtgtgtctctctcactactgtctctgataccagtaacatct 5913
Db 5641 ccatggtcgtggaagggtgtgtctctctcactactgtctctgataccagtaacatct 5700
Qy 5914 tcatcagggccagacactgttaaatgcaaaagctatctctcctgtaatgtaagaatgagatg 5973
Db 5701 tcatcagggccagacactgttaaatgcaaaagctatctctcctgtaatgtaagaatgagatg 5760
Qy 5974 tggggtcggggaagaacagagatcttgatgtgtgagggccaagaatgacattagaataa 6033
Db 5761 tggggtcggggaagaacagagatcttgatgtgtgagggccaagaatgacattagaataa 5820
Qy 6034 aggaatggaagaatataatagaagaagaacaggaagcctgtctgtgcaagaattctgctg 6093
Db 5821 aggaatggaagaatataatagaagaagaacaggaagcctgtctgtgcaagaattctgctg 5880
Qy 6094 gcaatcctcctgtgtgagctgtgtggtcctgtgaggttaatgggctgtgaaatacatcaa 6153
Db 5881 gcaatcctcctgtgtgagctgtgtggtcctgtgaggttaatgggctgtgaaatacatcaa 5940
Qy 6154 ctctcaagaatgtaaacaggaagatacactgttaccagagagatgcttcccttaacaaaa 6213
Db 5941 ctctcaagaatgtaaacaggaagatacactgttaccagagagatgcttcccttaacaaaa 6000
Qy 6214 ata-gtacttatcaaacatccatgaagtaacatcaagaacatgggctactgtccctcagttt 6272
Db 6001 atagtatcttatcaaacatccatgaagtaacatcaagaacatgggctactgtccctcagttt 6060
Qy 6273 gatgcatcacagaagctgtgtactgtggagagaacagctggaatcttctgcccctttaga 6332
Db 6061 gatgcatcacagaagctgtgtactgtggagagaacagctggaatcttctgcccctttaga 6120
Qy 6333 ggaatccccagaagaagatgtgcaaggttggtagtggggtgagatctcgaaacttgggctc 6392
Db 6121 ggaatccccagaagaagatgtgcaaggttggtagtggggtgagatctcgaaacttgggctc 6180
Qy 6393 gtgaagtaatgagaanaaaatctgtctgttaactatgtggaaggaacaaacgaagctcct 6452
Db 6181 gtgaagtaatgagaanaaaatctgtctgttaactatgtggaaggaacaaacgaagctcct 6240
Qy 6453 acagcaatgcttggatctgctgctgctcctctgtgtgttctcgtgtgaacccaacagcgc 6512
Db 6241 acagcaatgcttggatctgctgctgctcctctgtgtgttctcgtgtgaacccaacagcgc 6300
Qy 6513 atgatacccaagcccggtctctgtggaattgtgcccctaagtctgtctcaagaaggag 6572
Db 6301 atgatacccaagcccggtctctgtggaattgtgcccctaagtctgtctcaagaaggag 6360
Qy 6573 agatcagtagtctgtacatccatagtaatggaagaatgtgaagcctcttgcataagatg 6632
Db 6361 agatcagtagtctgtacatccatagtaatggaagaatgtgaagcctcttgcataagatg 6420
Qy 6633 gcaatcagtagtctgtacatccatagtaatggaagaatgtgaagcctcttgcataagatg 6692
Db 6421 gcaatcagtagtctgtacatccatagtaatggaagaatgtgaagcctcttgcataagatg 6480
Qy 6693 tttggagatgtgtatatacatagttgtatgaatgaacaggtcccaacccggaactaaagc 6752
Db 6481 tttggagatgtgtatatacatagttgtatgaatgaacaggtcccaacccggaactaaagc 6540
Qy 6753 gtccaggaattctctgtgactgtacattctccgtgaagtgcttctaaagagaacaccggaac 6812
Db 6541 gtccaggaattctctgtgactgtacattctccgtgaagtgcttctaaagagaacaccggaac 6600
Qy 6813 atgtcaataataccagctccatcttcatctctctcgtggccaagatattagaatctc 6872
Db 6601 atgtcaataataccagctccatcttcatctctctcgtggccaagatattagaatctc 6660
Qy 6873 tcccagaacaaagacgagctccacataagaagactactgttctccagacaacacttgac 6932
Db 6661 tcccagaacaaagacgagctccacataagaagactactgttctccagacaacacttgac 6720
Qy 6933 caagiatctgtgaactctgtgcaaggaacaaagtgaatgataccacttaaaagactctca 6992
Db 6721 caagiatctgtgaactctgtgcaaggaacaaagtgaatgataccacttaaaagactctca 6780
Qy 6993 ttacacaaaacacgaacgtagtgaagctgtgcaagttctccacatcttctcagagatgag 7052
Db 6781 ttacacaaaacacgaacgtagtgaagctgtgcaagttctccacatcttctcagagatgag 6840
Qy 7053 aaagtgaagaagaagctatgataagaagatccgttctcatagcgggtgtgctgaagtaaga 7112
Db 6841 aaagtgaagaagaagctatgataagaagatccgttctcatagcgggtgtgctgaagtaaga 6900
Qy 7113 ggaactagaacttctcctgtgacacatgtgaagtggtgtgtggaagaagaagcagaagttgat 7172
Db 6901 ggaactagaacttctcctgtgacacatgtgaagtggtgtgtggaagaagaagcagaagttgat 6960
Qy 7173 gtgggaagaagaagaactgtgatactgttactgtatcattcaatgcaatgcaatcaatgca 7232
Db 6961 gtgggaagaagaagaactgtgatactgttactgtatcattcaatgcaatgcaatcaatgca 7020
Qy 7233 atgaaacaaaatctccatcacaggggagtgccctgtgagctatgtctgtatgagctct 7292
Db 7021 atgaaacaaaatctccatcacaggggagtgccctgtgagctatgtctgtatgagctct 7080
Qy 7293 caagtgaagaagctgaattagtttttaactatacctaagtgaacacttatatggaac 7352
Db 7081 caagtgaagaagctgaattagtttttaactatacctaagtgaacacttatatggaac 7140
```


QY 217 gtccctgtgtgagctctgacgctgcttccagggctcccgagccacacgctggcgctg 276
|||||
Db 1 gtccctgtgtgagctctgacgctgcttccagggctcccgagccacacgctggcgctg 60
QY 277 ctggctgaggaacatgctgtgttgccctcaagctgaggtgtgctgtgtggaacactta 336
|||||
Db 61 ctggctgaggaacatgctgtgttgccctcaagctgaggtgtgctgtgtggaacactta 120
QY 337 ctctcagaagaacacacatgctcagctgttactggaagtgtgcgtgcctctattatct 396
|||||
Db 121 ctctcagaagaacacacatgctcagctgttactggaagtgtgcgtgcctctattatct 180
QY 397 tccctgacctgacctgtgttcgctgagctacccacctatgaacacatgagatgcatt 456
|||||
Db 181 tccctgacctgacctgtgtgttcgctgagctacccacctatgaacacatgagatgcatt 240
QY 457 ttccaaataaagacatgacctctgcaggaacacttccctgggttccagggaattatctgta 516
|||||
Db 241 ttccaaataaagacatgacctctgcaggaacacttccctgggttccagggaattatctgta 300
QY 517 atgccaacacacccctgttccctgtaccgacctctctggggagctcccgaggtgtgtgga 576
|||||
Db 301 atgccaacacacccctgttccctgtaccgacctctctggggagctcccgaggtgtgtgga 360
QY 577 accttaacaatccatctgtgtgcgctgttctcagaatgctcggaagctctttatca 636
|||||
Db 361 accttaacaatccatctgtgtgtgcgctgttctcagaatgctcggaagctctttatca 420
QY 637 gccagaagaacacacagcatgaaagagacatgacgcaaaagtcttgaacaattacagcagatca 696
|||||
Db 421 gccagaagaacacacagcatgaaagagacatgacgcaaaagtcttgaacaattacagcagatca 480
QY 697 agaaatccagcttaacacttgaagcttcaagatcttctgtgtgacaattgaaccttctcg 756
|||||
Db 481 agaaatccagcttcaacacttgaagcttcaagatcttctgtgtgacaattgaaccttctcg 540
QY 757 ggttcctatctcaacactctctctcccaagctctactgtgacaagaatgctgtgagcgctg 816
|||||
Db 541 ggttcctgtatctcaacactctctctcccaagctctactgtgacaagaatgctgtgagcgctg 600
QY 817 atgtcaattctccacaaggtatttttgcagaagctaccagttacatttgcacaagtctgtga 876
|||||
Db 601 atgtcaattctccacaaggtatttttgcagaagctaccagttacatttgcacaagtctgtga 660
QY 877 atgatatcaaatcatgagaagatgattccaactgtgtgaccagaagaattctcgagcttgcg 936
|||||
Db 661 atgatatcaaatcatgagaagatgattccaactgtgtgaccagaagaattctcgagcttgcg 720
QY 937 gctbaccacaaggaacactgtgctgcagcagagcgagtaactcgttccacaatgagacatcc 996
|||||
Db 721 gctbaccacaaggaacactgtgctgcagcagagcgagtaactcgttccacaatgagacatcc 780
QY 997 tgaagccaatctctgagagacacttaactctacatctccctcccgagcaaggaatgtgcg 1056
|||||
Db 781 tgaagccaatctctgagagacacttaactctacatctccctcccgagcaaggaatgtgcg 840
QY 1057 aagccacaacaaacatgctctcatagcttctggagctctgcgccaagcgctgttcaagatga 1116
|||||
Db 841 aagccacaacaaacatgctctcatagcttctggagctctgcgccaagcgctgttcaagatga 900
QY 1117 gaagctgtgagtgacatgctgcagagagtgatgttctgcacaaatgtgaacagctcagct 1176
|||||
Db 901 gaagctgtgagtgacatgctgcagagagtgatgttctgcacaaatgtgaacagctcagct 960
QY 1177 cctccaccacaatcttacaagcgctgtgtctgtattgtgtctgcggagctcccgaggaggagg 1236
|||||
Db 961 cctccaccacaatcttacaagcgctgtgtctgtattgtgtctgcggagctcccgaggaggagg 1020
QY 1237 ggtctgaagatcaagctctcctaactgtatgaggaacaaactacaaagccctcttggag 1296
|||||
Db 1021 ggtctgaagatcaagctctcctaactgtatgaggaacaaactacaaagccctcttggag 1080
QY 1297 gcaatggaactgaggaagatgctgaaaccttatatgacaacttacaactccttactgca 1356

Db 1081 gcaatggaactgaggaagatgctgaaaccttatatgacaacttacaactccttactgca 1140
|||||
QY 1337 atgattgtatgaagaatttgaagcttagctctcttcccgatatattctgaaagcttga 1416
|||||
Db 1141 atgattgtatgaagaatttgaagcttagctctcttcccgatatattctgaaagcttga 1200
QY 1417 agccctgtctgttggagaagatccctgtatatacctgtaacactccagccaagcgaggtca 1476
|||||
Db 1201 agccctgtctgttggagaagatccctgtatatacctgtaacactccagccaagcgaggtca 1260
QY 1477 tggctgaggtgtaacaagaccttccaggaactgtgtgttccatgactctggaagcatt 1536
|||||
Db 1261 tggctgaggtgtaacaagaccttccaggaactgtgtgttccatgactctggaagcatt 1320
QY 1537 gggaggaactcagccccaagatctggaactctcagggagaacagccaagaaatgagcatt 1596
|||||
Db 1321 gggaggaactcagccccaagatctggaactctcagggagaacagccaagaaatgagcatt 1380
QY 1597 tccggaatgctgtgagacagcgaggaacatgacacacttctgggaacagagcttgaatgct 1656
|||||
Db 1381 tccggaatgctgtgtgagacagcgaggaacatgacacacttctgggaacagagcttgaatgct 1440
QY 1657 tagatttgacagccccaagacatgctgtgcgttcttggccaagcacccagagaatgtccagt 1716
|||||
Db 1441 tagatttgacagccccaagacatgctgtgcgttcttggccaagcacccagagaatgtccagt 1500
QY 1717 ccagatgaatgctgtgtgtatcacaccttggagaagaagcttctaaagagatcaacagcaatcc 1776
|||||
Db 1501 ccagatgaatgctgtgtgtatcacaccttggagaagaagcttctaaagagatcaacagcaatcc 1560
QY 1777 ggaacatctcgtctcaatgtagatgtgttcaaaccttgaacaaactgaacccaatgaacag 1836
|||||
Db 1561 ggaacatctcgtctcaatgtagatgtgttcaaaccttgaacaaactgaacccaatgaacag 1620
QY 1837 aagctgtgctcaatcaacaagcttccatgtagctgtgtagtgaagaagaatctcgtgcgtga 1886
|||||
Db 1621 aagctgtgctcaatcaacaagcttccatgtagctgtgtagtgaagaagaatctcgtgcgtga 1680
QY 1897 ttgtgttcaatggaatttactccagcagcagcatgtagctgtcccatcatgtcaagtaacaga 1956
|||||
Db 1681 ttgtgttcaatggaatttactccagcagcagcatgtagctgtcccatcatgtcaagtaacaga 1740
QY 1957 tccgaatgagacatlgacaaatgtggaagagacaataaatacaagatgtgtagctggagcc 2016
|||||
Db 1741 tccgaatgagacatlgacaaatgtggaagagacaataaatacaagatgtgtagctggagcc 1800
QY 2017 ctgtgtccctcgaagctgaaccccttggagacatgctgtacgcttggggggctctgcctact 2076
|||||
Db 1801 ctgtgtccctcgaagctgaaccccttggagacatgctgtgtacgcttggggggctctgcctact 1860
QY 2077 tgcagatgtgtgtgagcagcgaacatcaacaggtgtctgacggcgcccgaggaagaaactg 2136
|||||
Db 1861 tgcagatgtgtgtgagcagcgaacatcaacaggtgtctgacggcgcccgaggaagaaactg 1920
QY 2137 --gtgtctatgtacaagatgctcctatccctgttaagctgtatgacatcttctgcgggt 2194
|||||
Db 1921 ggtgtctatgtacaagatgctcctatccctgttaagctgtatgacatcttctgcgggt 1980
QY 2195 gatgagccggtcaatgcccccttctatgagctgtgcgggttacttaagtgagctgtat 2254
|||||
Db 1981 gatgagccggtcaatgcccccttctatgagctgtgcgggttacttaagtgagctgtat 2040
QY 2255 catcaagggatcgtgtatgagaagaagcagcgtgtgaagaagacatgctgagatcatgag 2314
|||||
Db 2041 catcaagggatcgtgtatgagaagaagcagcgtgtgaagaagacatgctgagatcatgag 2100
QY 2315 cctggaacacagcactcctgtgttaagctgtgtcaattagtagcctcactctctgt 2374
|||||
Db 2101 cctggaacacagcactcctgtgttaagctgtgtcaattagtagcctcactctctgt 2157
QY 2375 gaggcgtgctgtgagtgatctatcctgaagttaagaaacccgtgtccctcagtgatcc 2434
|||||

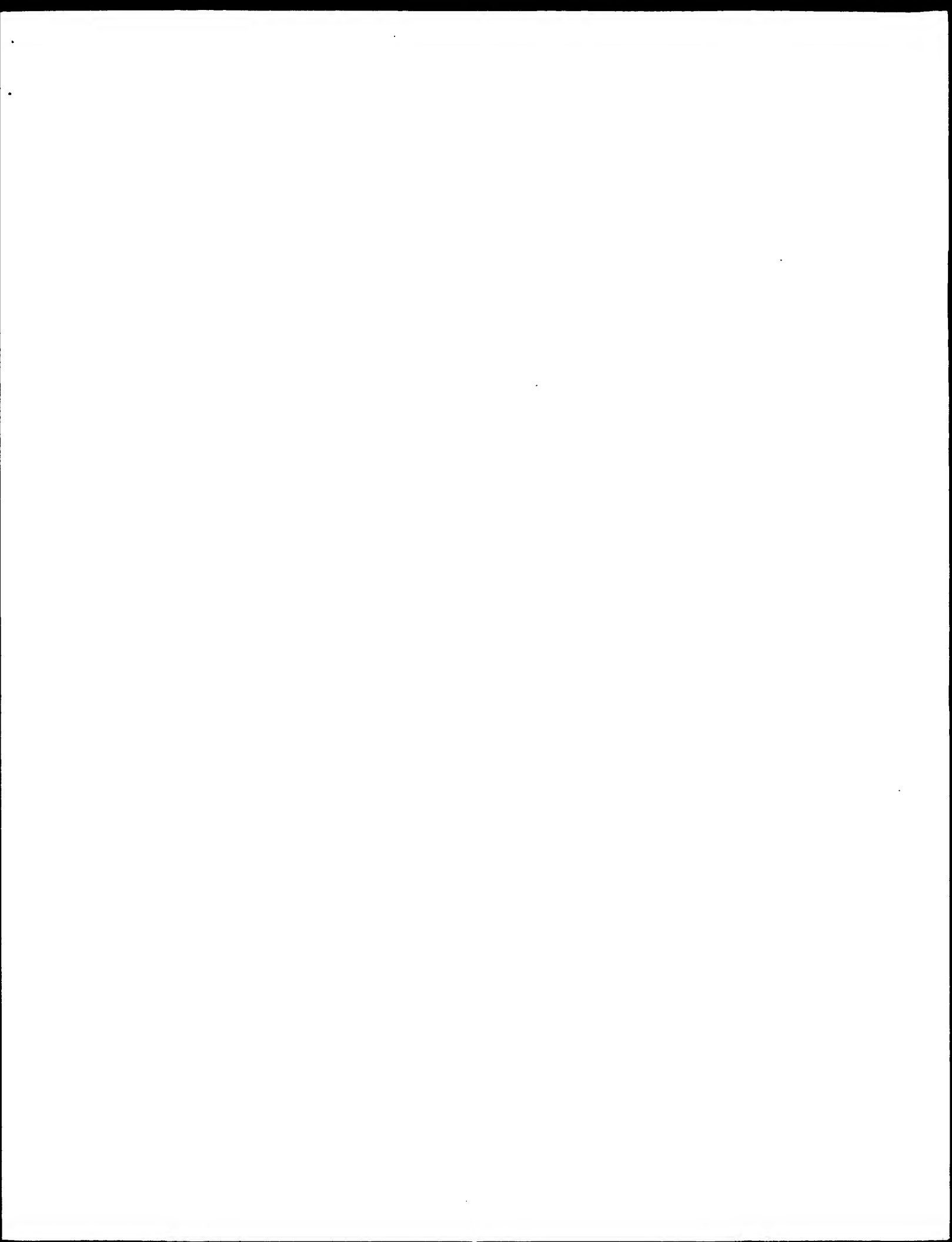
OY	4594	agugaccatcgcacagcttcccacagccaatgaaccttccagatvggaatgga	4653
Db	4378	agtggaccatctgcacagcttcccacagccaatgaaccttccagatvggaatgga	4437
OY	4654	caatgacgaacccctcaactcgtacgtacgtatgacagcgacaatatcaagaatgtgc	4713
Db	4438	caatgacgaacccctcaactcgtacgtacgtatgacagcgacaatatcaagaatgtgc	4497
OY	4714	ctgtgtgtcccccaggggcagggggctgtcctctccacaagaatacaaacctgcag	4773
Db	4498	ctgtgtgtcccccaggggcagggggctgtcctctccacaagaatacaaacctgcag	4557
OY	4774	atatccctcaagaccctgcagacagaagaataattgtgatatctgtatgaagcgatgtgc	4833
Db	4558	atatccctcaagaccctgcagacagaagaataattgtgatatctgtgtgaagcgatgtgc	4617
OY	4834	agatcatagcaaaaagcttaaaagaatactctgtgtgatgtattagtatbgtcggt	4893
Db	4618	agatcatagcaaaaagcttaaaagaatactctgtgtgatgtattagtatbgtcggt	4677
OY	4894	tttccctgggtgtgcagttaattactccaagacccttcctccgagccaagaattatgatgtcca	4953
Db	4678	tttccctgggtgtgcagttaattactccaagacccttcctccgagccaagaattatgatgtcca	4737
OY	4954	tcaaaaacaatgaaagaaacaactaaagcttgcgcgaaggaagatctgcagatcgatttcca	5013
Db	4738	tcaaaaacaatgaaagaaacaactaaagcttgcgcgaaggaagatctgcagatcgatttcca	4797
OY	5014	acagatctgggaagaatttatgacagcgctctgacaccaagaataatgttcaaggtgtgttca	5073
Db	4798	acagatctgggaagaatttatgacagcgctctgacaccaagaataatgttcaaggtgtgttca	4857
OY	5074	ataacaagggtctgtgcatactagctcttctctgaatgtcatcaacaatgtccatttccc	5133
Db	4858	ataacaagggtctgtgcatactagctcttctctgaatgtcatcaacaatgtccatttccc	4917
OY	5134	ggggccaacctgcgaaggggagaaacacctgaagcattatggaaattactgtcttcaatcattc	5193
Db	4918	ggggccaacctgcgaaggggagaaacacctgaagcattatggaaattactgtcttcaatcattc	4977
OY	5194	ccctgaaatctcaaccaagaacacagctctccagagtgtgctctgtatgccacatcaatggatgt	5253
Db	4978	ccctgaaatctcaaccaagaacacagctctccagagtgtgctctgtatgccacatcaatggatgt	5037
OY	5254	tccttgtgtccatctgtgttcaacttttgcaatgtcccttgcgtcccaagccagcttctgtat	5313
Db	5038	tccttgtgtccatctgtgttcaacttttgcaatgtcccttgcgtcccaagccagcttctgtat	5097
OY	5314	tcctgaaatccagagcggtgtacgaagaagcaaaacacctgaagtgttaacagtggaatgagc	5373
Db	5098	tcctgaaatccagagcggtgtacgaagaagcaaaacacctgaagtgttaacagtggaatgagc	5157
OY	5374	ctgtcatcctaactgtcttcaaatttgtgtctbgtgatatgtgcacaatagttgtccctgtcca	5433
Db	5158	ctgtcatcctaactgtcttcaaatttgtgtctbgtgatatgtgcacaatagttgtccctgtcca	5217
OY	5434	caatgtgcatattatcatcttcatctgtctccacagagaagtcctatgtgtcccccacaatc	5493
Db	5218	caatgtgcatattatcatcttcatctgtctccacagagaagtcctatgtgtcccccacaatc	5277
OY	5494	tgcctgtgcagaccctctactcttctgtgtatgggtgtgtcaatcaactctcaatgttacc	5553
Db	5278	tgcctgtgcagaccctctactcttctgtgtatgggtgtgtcaatcaactctcaatgttacc	5337
OY	5554	cagctcctctgtgttcaagaatccccaagacagcctatgtgtgtctcaacagcgtgaac	5613
Db	5338	cagctcctctgtgttcaagaatccccaagacagcctatgtgtgtctcaacagcgtgaac	5397
OY	5614	tcttcatattggaataatgaagaggtgtgcacaccttgtgtgtgaagctgttccacgacacata	5673
Db	5398	tcttcatattggaataatgaagaggtgtgcacaccttgtgtgtgaagctgttccacgacacata	5457
OY	5674	agctgaaataataatcaatgaatcctctgaatctgcgtgtctctgttcttccacaatttttccc	5733

Db	5458	agccggaataataccaatgataatcccgaaagtcggtgtcttgatcttcccaattttgccc	5517
Qy	5734	ttggagcagaaggtctcatcgtacatctggtgaaaaaccagaagcaatggctgatatgcccctggaaagt	5793
Db	5518	ttggagcagaaggtctcatcgtacatctggtgaaaaaccagaagcaatggctgatatgcccctggaaagt	5577
Qy	5794	ttggggagaatcgctgtgtgttgcacaaattctcttggagctgtgtggagcaaacctcttcg	5853
Db	5578	ttggggagaatcgctgtgtgttgcacaaattctcttggagctgtgtggagcaaacctcttcg	5637
Qy	5854	ccatgagccgtgtgaaggggtgtgttcttctcctaactgcttctgatacttgatccagtaacgattct	5913
Db	5638	ccatgagccgtgtgaaggggtgtgttcttctcctaactgcttctgatacttgatccagtaacgattct	5697
Qy	5914	tcatcaaggcccaagacctgttaatagtcaaaactatcttccctctgaatgatatgaataaagt	5973
Db	5698	tcatcaagcccaagacctgttaatagtcaaaactatcttccctctgaatgatatgaataaagt	5757
Qy	5974	ttgaagcgggaagaaacagaaagatctctgtgaatgtgtggagccagaatgacatctctaagaatca	6033
Db	5758	ttgaagcgggaagaaacagaaagatctctgtgaatgtgtggagccagaatgacatctctaagaatca	5817
Qy	6034	aaggagttgacgaagaataataataagaaggaagcagaacgcgtctgtgtacagagtttgcgttg	6093
Db	5818	aaggagttgacgaagaataataataagaaggaagcagaacgcgtctgtgtacagagtttgcgttg	5877
Qy	6094	gcatctccctccgtgtgtgaatgtgtcttgggctccctggagttatgtgggctgtgaataatcataa	6153
Db	5878	gcatctccctccgtgtgtgaatgtgtcttgggctccctggagttatgtgggctgtgaataatcataa	5937
Qy	6154	ctttcaagaatgttaacaaggagataccaactgtttaccagagagaaatgtcttctcttaacaaa	6213
Db	5938	ctttcaagaatgttaacaaggagataccaactgtttaccagagagaaatgtcttctcttaacaaa	5997
Qy	6214	ata-gtatcttatacaaacatcccatgtgaatgacatacaaaatgtgtactgtccctcaagttt	6272
Db	5998	ataagttactcttaaccaaacatcccatgtgaatgacatacaaaatgtgtactgtccctcaagttt	6057
Qy	6273	gatgcatcacaagaagctgtgtgactgtggagaagaacacgtgtgaattcttggccctttgaga	6332
Db	6058	gatgcatcacaagaagctgtgtgactgtggagaagaacacgtgtgaattcttggccctttgaga	6117
Qy	6333	ggagtcccaagaagaaagatgttggcgaaggtttgtgtgtgtgtggatcttcggaactgtggccctc	6392
Db	6118	ggagtcccaagaagaaagatgttggcgaaggtttgtgtgtgtgtggatcttcggaactgtggccctc	6177
Qy	6393	gtgaagctatctgagaagaaaataatgtcgtgtgaactatagtgtgaagtgagacaaacgaacgactctct	6452
Db	6178	gtgaagctatctgagaagaaaataatgtcgtgtgaactatagtgtgaagtgagacaaacgaacgactctct	6237
Qy	6453	acagccatgctcttgaatcgcgcgggcctccctgtgtgtgttctctgtatgaaaccccaacgaagc	6512
Db	6238	acagccatgctcttgaatcgcgcgggcctccctgtgtgtgttctctgtatgaaaccccaacgaagc	6297
Qy	6513	atcgagctcccaagcccgccgcttctcttggaaattgtgtccctcaagtgttctcaagaaggg	6572
Db	6298	atcgagctcccaagcccgccgcttctcttggaaattgtgtccctcaagtgttctcaagaaggg	6357
Qy	6573	agatacagtagtcttacaatcctcatagtatagtgaagaaatgtgaagctctcttgcactagaagt	6632
Db	6358	agatacagtagtcttacaatcctcatagtatagtgaagaaatgtgaagctctcttgcactagaagt	6417
Qy	6633	gnaatcatcgtcatcgtatggaaggtttcaagtgtccttggagtgatgtccagcatcttaaaaaatagg	6692
Db	6418	gnaatcatcgtcatcgtatggaaggtttcaagtgtccttggagtgatgtccagcatcttaaaaaatagg	6477
Qy	6693	tttggagatgtgtttacaataagttgttgcagatactgacagaggttccaacccggaacctgtgaagct	6752
Db	6478	tttggagatgtgtttacaataagttgttgcagatactgacagaggttccaacccggaacctgtgaagct	6537
Qy	6753	gtccaagatcttcttggactgtgaatcttccctgtgaagtgcttcttaaaagagaacacacccggaac	6812

Db 6538 gtccagattcttcttgacttgcatlctcctggaagtgtcttaaaagagaacacccggaac 6597
 QY 6813 atgctaaatccagcttccatctcattctctctctgccaagatattcaacatccctc 6872
 Db 6598 atgctaaatccagcttccatctcattctctctctgccaagatattcaacatccctc 6857
 QY 6873 tcccaagacaaaagcgaactccacataagaaactactctgttctccagacaactgtac 6932
 Db 6658 tcccaagacaaaagcgaactccacataagaaactactctgttctccagacaactgtac 6717
 QY 6933 caagtatttgaactttgccaagggacaaagatgatagtacacacttaaaagaccttca 6992
 Db 6718 caagtatttgaactttgccaagggacaaagatgatagtacacacttaaaagaccttca 6777
 QY 6993 ttacacaaaacccagacagtagtggacgttgcagttctccacatcttctccagagatgag 7052
 Db 6778 ttacacaaaacccagacagtagtggacgttgcagttctccacatcttctccagagatgag 6837
 QY 7053 aaagtgaagaagaagctctgtatgaagaatccgttccatccaggggtggtcgtgaagaaga 7112
 Db 6838 aaagtgaagaagaagctctgtatgaagaatccgttccatccaggggtggtcgtgaagaaga 6897
 QY 7113 ggaactgaacttccctctgccaatgtagaagtgtgtggaagaagaagccagaagttgat 7172
 Db 6898 ggaactgaacttccctctgccaatgtagaagtgtgtggaagaagaagccagaagttgat 6957
 QY 7173 gtgggaagaagaactgtaactgtactgtatactatcaatgcaatgcaatcaatgca 7232
 Db 6958 gtgggaagaagaactgtaactgtactgtatactatcaatgcaatgcaatcaatgca 7017
 QY 7233 atgaaaaacaaatccattacaggggagagtccttggtagcctatgtctgtatgtctct 7292
 Db 7018 atgaaaaacaaatccattacaggggagagtccttggtagcctatgtctgtatgtctct 7077
 QY 7293 caagtgaagaactgtaattagtttttaacctataacctatgtaaaactatattgaac 7352
 Db 7078 caagtgaagaactgtaattagtttttaacctataacctatgtaaaactatattgaac 7137
 QY 7353 ccaatgacataatggttttgaactcaac-ttttttttttttttttttttttttttttttt 7411
 Db 7138 ccaatgacataatggttttgaactcaac-ttttttttttttttttttttttttttttttt 7197
 QY 7412 catlgggtgtgcaacaataatcatcaatcaatcatlggccaagcattatgatacaaatc 7471
 Db 7198 catlgggtgtgcaacaataatcatcaatcaatcatlggccaagcattatgatacaaatc 7257
 QY 7472 aaaagtgataatgcaatccatctcaactaagccaatgccaatgccaagagactggtcccg 7531
 Db 7258 aaaagtgataatgcaatccatctcaactaagccaatgccaatgccaagagactggtcccg 7317
 QY 7532 gtgacacatccattgtctgccaatgtagtgcagagttatgtagccaagtttttcagaa 7591
 Db 7318 gtgacacatccattgtctgccaatgtagtgcagagttatgtagccaagtttttcagaa 7377
 QY 7592 agtttgaagacacatggtgtgtcatgtcacttttggtaaaagctgctcgtccagatct 7651
 Db 7378 agtttgaagacacatggtgtgtcatgtcacttttggtaaaagctgctcgtccagatct 7437
 QY 7652 atcaaatatgaataatagtttgaagaatgtgccaatgccaatgccaatccctgtttgat 7711
 Db 7438 atcaaatatgaataatagtttgaagaatgtgccaatgccaatgccaatccctgtttgat 7497
 QY 7712 tccctctgaagaagctgttctgtgtgagtaacaatgcaaaaatgtggtgtctctag 7771
 Db 7498 tccctctgaagaagctgttctgtgtgagtaacaatgcaaaaatgtggtgtctctag 7557
 QY 7772 caacggaaaactgtgtccattgtatataatgtccatgtctcgaagccatggtgtctacaagg 7831
 Db 7558 caacggaaaactgtgtccattgtatataatgtccatgtctcgaagccatggtgtctacaagg 7617
 QY 7832 tcatcctttagagactctaaatatactagatccctgtaagaagcaagaatcaacagc 7891
 Db 7618 tcatcctttagagactctaaatatactagatccctgtaagaagcaagaatcaacagc 7677

QY 7892 caaactgtcggggtcgtgcaagctgtcgaagccagggcatgggattaaagatgtggtt 7951
 Db 7678 caaactgtcggggtcgtgcaagctgtcgaagccagggcatgggattaaagatgtggtt 7736
 QY 7952 caaactgaaggagcctgtgccaattgttccctgaactgtctcgaacatgtaactgtcat 8011
 Db 7737 caaactgaaggagcctgtgccaattgttccctgaactgtctcgaacatgtaactgtcat 7796
 QY 8012 ctcaagatgtttatctgacacaagatgattatcttctgcttttgaatatactagaana 8071
 Db 7797 ctcaagatgtttatctgacacaagatgattatcttctgcttttgaatatactagaana 7856
 QY 8072 tgaag 8076
 Db 7857 tgaag 7861

Search completed: September 14, 2002, 07:48:35
 Job time: 72627 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2002, 10:15:42 ; Search time 277.92 seconds
(without alignments)
9228.933 Million cell updates/sec

Title: US-09-595-526b-1
Perfect score: 10442
Sequence: 1 ggcgcggaccgcgagagcg.....aaaaaaaaaaaaaaaaaa 10442

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Issued_Patents_NA: *
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCrUS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	430.8	4.1	5894	3	US-08-665-259-24
2	430.8	4.1	5894	3	US-08-762-500-24
3	430.8	4.1	6525	3	US-08-762-500-74
4	96.2	0.9	240	1	US-08-628-417-6
5	93.8	0.9	2447	2	US-09-014-969-14
6	91.4	0.9	1117	4	US-09-247-373B-33
7	86.6	0.8	1474	4	US-08-821-994-64
8	86	0.8	260	2	US-08-520-678A-29
9	85.2	0.8	1582	4	US-08-897-126-29
10	85.2	0.8	1582	3	US-08-545-196B-12
11	85	0.8	3410	4	US-09-020-956-110
12	85	0.8	3410	4	US-09-030-607-110
13	85	0.8	3410	4	US-09-439-313-110
14	85	0.8	3410	4	US-09-471-528-22
15	84.4	0.8	144	1	US-08-702-344-26
16	84.4	0.8	2671	6	US-08-5168051-9
17	84	0.8	1129	4	US-09-227-357-40
18	83.6	0.8	1066	1	US-08-157-101A-4
19	83.6	0.8	1641	1	US-08-300-903A-8
20	83.4	0.8	1736	3	US-09-182-816-22
21	83.4	0.8	1736	3	US-09-182-816-24
22	83.4	0.8	1736	3	US-09-471-528-22
23	83.4	0.8	1736	3	US-09-471-528-22
24	83.4	0.8	1736	4	US-09-634-530-22
25	83.4	0.8	1736	4	US-09-634-530-24
26	83.2	0.8	140	1	US-08-628-417-5
27	83	0.8	1441	4	US-08-821-994-63

28	83	0.8	1817	1	US-08-473-981A-5	Sequence 5, Appli
29	83	0.8	1817	2	US-08-474-087-5	Sequence 5, Appli
30	82.6	0.8	2280	3	US-08-813-150-1	Sequence 1, Appli
31	82.4	0.8	1602	1	US-08-530-950-3	Sequence 3, Appli
32	82.4	0.8	1602	3	US-08-888-429A-3	Sequence 3, Appli
33	82.4	0.8	1602	4	US-09-149-879-3	Sequence 3, Appli
34	82.2	0.8	1813	4	US-09-071-224-3	Sequence 3, Appli
35	82.2	0.8	2852	3	US-09-027-137-2	Sequence 3, Appli
36	82	0.8	1454	4	US-09-372-422A-19	Sequence 19, Appli
37	82	0.8	1882	4	US-09-370-253-1	Sequence 1, Appli
38	82	0.8	6671	1	US-08-280-443-1	Sequence 1, Appli
39	82	0.8	6671	1	US-08-457-459-1	Sequence 1, Appli
40	82	0.8	6671	1	US-08-555-678-1	Sequence 1, Appli
41	82	0.8	6671	5	PCR-US95-02275-1	Sequence 1, Appli
42	81.4	0.8	1279	3	US-09-248-335-25	Sequence 25, Appli
43	81.4	0.8	1493	1	US-08-340-820-24	Sequence 24, Appli
44	81.4	0.8	1493	1	US-08-593-535-24	Sequence 24, Appli
45	81.4	0.8	2184	4	US-08-955-918C-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-665-259-24
; Sequence 24, Application US/08665259
; Patent No. 6028173
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klingler, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,259
; FILING DATE: 17-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-9.1
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..5053
; US-08-665-259-24

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,500
FILING DATE: 09-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,259
FILING DATE: 17-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10469
FILING DATE: 17-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: 105-9.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 5894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..5053
US-08-762-500-24

Query Match 4.1%; Score 430.8; DB 3; Length 5894;
Best Local Similarity 56.1%; Pred. No. 5.2e-89;
Matches 944; Conservative 0; Mismatches 692; Indels 48; Gaps 5;

QY 2050 ggtacgtctgggggggcttcgctactctgagatgtgtggagagcaatcattcaagg 2109
DB 555 ggtacgtctgggggggcttcgctactctgagatgtgtggagagcaatcattcaagg 614
QY 2110 tgcctgagggcagcagaga-----agaaactgtgtctatatgcaacaga 2154
DB 615 accatgcccagatccgcccacacacgacgctgtccagagactgacggtgacacaaagagt 674
QY 2155 tgcctatccctgttactgttgaatcattcttcgaggtgagtcgagtcagtcaccc 2214
DB 675 tcccgatcccgccgcttcatcagacaccccttctcgtgacccatccagacacgctgccc 734
QY 2215 tcttcagcgtctggcctgagattactcagtggtgtgatacacaagggcaltgtatg 2274
DB 735 tctgctgctgctgacgcttccacacgacgctgacacacacacacacacacacacac 794
QY 2275 agaaagagcaagcgtgaaagagcaatgcatatgagtcgagtcgagtcgagtcgagtc 2334
DB 795 agaaagagcaagcgtgaaagagcaatgcatatgagtcgagtcgagtcgagtcgagtc 854
QY 2335 ggtttagcgtctgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 2394
DB 855 ggaagtcctggttctcctgttcttcttcttcttcttcttcttcttcttcttcttctt 914
QY 2395 tcatcctgaagta-----ggaactgctgctcctcaagtcagtcagtcagtc 2439
DB 915 tgccttctgctgacgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtc 974
QY 2440 tgggtgttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 2499
DB 975 tgggtgttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1034
QY 2500 ggaactcttctcagagcaacacgagcagcagcagcagcagcagcagcagcagcagcagc 2559
DB 1035 gcaactcttctcagagcaacacgagcagcagcagcagcagcagcagcagcagcagcagc 1094
QY 2560 tgaactcctcagcgtctgt 2619
DB 2619 tgaactcctcagcgtctgt

DB 1095 ccttaccatcccttacttcttctgctggcccttgcgttacaactgcatgacttgcagccagac 1154
QY 2620 tcttcgttaccctgctgtctcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2679
DB 1155 tcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1214
QY 2680 ttgagagcagggcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 2739
DB 1215 ttgagagcagggcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 1274
QY 2740 atggtcttcaatctcaccacttgcattcctcagtcagtcagtcagtcagtcagtcagtcagtc 2799
DB 1275 acgacttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1334
QY 2800 tgaagactgttgaatgagtcgttcttcttcttcttcttcttcttcttcttcttcttctt 2859
DB 1335 tgggtgacttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1394
QY 2860 atttcttgcaccacagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 2910
DB 1395 acttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1454
QY 2911 gccacccgtgttccacacag 2970
DB 1455 aagaagacagtgaccccgag 1514
QY 2971 acttgaagcgt 3028
DB 1515 acttgt 1574
QY 3029 ----gttgcctgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 3084
DB 1575 acagagcggcgcttgcagagac 1634
QY 3085 ttggccaacatlgagcggggag 3144
DB 1635 ttggccaacatlgagcggggagagagagagagagagagagagagagagagagagagag 1694
QY 3145 cgacctgt 3204
DB 1695 ccaccagtgagcggcgcttgcagagacacacacacacacacacacacacacacacacacac 1754
QY 3205 ggcagaaactgt 3264
DB 1755 ggaagagcgt 1814
QY 3265 aacacatctgttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 3324
DB 1815 agcacttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1874
QY 3325 ttgagcagatgt 3384
DB 1875 tcmaagcagatg----ctgcacatcattcgccctggagagacacacacacacacacacac 1931
QY 3385 agcttcaagtgag 3444
DB 1932 tcttgagcggggag 1991
QY 3445 aggttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 3504
DB 1992 aggttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 2051
QY 3505 gggagctgtctgaaataacagcaagcgcacacatattctctcacaacacacacacacac 3564
DB 2052 gggatcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 2111
QY 3565 atgaagcagcgtctgt 3624
DB 2112 acgagcgtgacgtctgt 2171
QY 3625 ttggtcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 3684
DB 2172 gctggtcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 2231

QY 3685 agaa 3688
Db 2232 AGGA 2235

RESULT 3
US-08-762-500-74
Sequence 74, Application US/08762500
Patent No. 6030806
GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Burns, Timothy C.
APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Klinger, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: One Mountain Road
CITY: Framingham
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,500
FILING DATE: 03-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,259
FILING DATE: 17-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10469
FILING DATE: 17-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IGS-9.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 6525 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 573..5684
US-08-762-500-74

Query Match 4.1%; Score 430.8; DB 3; Length 6525;
Best Local Similarity 56.1%; Pred. No. 5,5e-89;
Matches 944; Conservative 0; Mismatches 692; Indels 48; Gaps 5;

QY 2050 gtaagctcggggggttcgcactctgacagatggtgtagaagcaatcatcaagg 2109
Db 1186 GGTACATCGGAAAGGCTTCTGGCCGTGACATGCTGTGAGACCGGGCATCATGAGT 1245
QY 2110 tctgacgggacacagaa-----agaaactgtgtctatcatgcaacaga 2154
Db 1246 ACCATGCGATGCGCGCCACACCGCATGCTTCCACAGAGACTGACGATCAAGAGGT 1305

QY 2155 tgcctatccctgttaagttatgaatcttctcgagggtatgaagccgtcaatgcc 2214
Db 1306 TCCCGTACCCCGCGCTTCAATCGAGACCCCTTCTGTCGCGCCATCGAGTACCAGTCC 1365
QY 2215 tcttcatgacgtggtcggtgattactcagtcgtgtgatacatcaaggacgtgatg 2274
Db 1366 TCTCTGCTGTGCTCAAGCTTCAACCTACCGCGCTCACCATTGCGCGTCTGTCTGTA 1425
QY 2275 agaaggaagcaagctgaaagaaagacatgcgatalcgtgagccttgaaacacatact 2334
Db 1426 ACAAGAAAGAGAGCTGAAGAGTACATGCGCATGATGGGCTCAGCAGCTGCTGCACT 1485
QY 2335 gtttagctgttcatgtagtaccatctctctgtgtagcgtcggtgtatg 2394
Db 1486 GAGAGCTGTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1545
QY 2395 tcatctgaagta-----ggaacactgctccctcaagtatccagcg 2439
Db 1546 TCTCTTCTGTGTCAAGGTGAAGCCAAATGTAGCCGTCTCTCCCGCAGCACCCTCC 1605
QY 2440 tgggttcttctctcgtcgtgtgtgtgtagaactctgcaatgcttctgalt 2499
Db 1606 TGTCTGCGCCTTCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1665
QY 2500 gaaacttcttccagagcaactcgtgagcagcgtgtggtggtatcatcttcaagc 2559
Db 1666 GCACCTTCTTCAAGCAAAACATGAGCAGCAGCTTGGAGGCTTCTTCTTCTTCTTCA 1725
QY 2560 tgaactgacctagctcgtgtgtgtgtagcagagacatggtggtcacaacaga 2619
Db 1726 CTTAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1785
QY 2620 tcttgcagcctgctcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2679
Db 1786 TCTGCTCTGCT 1845
QY 2680 ttgaaggaagcaggtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 2739
Db 1846 TTGAGGCGAAGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1905
QY 2740 atggtcctaactcaacacactcgaatcgaatgagtgagtgagtgagtgagtgagtg 2799
Db 1906 ACGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1965
QY 2800 tgaagcctgttgaatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 2859
Db 1966 TGTGACTGTGATGAGGAGGCGCTTCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGG 2025
QY 2860 atttctctgacacaaagtcctactggttgcgaggaagtgtatg-----agaaga 2910
Db 2026 ACTTCTCATCATGCGCT 2085
QY 2911 gccacactgttccaacacagagaagatgcaaatctgcatgaggaaggaacacccc 2970
Db 2086 AAGAAAGACATGACCCCGAGAAACACTCAGAAACGAGTACTTGAAGCCGAGCAAG 2145
QY 2971 acttgaagcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 3028
Db 2146 ACTGTGTGCGGGGATCAAGATCAAGCACTGTCTCAAGGTGTTCAGGTTGGGAATTA 2205
QY 3029 ----gtgtgtgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 3084
Db 2206 ACAAGGGGGCGCTGAGAGACTGTAACTGAACCTGTAGAGGAGGAGAGATACCGTCTG 2265
QY 3085 tgggacacatgagcgaggaagagacacacatgtcaatctcgtacccggtgtgtccccc 3144
Db 2266 TGGGCGACAAAGGAGCGGGAGAGACCAACCCCTTCTCATGCTTCAAGGCTCTTTC 2235
QY 3145 cgacctgggagcagcctacatctcgtggaagaaagacatctgctgtagatgagcaccat 3204
Db 2236 CCACCATGTGAGCGGCAATATCATGAGCGGATTAATAATTTCCAGAGCATGTGTTCA 2285

TOPOLOGY: Linear
MOLECULE TYPE: cDNA
US-09-014-969-14

Query Match 0.9%; Score 93.8; DB 2; Length 2447;
Best Local Similarity 63.0%; Pred. No. 7, 6e-12;
Matches 143; Conservative 1; Mismatches 83; Indels 0; Gaps 0;

QY 10216 ttccacacagattcttaagtaatcattcattaaaggagaaagaaagaaatctt 10275
DB 2209 TTGTACTTTAAATGTCACAAATTAACCTTTGGAGAAAAAARAAAAA 2268
QY 10276 tgcatacgaacttataagagattaaatgcatattcttggtgataatag 10335
DB 2269 AA 2328
QY 10336 agtcacaaataaagctgtgacagctctgttaaaaaaagaaagaaagaa 10395
DB 2329 AA 2388
QY 10396 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 10442
DB 2389 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2435

RESULT 6

US-09-247-373B-33
Sequence 33, Application US/09247373B
Patent No. 6168954
GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CI-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
SEQ ID NO 33
LENGTH: 1117
TYPE: DNA
ORGANISM: SOYBEAN
FEATURE:
NAME/KEY: unsure
LOCATION: (1101)
OTHER INFORMATION: M-A OR C
NAME/KEY: unsure
LOCATION: (1104)
OTHER INFORMATION: M-A OR C
NAME/KEY: unsure
LOCATION: (1116)
OTHER INFORMATION: N-G or A or T or C
US-09-247-373B-33

Query Match 0.9%; Score 91.4; DB 4; Length 1117;
Best Local Similarity 72.0%; Pred. No. 1, 8e-11;
Matches 116; Conservative 2; Mismatches 43; Indels 0; Gaps 0;

QY 10282 tcataacttataagatatttaaatgcatattcttggtgataatagagtcac 10341
DB 952 taatatattatattgagcattatcataattcattctttaaaaaa 1011
QY 10342 aaataaagctgtgacagctctgttaaaaaaagaaagaaagaaagaa 10401
DB 1012 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1071
QY 10402 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 10442
DB 1072 aaaaaaaaaaaaaaaaaaaaaaaaaa 1112

US-08-821-994-64
Sequence 64, Application US/08821994A
Patent No. 6228643
GENERAL INFORMATION:
APPLICANT: Greenland, Andrew J
APPLICANT: Thomas, Ian
TITLE OF INVENTION: Promoters
FILE REFERENCE: PPD 50108
CURRENT APPLICATION NUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-22
EARLIER APPLICATION NUMBER: PCT/GB97/00729
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: GB 9606062.9
EARLIER FILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 64
LENGTH: 1474
TYPE: DNA
ORGANISM: Brassica napus
US-08-821-994-64

RESULT 7

Query Match 0.8%; Score 86.6; DB 4; Length 1474;
Best Local Similarity 65.0%; Pred. No. 2, 6e-10;
Matches 128; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 10246 ttcatataagaaagaaagaaagaaatcttgatgcatcattatataagatt 10305
DB 1255 tccgcatacagattgctgcgtataatccttgcgcatacattcattggtcaaa 1314
QY 10306 aatgcataattctatgltgataataatgagtcacaaataagctgtgacggtctgt 10365
DB 1315 gaagattgattgtgttattatgaagagataataaagatataattctct 1374
QY 10366 taaaaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 10425
DB 1375 taaaaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 1434
QY 10426 aaaaaaaaaaaaaaaaaa 10442
DB 1435 aaaaaaaaaaaaaa 1451

RESULT 8

US-08-520-678A-29/C
Sequence 29, Application US/08520678A
Patent No. 5874565
GENERAL INFORMATION:
APPLICANT: Rice, Charles M.
APPLICANT: Kolykhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
NUMBER OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haterkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,678A
FILING DATE:

```

: INFORMATION FOR SEQ ID NO: 29:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 260 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:   MOLECULE TYPE: DNA (genomic)
: US-08-897-126-29
:
: Query Match
:   Best Local Similarity 75.4%; Score 86; DB 4; Length 260;
:   Matches 107; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
:
: Qy 10299 agtattaaatgcattctctatgttgaataataatgagtcacaataaagcttgaca 10358
:   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
: Db 249 AGGCGTAAATGAGCCAGCCACTTAAGAAGCAAAATTAGAACTCGAAAGAAAGAAAGAAA 190
:
: Qy 10359 gtctctgttaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 10418
:   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
: Db 189 AAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 130
:
: Qy 10419 aaaaaaaaaaaaaaaaaaaaaa 10440
:   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
: Db 129 AAAAAAAAAACAAAAAACGAA 108
:
: RESULT 10
: US-08-545-196B-10
:   Sequence 10, Application US/08545196B
:   Patent No. 6080577
:   GENERAL INFORMATION:
:     APPLICANT: MELKI, JUDITH
:     APPLICANT: MUNNICH, ARNOLD
:     TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
:     NUMBER OF SEQUENCES: 65
:     CORRESPONDENCE ADDRESS:
:       ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
:       STREET: PO BOX 747
:       CITY: FALLS CHURCH
:       STATE: VA
:       COUNTRY: USA
:       ZIP: 22040-0747
:     COMPUTER READABLE FORM:
:       MEDIUM TYPE: Floppy disk
:       COMPUTER: IBM PC compatible
:       OPERATING SYSTEM: PC-DOS/MS-DOS
:       SOFTWARE: Patent Release #1.0, Version #1.30
:     CURRENT APPLICATION DATA:
:       APPLICATION NUMBER: US/08/545,196B
:       FILING DATE: 19-OCT-1995
:       CLASSIFICATION: 435
:     ATTORNEY/AGENT INFORMATION:
:       NAME: FARACI, C. J.
:       REGISTRATION NUMBER: 32,350
:       REFERENCE/DOCKET NUMBER: 2121-110P
:       TELECOMMUNICATION INFORMATION:
:         TELEPHONE: (703) 205-8000
:         TELEFAX: (703) 205-8050
:       INFORMATION FOR SEQ ID NO: 10:
:         SEQUENCE CHARACTERISTICS:
:           LENGTH: 1582 base pairs
:           TYPE: nucleic acid
:           STRANDEDNESS: double
:           TOPOLOGY: linear
:           MOLECULE TYPE: cDNA
:           US-08-545-196B-10
:
: Query Match
:   0.8%; Score 85.2; DB 3; Length 1582;
:   Best Local Similarity 79.6%; Pred. No. 5.7e-10;
:   Matches 113; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

```

QY	10302	atthaaatgcatcttccctgtgtga-ctaaagagcgcacaaataacgttgcagt	10360
Db	1424	ATTGACTGTTTTTTCTATCTTATATGTTAAAGTAAATVATAAATAATTAAAT	1483
QY	10361	tcgtctgaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa	10420
Db	1484	TTTTTTTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	1543
QY	10421	aaaaaaaaaaaaaaaaaaaaa	10442
Db	1544	AAAAAAAAAAAAAAAAAAAAA	1565

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

	Query Match	0.8%;	Score 85.2;	DB 3;	Length 1582;
	Best Local Similarity	79.6%;	Pred. No. 5.7e-10;		
	Matches 113;	Conservative	0;	Mismatches 28;	Indels 1; Gaps 1
QY	10302	atataaatgcatatcttcatagtgtga-atataatgagtcacacaaataaagctgacagt	10360		
Db	1424	ATGTGACTGTTTTTTCCTATCTTCATATAGCTTTAAAGATATATATATAATTTTAA	1483		
QY	10361	tctgttaaaaaa	10420		
Db	1484	TTTTTTTAAAAA	1543		
QY	10421	aaaaaaaaaaaaa	10442		
Db	1544	AAAAAAAAAAAAA	1565		

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

```

Query Matched Score 85; DB 4; Length 3410;
Best Local Similarity 81.5%; P-Val 9.6e-10;
Matches Conservative 1; Mismatches 21; Indels 0; Gaps 0;

QY 10334 tgtatattaatggtcacaataaaagctgtgtacagtcgttttaaaaaaaaaaaaaa 10383
      |||||
DB 3282 TATATTGTATTGCTGCACAAATAAAGCGTTCCTTAATGTCTTAATTTAAAAA 3341

QY 10384 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 10442
      |||||
DB 3342 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3400

```

```

RESULT 13
US-09-030-607-110
; Sequence 110, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
;

```


	Query Match:	0.8%;	Score 85;	DB 4;	Length 3410;	
	Best Local Similarity	81.5%;	Pred. No.	9.6e-10;		
	Matches	97;	Conservative	1;	Mismatches	21; Indels 0; Gaps 0;
QY	10324	tgtacatacatagtcacacaataagaagtctgycacgttctcgtttaaaaaaaaaaaaaaa	10383			
Db	3282	TATTAAGTTTATGCGTCACAAATTAAAGCTTTCTTAATGTCTTTAAAAAAAAAAAAA	3341			
QY	10384	aaa	10442			
Db	3342	AAATAA	3400			

```

QY      10324 tglatatatgagtgactacaataaaagcgtgcagttctgtttaaaaaaaaaaaaaa 10383
Db       3282 tataaagtlltatgglycacaaaattaaaggcttcttatattgtttaaaaaaaaaa 3341

QY      10384 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 10442
Db       3342 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 3400

RESULT   15
US-08-702-344-26
; Sequence 26, Application US/08702344
; Patent No. 5723315
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Lavallee, Edward
APPLICANT: Racine, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,344
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-702-344-26

Query Match          0.8%; Score 84.4; DB 1; Length 144;
Best Local Similarity 74.6%; Pred. No. 2.3e-10;
Matches 103; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY      10305 aaatgcatttcattcatgttgtaatatcatgaagtcacaaataaagctgtagcagttctg 10364
Db       1 AAAAAAAAAAANNNTTTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 60

QY      10365 tttaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 10424
Db       61 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 120

QY      10425 aaaaaaaaaaaaaaaaaa 10442

```

Mon Sep 16 10:19:47 2002

us-09-595-526b-1.rni

Page 10

Db 121 AAAAAAAAAAAAAAAAAA 138

Search completed: September 14, 2002, 07:01:42
Job time: 74760 sec

MEDLINE	20530913
PUBMED	11076861
REFERENCE	4 (sites)
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5 (bases 1 to 3065)
AUTHORS	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Balderelli,R., Bono,H., Brownstein,M., But,C., Carninci,P., Fukuda,S., Fukushima,Y., Furuno,M., Hanaoka,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hirooka,T., Horii,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koye,S., Kurihara,C., Matsuyama,T., Miyazaki,i., Nishii,K., Nomura,K., Numataki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasai,D., Schimi,L., Shibata,K., Shibata,Y., Shingagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gscc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details
FEATURES	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAAGAGACAGATTCGCAGTAAATTGAATTAATCCCCCCCCC 3']. CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAAGAGACAGATTCGCAGTAAATTGAATTAATCCCCCCCCC 3']. CDNA was cleaved with BamHI and XhoI. CDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B
FEATURES	Location/Qualifiers
source	1..3065 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="MGI:MGI:1912764" /db_xref="taxon:10090" /clone="4921353G24" /sex="male" /tissue_type="testis" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult"
gene	1..3065 /gene="Abca1"
misc_feature	1..3065 /gene="Abca1" /note="ATP-binding cassette, sub-family A (ABCI), member 1"
BASE COUNT	data source:MGI, source_key:MGI:99607, evidence:ISS 930 a 581 c 567 g 987 t
ORIGIN	
Query Match	6.8%; Score 714; DB 11; Length 3065;
Best Local Similarity	63.4%; Pred. No. 7,6e+68;
Matches 2058; Conservative	0; Mismatches 954; Indels 234; Gaps 54;
7168 ttgatgttggaagaagttaactgatactgatacattacatgcataatgcataatca 7227	

Db	2	TTTTCTGTGGAGAACAAACAACTGATATCTGTACTGACACGATTTCATTCGAAATGCCACTTCA	61
Qy	7228	atgcatagcataaacaanaattccattacaggggcagtgcccttgagcctatgctctgatalg	7287
Db	62	ATGCACAGCAAGAAACCAATATTCATTACAGGGGACGATGCGCTTGTAGCGCTTGTGCTTGAAG	121
Qy	7288	gctctccaggtgaaa--gacttgaaattagttttttacc--tataccatgctgaaactctat	7344
Db	122	GCTGCTGTGTGTAATAATGACTGTGAAGTTAGTTCATTAACCTTATACAGATGGAACCTGG	181
Qy	7345	tatgcatacccaatgcagacatagatgggtttgcgaactcaactttttttttttttgtccggt	7404
Db	182	TGTGGAACCAAGACAGACTCTGTGGTTTGA-----TTCACTCTTTTGTGTTGCTGCT	232
Qy	7405	gtattccattgggggtttgcacaataattcatcaagtaatcatgycgcagctattgat	7466
Db	233	GTATTTCTACTAGAGATWGCAACCAACACTCTATCAATTAATGATCAATGGCCACTGTATATCAAA	292
Qy	7465	caaaatcaaaaggttaatgcacatccc--tcatcaactaagccatgcacgtccgcagagagat	7522
Db	293	GTCAAAAGGCACACACATCTCTGTCCATTAAAGCCATTAAAGCATAGCTGACACCAAAACAG	352
Qy	7524	gtttcccggtgcacatccattgctgtgcgaatgsgtgcgcagatattagtgcgaagt	7583
Db	353	GTTTTCCCGGTACACATCCATTCGTGTGCAATGATGTGCAGAGTTACATGAGTCCCAAGTT	412
Qy	7584	tttccgaaagctttgcagcacacatggtgtgtgcacagtcacactttgtgcgaagcgcctgct	7643
Db	413	GCTCAGAAAGTCTGACGACTGA--GTGTGTCACAAAACATTTTGTGAAAACCGCCCTACT	471
Qy	7644	cagagctcataacaattggaatatcagttgac--agaatggtgcacagcgtggtcactacatcc	7702
Db	472	GTCGGT--TGACATCATTTAAATATCAGGTGCAAAAACGGGCCACATGTGACTTAATATCC	530
Qy	7703	tgctttgattccccctgataagcgtgtctgtgtgcagtaacatgcacaaanaatgltggt	7762
Db	531	CATTTTCTTCTCTCTTTGATGAGCTGCTTTGTGCTGCTTTGTGTAACAAA---TGtGc	586
Qy	7763	gtctctagcacagggaaactggttccatctgatalatctgctatgcttcgcagcatggt	7822
Db	587	ATCTCTTAACCCAGAGTACTGTGGTTCCTTTGTCAGAGTTGCCAATGCCCTGTATGAC	646
Qy	7823	tctaaaggtcatcccttatagagctcttaatatatc--tagatctcgtgtaagagcgaag	7881
Db	647	TTGCCATAG--CATTTTCTAGACATTTTTCAAATPACATTAGATATCCCTTAACACACAAAG	705
Qy	7882	aatcaacagccaactcgtcggcgctgaacgctctgaacgcagggacatgggattgaag	7941
Db	706	ATTAGACGCCAAACTGCTGGGGCTGCAACGGGCTCAAGTTCAAGGGGTGTGCAATGAATAT	764
Qy	7942	atgtgctgtcaaaactagggaaagcctgtgccacttgtccctgactgctcgtctaacaa--	7998
Db	765	CCAGTGCATTTTACACGT--GGCAGAGTCTGGGTGTGGTGTGCGACGTGCTCTTACACAA	823
Qy	7999	---tggtaactgatactcaaga-----tgitatctgcacaaaggtta--tattctgcgc	8050
Db	824	GATGGGTACACTACACCTTGATGATCCCTCATTTATTAACAGAAATCTGTGTTCTTCTTAC	883
Qy	8051	tttttgaatcaatcagaanaatgaaagaatgtaggtgttatctttgcacaaaatggtttgac	8110
Db	884	TGTTTGATTAATCTAGAAAATGAAGGGGGCATTTTATTTTGAACAAAATGTTTGCA--	942
Qy	8111	tttttaatgtatttgaatcttaagtctctatcagtgactcctgaactccttagaatgccc	8170
Db	943	TTGTAGTATATTATTTGAATTTTAACTTTTATTCAAATGCTTTCGGAAGCTTGTGAACCTGTAC	1002
Qy	8171	tctttgtagaacacctgtagtagagaggtatgtagccactgcgcacactattttttct	8230
Db	1003	ACGTGTATGTCACTCACATAGAGGAATGTGCCCGACTGCTTCATGCTTTATTTTCT	1062
Qy	8231	t-----atgtaaagtgtcatatcagtcagatgactgctgtagaagcaatgtagtgc	8284

Db 1063 TGGTAATTTGAGATAGATGTCTGACTAGCGAGTGACCAAGAAAACATGTGGTAGTC 1122
QY 8285 aggaatcaatgacatcatatttgatcttcacatcatattagatcatcttaactca 8344
Db 1123 AACATCTGAGGCCA-----TATTTTAAAGATCTGTAGAGCACTATTCATTTC 1170
QY 8345 ctctcaatcaaatatttttgatgtagctgtagctggaagatgtagtgaagta 8404
Db 1171 GGTTCAGATGAGATATTTTGAACATCATATATGTAAATGCTTGATTA----- 1222
QY 8405 taagatagagatcatatgaagctacacactcctcgtgcattcattcaactcag 8464
Db 1223 -----GAGATGAGGGGGAGCTAGCAGATTTCTGTGCCAT-TTATTCAGCTGATG 1272
QY 8465 gttcaaatataggttgcttggtgtaggagccactgtaaacatattgagcagcc 8524
Db 1273 ATGTACAGATGTAGGT-----TATTTTGTAAATTCACATGAAAGATATGGCCACAC 1326
QY 8525 tttttttttttttaaattgacaaatgcaaaagccaaagatataagtgatcaagt 8584
Db 1327 CTGGCTTACTTG-----ATAGCATCAATACAGAAAGCCAAAGAGACACT----- 1371
QY 8585 ttaacaatgaattcttcaacagggaaacagctagctgtaaacactgctgaatacaca 8644
Db 1372 ---AGTAAACCCCTCTTCCAGGAGAGAGCTAGTGAATCTCTCGATACAAATCG 1428
QY 8645 acttggttattg-----cattagtaacctcaaatattgcttgtagatattgg 8697
Db 1429 ATGCGCTTGACCTTGGGATCCTCACCATATGGGCAAAACATGGGCTTTGACAGATGAGA 1488
QY 8698 ataccocatataa---tctgacagctcaaatcttctccttcaactcaactgagcaaga 8754
Db 1489 GACACCCACTTAAACCTCTGAGAGATCTGAAATGTTCACTCTTCCGATTAACCAATG 1548
QY 8755 aaaaataaaaaaacaataacttccacatagagca-ttttcagagttcttcaacccag 8813
Db 1549 ATGGAACCAATCAACAACCTGCCAGCTGAAATATTTTTCACAGCTTTTCAACCCAA 1608
QY 8814 tcttattttct-----agtcagtaaacatttgtaaaaatactgcttccactaacta 8867
Db 1609 GCTTATATTTGTTTCATCTGCAAGCAACGTGAAAAAATAGTATTTTCCACAGTCTCA 1668
QY 8868 ctgttaactgcttgaagaaaaaataatagagaactattgttgggg--aaagtc 8925
Db 1669 ATGTATCGCTTTCACACAAACAAATATAGATTAAGTCTCTATTTGGCAAGTTTC 1728
QY 8926 aagtgacttcaatataacttaactctcaccatttccaaatltgaaataaac 8985
Db 1729 AAGTAGCTTTGCTATC-----CTTATTTACTTCTTCTAAATAAT----- 1770
QY 8986 gctaaagtgttaagcttcaagtttcaaatatcttctctatatttttaatttaacga 9045
Db 1771 --TGGAGAAATAGATTTTCAGATCTATTTCAAA-----TTATGTTTATATTA 1814
QY 9046 atatatataccactcctgtaaaaaaataatgattgtttagaagttlaaagcaat 9105
Db 1815 ATGTATATGTAATTCATTTGCTTGAAGGAATAATGACAAGTTT---GATACATAATGTCAC 1871
QY 9106 attgatttaataataagaatgaagacatattccaaactagtgatagatgcatc 9165
Db 1872 ATAGGTTTCTAAATGA--TAAAGAAAGTGTTTCCAGTAGTATTTGGCATACCTATTCAT 1930
QY 9166 gaaattttagatcttcaaaaaatacagaattatagaaataattctctcctcaatcaat 9225
Db 1931 TTTTAGTA-----TCAAAATATCCGAATCAAAAGAGCATGTGCTT-----TAT 1973
QY 9226 ttttcaaaatcaagttatggtttcctcatcttactaaatcgta tctcaattctcalt 9285
Db 1974 TTTTCAAAACAAACTTCGTTGGCTTCTCTAGTCACATTAACACATGACAGC----- 2027
QY 9286 atagtaaatctatgagcaactccttaactcgggttcctctgatttcaaggcatatttaa 9345
Db 2028 -----CCTTAGAAATAATCTTGTTTTAAATTACTCAGATTTTGAAGC-----CAC 2073

QY 9346 aaaaatcaaaagcactgtagacatatttgaagaaaacagacatlttaacagattgaa 9405
Db 2074 AAACACACAAAAAGTAAAGCCACCATTTTGAABAACAAATCAATTAGATGATTTAA 2133
QY 9406 aggaacctctcgaagctaaacaactcatalagttatatacttcaactcaactgta 9465
Db 2134 A-ATCTTTCTGAGCTTAAGACAAATCTGTACTAT-----ATGTACTCTTTAC 2183
QY 9466 cctttaaataagtaatttttcaatttccctgltgtaaacctaatgltgtagaaatt 9525
Db 2184 ACTATCTGAAGAGCAATCTTCAAC--TTTCTGTTTAAAGTAATTTATTTAAGAAAGTTA 2241
QY 9526 taccactataactcaataagcaaatcttgatatactccctggtgaatgtaactag 9585
Db 2242 AAATCAATCTATCT--TCAAAATGAATTTCTTACATTTCCCTATGAGATGTGCAATG 2299
QY 9586 tgaatcagaatctcacaataacgltgtaaaaattctgclltgcaacttggagc 9645
Db 2300 TGAG-TTGAGAAATTTCCAA-----GTGCAAAACACTTCTGTTT---ACTTAAATA 2347
QY 9646 acctcaaaaactataaacaactgtaataatgagaataacagaagaaataaagccc 9705
Db 2348 AAATAGTGAAGAACTTACTAAGTGAATATGAGAAAGCAAAAGAA--AGTGAAGTCC 2404
QY 9706 tctatcataatgcccagacaattcattgtttaaaaaaacaacaacccacactagc 9765
Db 2405 TCTCGTAGATATACATGATATATTTCA---TTATGAACAAACAAACCTCAAACTACTG 2461
QY 9766 tattcatalactgtaactgaagaatgctltgtagacttaa-altgtagacatcat 9824
Db 2462 TATTTGGTGTGTACCGGAGAGCATATGGCTCATGATTAATATGTATCATATCATAT 2521
QY 9825 catcactgtagtaactgaactgtaaacatgagccattgctggttcttctctgtagtgn 9884
Db 2522 TGCTCTCTGTATAGTACGATTTGACTTAAAGGATTT--TTTGTTGCTTCTCATGTTGT 2580
QY 9885 atatacaggttaaaaatlttccaaagacatgctgtaactgaactgaactga--ccttga 9943
Db 2581 ATATATCAGGTAAAT--TGTTCCAAAGACCATGTGTATATGATGAGGACCACTTTGA 2639
QY 9944 tatgaacactaaatttgaaccccttggtlatatctactag-aataatgtaataactgnaga 10002
Db 2640 TATGAAATTAATTTGTAATTTGATTTACTTACTATTTGCTGTAATATAGTAACGCCACAGT 2699
QY 10003 aatatgcttaattcttcaaaaatggtgcatccccccttaaanagtctatccataag 10062
Db 2700 AATACGTGTTGATTCAAAACGTGTCATCCCTTTTGTAGAACATTTATATTTCCATTA 2759
QY 10063 gattagcttgctatcccttcttaacccttaagatgaagcgttlttgctccttgg 10122
Db 2760 GGATTCGGTATGTTCTTTTCCCTCTGCTCCTAGATGAACCTGGTTTGGCTTTTCT 2819
QY 10123 calcatggccctcattcccaagcatttaacgtgctgtaagggatcatatttgcaat 10182
Db 2820 TATCATGGCCCTCATTCACAGCACTTATGCTGTCTGTAT--GGAATTTTGTGCACT 2878
QY 10183 ggaatattcgtgaattgcaaaactagaacaaagtlttaacaacagatttcaagttaatc 10242
Db 2879 GGAATATCTGAGTTTCCAAACCTAGACAAAGTTTGAAGAGCATTTGAAGTTAAATC 2938
QY 10243 atttcaataaagaaagaaaga--aaaaaatctgtatgcaataacttatalgaag 10300
Db 2939 GTTTTCATTAACAAAAAATAAACTGAAAAAATTTGATGTGAATATCTTATATGACG 2998
QY 10301 tattaagaatcatattctatgltgtaataatagtgatcaaaaataaagcgtgtagc 10360
Db 2999 TGT-----TTTAAAGCTTGTATGTATGATGATCAAAATTAACGTGACAGT 3054
QY 10361 tctggt 10366
Db 3055 CCTGCT 3060

```

RESULT 2
B1754756 809 bp mRNA linear EST 25-SEP-2001
LOCUS 603025477F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5195995 5',
DEFINITION mRNA sequence.
ACCESSION B1754756
VERSION B1754756.1 GI:15746334
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 809)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11490 row: 1 column: 20
High quality sequence stop: 768.
Location/Qualifiers
1..809
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5195995"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library site is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH-MGC Library."
BASE COUNT 151 a 199 c 220 g 239 t
ORIGIN
Query Match 6.6%; Score 692.4; DB 10; Length 809;
Best Local Similarity 99.6%; Pred. No. 2.8e-65;
Matches 715; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY 2118 ggaacgagaaagaactgctctatgacagagatgcctatccctgttagcttga 2177
Db 1 GGCACCGAAGAAACTGCTGCTATATGCAACAGATCCCTATCCCTGTTACGTGAT 60
QY 2178 gacatctctcggggtgtagccggtcaatgagccctcttaagcgtggcctgatt 2237
Db 61 GACATCTTCTGGCGGTGATGAGCCGGTCAATGCCCTCTTCATGACGCTGGAGATT 120
QY 2238 tactcagtgctgtagtcaatcaggatcgatgtagaagagacgctgaaagag 2297
Db 121 TACTCAGTGGCTGATCATCAAGGCGCATCGTATGAGCAAGAGCAGCGCTGAAAGAG 180
QY 2298 accatcgatcatgagcctgagcaacacatcctctgtttagcgtgattagtagc 2357
Db 181 ACCATCGGATCATGGCGCTGAGCAACAGCATACCTGTTAGCTGGTTCTTTAGTAGC 240
QY 2358 ctcaatctctctctgtgtagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 2417
Db 241 CTCATTCCTCTCTCTGAGCGCGCTGCGCTGAGTGCATCCTGGAAGTAGAAGAACTCG 300
QY 2418 ctgacctagagtagatcccaagcgtgtgtgtgtctctccgtctcgtgtgtgtgaca 2477

```

```

Db 301 CTGCGCTACAGTGAATCCAGCGGTGTTGTTCTCTCCCTGTCGTTGCTGTGTACCA 360
QY 2478 atccctgagctcttcctattagcaacctctcccaagagcaaccctggagcagctgt 2537
Db 361 ATCCGTGAGTGTCTTCTGATATGACACTCTTCTCCAGAGCAACCTGGACAGCCTGT 420
QY 2538 ggggagcatcattacttaacagcgtgtacccctcagctcgtgtgtgtgtgtgtgtgtgt 2597
Db 421 GGGGCGCATCATCTACTTACCGCTACCTGACCGCTACCGCTGCTGTGTGTGTGTGTGTGT 480
QY 2598 taagtgagcttcaactcaatcaatcttgcctgtagcctgtgtgtgtgtgtgtgtgtgt 2657
Db 481 TACGTGGCTTACACTCAAGATCTTGCCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 540
QY 2658 ggcctgtagtacttgcctctttttagagagagagcatttggagtgagtgagagacatg 2717
Db 541 GCGTGTGATGACTTGTGCTCTTTTGGAGAGCAGGCGCATTTGGAGTGCAGTGGACACCTG 600
QY 2718 ttgagagctcctgtgtg-aggaagatggtcattcaatcaccactgtatctccatgact 2776
Db 601 TTGAGAGTCTCTGTGGAAGAGATGGCTTCAATCAGCACTTGGCTCTCCATGATGCT 660
QY 2777 gttgagaccttctcctat-agggtgtagactgtgtagcattgagcgtgtcttccagg 2833
Db 661 GTTGACACCTTCTCTATGAGGGGTGATGACCTGTGATTTGAGGCTGTCTTTCCAGG 718

RESULT 3
BG482804 705 bp mRNA linear EST 21-MAR-2001
LOCUS 602502594F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4616207 5',
DEFINITION mRNA sequence.
ACCESSION BG482804
VERSION BG482804.1 GI:13415083
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 705)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1370 row: k column: 24
High quality sequence stop: 688.
Location/Qualifiers
1..705
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4616207"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1:
SfiI (ggcgctggcg); Site:2: SfiI (ggcattatggcg); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTTAGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGCCGACATG-dr(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
Ca). Note: this is a NIH-MGC Library."
BASE COUNT 255 a 109 c 86 g 255 t

```


ORIGIN

Query Match 6.3%; Score 656.8; DB 10; Length 705;
Best Local Similarity 98.6%; Pred. No. 1.9e-61;
Matches 694; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

QY 8753 gaaaataataaacaacaataactcacaatgagagcattttcagagtttctaccaca 8812
DB 1 GAAAAATATATAAACAACAAATACCTTCATATGAGAGCATTTTTCAGAGTTTCTTAACCA 60
QY 8813 gcttaattttctagtcagtaacatttgtaaaataactggttcacttaacttcgtt 8872
DB 61 GCTTATTTTCTAGTACAGTAAACATTTTATAAAATFACTGTTTCACTAATTAATCTGTT 120
QY 8873 aactgcttgagagaaaaaataatagagagactatgtttggggaagtcaagtat 8932
DB 121 AACTGCTTGAGAGAAAAAATAATATGAGAGCATTTGTTGGGAAGTTCAAGTGAT 180
QY 8933 ctttaataatcttaactcttcacacttttccaataattgataatactaaag 8992
DB 181 CTTTCAATATCAATCTAATCTTCCACTTTTCCAGATTTGAAATTAACGCTAAG 240
QY 8993 ggttaagactcagattcaaatatcttcataatttttaattacaagaatattat 9052
DB 241 GGTAAAGACTTCAGATTCAATTAATCTTCTATATTTTAAATTTACAGAAATATAT 300
QY 9053 ataaccactgctgaaaaaagaaa-aaatgattgttttagaagttaaagtaattgat 9111
DB 301 ATAAACCCTGCTGAAAAAAGAAACAAATGATGTTTGAAGTTAAAGTCAATATTCAT 360
QY 9112 tttaataataagtaagagcatalttccaataactagtagtagagagcttgcaatt 9171
DB 361 TTTAAATATTAAGTAAGAAAGCAATTTTCCAAATACATGATGATGAGCACTTGCAATT 420
QY 9172 taacagatctcaaaaatacagaattatagataaattcttcacttaataatttca 9231
DB 421 TACAGATCTTCAAAAATACAGATTTATAGAAATATTTCTCCTCATTAATATTTTCA 480
QY 9232 aaatcaaatlatgttctcccaatttactaaatcgtatcttaacttctcaattataga 9291
DB 481 AAATCAAAATTAATGTTTCTCTCATTTTACTTAAATGATTTCTTCAATTTATAGTA 540
QY 9292 aatctatgagcaactcttactctcgttctcgtatgattca-aggccatatttaaaat 9350
DB 541 AATCTATGAGCACTCTTACTTCTGTTCTCTGATTTTAAAGGCCATATTTTACAAAT 600
QY 9351 caaaagcactgtgaactatttgaaagaaaacagacatttataacagattgaaagac 9410
DB 601 CACAAGGCACTGTGAACATTTTGAAGAAACACACATTTTAAATACAGATTGACAGGAC 660
QY 9411 cctctctgaagctagaacaacatcatagttatacatctcattca 9454
DB 661 CTCTCTGGAAGCTAG-ACCAATCTATAGTTTACTTCTTCATTA 703

RESULT 4
BI854140 854 bp mRNA linear EST 10-OCT-2001
LOCUS 603381449F1 NIH_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5388972 5',
DEFINITION mRNA sequence.
ACCESSION BI854140
VERSION BI854140.1 GI:15994887
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 854)
AUTHORS NIH-MGC http://mgi.mgi.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: CGAPs-Remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1991 row: b column: 13
High quality sequence stop: 801.
Location/Qualifiers
1..854
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5388972"
/clone_lib="NIH_CGAP_Mam4"
/issue_type="tumor, gross tissue"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Note: Site 2: SalI. Cloned unidirectionally. Primer: oligo dT. Average insert 2.5 kb. Library constructed by Life Technologies, catalog # 12018-016. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996). Note: this is a NCI_CGAP Library."

BASE COUNT 238 a 198 c 227 g 191 t
ORIGIN
Query Match 6.1%; Score 639.8; DB 10; Length 854;
Best Local Similarity 88.1%; Pred. No. 1.1e-59;
Matches 753; Conservative 0; Mismatches 97; Indels 5; Gaps 5;
QY 6040 tgaagaagatalatagaagaagcgaagcctgctgttgacaagattgctgagca-tt 6098
DB 4 TGACCAAGATCATATAGAGAGAGAGGAGAGGAGCCTGCAGTCAGACAGATGTCATCGGAGTC 63
QY 6099 cctctgtgagtgcttgggctcctgggagttatagggcttgaaatacataacttc 6158
DB 64 CTTCCCGAGAGAGGTTTGGACTCCTGGAGTTTAAAGGAGTGGAAAGTCAACACTTTTC 123
QY 6159 aagatgttaagaagagataacacactgttccagagaagatgcttccttaacaaaatagt 6218
DB 124 AAGATCTGACTGGAGACACCCCTGTGACAGAGGAGTGGCTTCTTAACAAAACAGC 183
QY 6219 atcttataaacaatcatalgaatatacagaacalgggctactgacctcaattgattgac 6278
DB 184 ATCTATCAAAATATATCATGAAGTACACCAAGAAATGGGCTACTGCTCATGTTGAGGCC 243
QY 6279 atcaagaagcgttgacatggagagaagacagtggaattcttgcctttgaagaagatc 6338
DB 244 ATCAAGAGCTGCTGACGGAAGAGAGCATGTGGAGTTCTTGCCCTCTAGGGAGATC 303
QY 6339 ccagagaagaagttgcaagattgltgagtgaggcgaactggagcctgltgaag 6398
DB 304 CCAGAAAAGGAAGTTGGCAAGTTGTGATGGCAATTTGCCAAACTGGGCTGTGAAG 363
QY 6399 tatgagaanaatalgctgtaactatagtgagagcaacaagcgaagcttctacagcc 6458
DB 364 TATGAGAGAAAATATGCAAGTAACTACAGTGGCGCAACAAACGACTCTCCACAGCC 423
QY 6459 atgagcttgatcggcgccctcctgtgtgttcttgatgagtaaccaacagagcatgat 6518
DB 424 ATGGCTTTGATTGGGGGACCTCTGTGTGTGTTCTGATGAACCAACACAGGATGGAC 483
QY 6519 ccgaagcccgagcttcttgatgagattgcccataatgltgcaagaagagagatca 6578
DB 484 CCTAAAGCCCGAGATTTTGTGGAAATGTGCCCCCAACATTTGCAAGAGGAGGAGATCT 543
QY 6579 gtatgcttatactcatagtagtagaagaatggaagcttgcactagaatgcaatc 6638
||||| ||||||| ||||||| ||||||| ||||||| ||

Db 544 GTAGTCCATACATCTATAGTATGGAAGAAATGGAAGCTCTTTGTACAAAGATGGCCATA 603
 QY 6639 atgagcaatgaaggttcaagtgcttgcagtgctcagcagctcaataaataagtttga 6698
 Db 604 ATGTGCAATGGAAGGTTGACAGTGCCTTGGCAGTGTCCACATCTGAAAAACAGGTTCCGA 663
 QY 6699 gatgttatacaatagttgtaagataagcaggtccacccgagcctgaagcctgcag 6758
 Db 664 GATGCTATACAAATAGTTGTACGAATAGCAGGCTCCACCTGACCTGGAAGCCTGTCCAG 723
 QY 6759 gattcttgacttgacttcctcctgaagtgctcctaagaagaacacccggaacatgcta 6818
 Db 724 GA-GTCTTGGACTTGCTTACCGGAGAGTGTCTTAAAGAGAA-ATGACACATGCTT 781
 QY 6819 caatacagcttcacatctcattatctctcgtccagagatcagcaatcctcctccag 6878
 Db 782 CAGNACCAAGCTCCATC-TCCTTGTATCTCTAGCCAGATA-TCAGCATCTCTCCACA 839
 QY 6879 agcaaaagagactc 6893
 Db 840 AGCAACAGCGGACTC 854

RESULT 5
 LOCUS BG436050 640 bp mRNA linear EST 14-MAR-2001
 DEFINITION 602508836F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4619552 5',
 mRNA sequence.
 ACCESSION BG436050
 VERSION BG436050.1 GI:13342556
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: CLOMTECH Laboratories, Inc.
 CDNA Library Preparation: CLOMTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM1379 row: g column: 09
 High quality sequence stop: 635.

FEATURES
 source Location/Qualifiers

1..640
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4619552"
 /clone_1ib="NIH_MGC_79"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: placenta; Vector: pDNR-LIB (Clontech);
 Site.1: SfiI (ggccgctcgcc); Site.2: SfiI (ggccattatggc
) 5' and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-ATCTAGAGCGGCGGCGGCGCATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
 library."

BASE COUNT
 ORIGIN

233 a 97 c 74 g 236 t
 Query Match 6.1%; Score 633.2; DB 10; Length 640;

Best local similarity 99.5%; Pred. No. 6.6e-59;
 Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8718 gtctcaaatcttctacatcctcaactagcagaagaaaaataaaaaaacaaatct 8777
 Db 1 GTCTCAAAATTTTCTATCTTCAATCACTAGTCAAGAAAAATATAAACACAAATACT 60
 QY 8778 tccatattgagcaatcttccagattctcaccagctctatcttctcagcaglaaca 8837
 Db 61 TCCATATGAGAGATTTTACAGGTTTCTTAACCCAGCTTATTTTCTAGCATTAACA 120
 QY 8838 ttgtcaaaaaaacggttccactactactgttactgtctctgagagaaaaaat 8887
 Db 121 TTTGTAAAAAATACGTCTTCACTAATACTACTGTAACTGTCTTGAAGAAAAAAT 180
 QY 8898 atgaagaacactgtcttgagggaagttcaagtgatctcttcaatactactactct 8957
 Db 181 ATGAGAGAACTATTTGTTGGGGAAGTTCAAGTCACTTTCAATTCATTAATCTTCT 240
 QY 8958 ccaactttccaaaaattgcaatataacgctaagtgtaagactcagattccaatta 9017
 Db 241 CCACATTTTCCAAAATTTGAATATTAAAGCTAAAGGTAAAGTCACTTCAATTA 300
 QY 9018 atcttctatatcttcttaattcagaatatataaccactgctgaaaaaaga 9077
 Db 301 ATCTTTCTATATTTTAAATTTACAGAAATATTAATTAATTAATTAATTAATTAAT 360
 QY 9078 aatgattctttagaagttgaagcaatattgatttcaatataagtaagagacat 9137
 Db 361 AATGATGTTTTTAAAGTTAAAGTCAATATGATTTTAAATTAATTAATTAATTAAT 420
 QY 9138 ttccaataactagtgatagtgatcggttgcgaattcaagtaacttccaaaaatacagaatt 9197
 Db 421 TTCCAAATACAGTATGATATGCGATCGTTGCAATTTTAAAGTATCTTCAAAAATACAGATT 480
 QY 9198 tatagaataatttcccccattatatttccaaatcaagtgatggttccattt 9257
 Db 481 TATGAAATATTTTCCCATTTATATTTTTCAAAATCAAAAGTTATGTTTCTCATTT 540
 QY 9258 lactaaatcgtatcttaattctcattatagtaaatctatgagcaactcctactcgg 9317
 Db 541 TACTAAATTCGTATTTCTATTTCTCATTTATAGTAAATCTATGAGCAACTCTTACTCGG 600
 QY 9318 ttccctgattcaagccatattttaaaaaataaaaa 9355
 Db 601 TTCCTGATTTCAAGGCGCATTTTAAATAATCAAAA 638

RESULT 6
 LOCUS B1182779/c 878 bp mRNA linear EST 10-JUL-2001
 DEFINITION UNL-P-FN-bp-c-01-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
 UNL-P-FN-bp-c-01-0-UNL 3', mRNA sequence.
 ACCESSION B1182779
 VERSION B1182779.1 GI:14657188
 KEYWORDS EST.
 SOURCE pig.
 ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 AUTHORS Caetano,A.R., Johnson,R.K. and Pomp,D.
 TITLE Generation and sequence characterization of a normalized cDNA
 library from swine ovarian follicles
 JOURNAL Unpublished (2001)
 COMMENT Contact: Pomp, D
 Department of Animal Science
 University of Nebraska, Lincoln
 Lincoln, NE 68583-0908, USA
 Tel: 402 472 6416
 Fax: 402 472 6362
 Email: dpomp@unl.edu

The sequence contained an oligo-dT track that was present in the

OY	8705	attaatctgcagcgtctaatttcaacttccttcacacacgacgaagaataataaa	8764
OY	8705	atttaattgcagcgtctaatttcaacttccttcacacacgacgaagaataataaa	8764
Db	194	ATTAAATCTGCAGCCTCAAAATTTTTCATCTCTTCAATCATTACGACAAGAAAAATATAA	253
OY	8765	aacaacaatactccatatatgatgagcattlltcaagagttlctcaaccagcttatlctc	8824
Db	254	AACAACAATACTCTCCATATGTGAGCATTTTTCAGAGTTTCTTAACCAGTCTTATTTTTTC	313
OY	8825	tagtcatgaagaacatttgttaaaaactcgttlccaactactactcgtttaactcgcttag	8884
Db	314	TAGTCAGTAAACATTGTGTAANAATTCGTCTTTCACATTAATCTTACTGTTACTGTTGGN	373
OY	8885	agaaaaagaaaaaatatgatgagaactatlglttgagggaagltc-aagtaccltccaatlc	8943
Db	374	AGAAAAGAAAAATATGACAGAACCTATGTTGGGAGATTCAAATGATCTTTCAAATATC	433
OY	8944	attactaacctcttcaccttlltcccanaatttgaatataaagcgtcaaaagggtaagact	9003
Db	434	ATTCTACTCTCTTCCACTTTTTCACAAATTTGAATATTAAGCGTAAAGGISTTAAGAC-T	492
OY	9004	cagattccaatatcattccttcataatttttcaaatltaacagaatalatataccccactg	9063
Db	493	CAGATTCCAATTAATCTTTCTATATTTTTTAAATTTACAGAATATATATATATATCCACG	552
OY	9064	ctgaaaagaagaaaaaatgatgltttagaagcttaaagctcaaatatgatgtttaaataatag	9123
Db	553	CTGAAAAGAAAAAATGATGTTTTCAGAGTTAAAGCTTAAGCATATTTGATTTTAAATATAG	612
OY	9124	taattgaagcatalatttccaatactagt-gatatagcactcgttgcaatt 9172	
Db	613	TAAATGAAGCATATTTCCAAATCACTAGTGATGATGATGCCATCCGTGCATTT 662	
RESULT	8		
AUI35588			
LOCUS	AUI35588	736 bp	mRNA linear EST 24-OCT-2000
DEFINITION	AUI35588 PLACE1 Homo sapiens CDNA clone PLACE1002437 5', mRNA sequence.		
ACCESSION	AUI35588		
VERSION	AUI35588.1 GI:10996127		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 736)		
AUTHORS	Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,T., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.		
TITLE	HRI human cDNA project		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3951 Fax: 81-438-52-3952 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute. Location/Qualifiers 1..736 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="PLAXION002437" /clone_lib="PLACE1" /tissue_type="placenta" /note="Vector:pMT18SFL3"		
FEATURES			
SOURCE			
BASE COUNT	163 a 199 c 199 g 170 t		5 others
ORIGIN			

Query Match	5.7%	Score 596.2	DB 9	Length 736
Best Local Similarity	96.9%	Pred. 5.5e-55		
Matches 629	Conservative	0	Mismatches 18	Indels 2
				Gaps 2
QY 1	gqccggagaccgcaagagccgagaccctctctccgggctcggcagagggcagggcgg	60		
Db 25	ggccgggagaccgcaagaccgagaccctctctccgggctcggcagagggcagggcgg	84		
QY 61	ggaactccggcaccacaagagcggtcttaaggcggttgccctgtgttttccccg	120		
Db 85	ggagctccggcaccacaagagcggtcttaaggcggttgccctgtgttttccccg	144		
QY 121	gtctgttttctccctctccggcagagctgttcaaggggtaggagaaagagacgcaaac	180		
Db 145	gttctgttttctccctctccggcagagctgttcaaggggtaggagaaagagacgcaaac	204		
QY 181	acaaaagtggaaaacaaagttaataagcagcagcagggcgctccctgtgtgagctctggcgc	240		
Db 205	acaaaagtggaaaacaaagttaataagcagcagcagggcgctccctgtgtgagctctggcgc	263		
QY 241	tgccctccagggctcccccagccacacgcctgggcgtgtcgtctgtagggagacatggtcgt	300		
Db 264	tgccctccagggctcccccagccacacgcctgggcgtgtcgtctgtagggagacatggtcgt	323		
QY 301	ggcctcaagctgtaggtgtgctgtgtggaagaaacctcacttcaagaagaacaaatgtc	360		
Db 324	ggcccccacactgaggtgtgtgtgtggaagaaacctcacttcaagaagaacaaatgtc	383		
QY 361	agctgttaactggaaggtgctctggcctcattatctcctgatacctgtatcgtctgcgc	420		
Db 384	agctgttactggaaggtgctctggcctcattatctcctgatacctgtatcgtctgtgcgc	443		
QY 421	tgagctacccaccctatgaaacaacatgaaatgcatttccaaataaagcgcactgtc	480		
Db 444	tgagctacccaccctatgaaacaacatgaaatgcatttccaaataaagcgcactgtc	503		
QY 481	caggaacaccttccttggttgaagggtatctatctgaatgcaaacaccccgcttccgt	540		
Db 504	caggaacaccttccttggttgaagggtatctatctgaatgcaaacaccccgcttccgt	563		
QY 541	accgcacccctggggagagctcccgaggttgtgttggaaacttlaacaacatcattg-tgct	599		
Db 564	accgcacccctggggagagctcccgaggttgtgttggaaacttlaacaacatcattg-tgct	623		
QY 600	cgccgtgttctcaagatgctcgagagctcttattatacagccagaagaaca 648			
Db 624	cgccgtgttctcaagatgctcgagagctcttattatacagccagaagaaca 672			
RESULT 9				
BP216316		783 bp	mRNA	linear
LOCUS				
DEFINITION	60189834.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102714 5',			
ACCESSION	BP216316			
VERSION	BP216316.1			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Enkalyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 783)			
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgaabs-remail.nih.gov			
	Tissue Procurement: ATCC			
	CDNA Library Preparation: CLONTECH Laboratories, Inc.			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
	DNA Sequencing by: Incyte Genomics, Inc.			

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1CM976 row: h column: 11
 High quality sequence stop: 593.

FEATURES

source
 1. 783
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4102714"
 /clone_lib="NIH_MGC_57"
 /tissue_type="g11oblastoma"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgccctcgcc); Site_2: SfiI (ggccattagcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT 261 a 126 c 120 g 276 t
 ORIGIN

Query Match 5.5%; Score 576; DB 10; Length 783;
 Best Local Similarity 95.7%; Pred. No. 7.7e-53;
 Matches 624; Conservative 0; Mismatches 25; Indels 3; Gaps 3;

QY 9121 aagtaatgaagcattcccaataactagatagcattggaattacagatc 9180
 Db 1 AAGTAATGAAGCATTTTCCATTAATCTAGATAGCATGTTGCATTTTACAGTATC 60
 QY 9181 ttcaaaatacagaattatagaataattctccattatatttcaaaatcaag 9240
 Db 61 TTCAAAATACAGAAATTTATAGATATTTCTCCATTTATATTTTCAAAATCAAG 120
 QY 9241 ttatggttccatcttacttaataatcgatcttaatttccattatagtaaatcatala 9300
 Db 121 TTATGTTTCCATCTTACTTAATAATCGATTTCTATTTCTCATTAATATATGATGA 180
 QY 9301 gcaactccctacttggttcctcctgatttcaaggccattttaaaatcaaaagcac 9360
 Db 181 GCAACTCCCTACTTGGTTCCTCTGATTTCAAGGCCATTTTAAATAAAGGCGAC 240
 QY 9361 tctgaactatttgaagaacacagacatttaatacagattgaaggccctctcga 9420
 Db 241 TGTGAACCTATTTTGAAGAAACAGACATTTTATACATTTGAAGACCTTCTGTA 300
 QY 9421 gctagaacacatctatgattatatacttcaataactgctgttaccctttaaatagta 9480
 Db 301 GCTAGAACAATCTATATGATATCATCTTCAATTAATCTGTGTTACCTTTTAAATAGTA 360
 QY 9481 atttttcaatttctgctgttaactaattggtgaagaatttttaccactctatct 9540
 Db 361 ATTTTTCATTTTCTGTAACCTAATTTGTGTAAGAAATTTTACCA-TCATATCT 419
 QY 9541 caataagaacaaattcttatatccctgtgaagtacacatctggaattcagaatt 9600
 Db 420 CAATCAAGCAAAATTTCTATATTTCCCTGTGGAATGTACCTATGTGAATTTCAAGAAAT 479
 QY 9601 ctcaaaatcgtgttcaaaaatttctgtcttgcactt-tgggaacacctcagaacatt 9659
 Db 480 CTCAAATACGTCTCAAAATTTTGTGTTGGCATCTTGCGGACACCTCAGAAATTT 539
 QY 9660 attaaacactgtgaataatgagaatcagaag-aaataataagccctctatacataaat 9718
 Db 540 ATTTAACAATGTGAATATGAGAAATTCAGAAAGAAATAATTAAGCCCTCTTATTAATTAAT 599
 QY 9719 gcccaagaacattcgtttaaaaaaaccaacactcacactactgtattt 9770

Db 600 GCCAGCACATTCATCTGTGAAAAAACAACACTCACATTAATGTTCAATT 651

RESULT 10
 BC400012 919 bp mRNA linear EST 12-MAR-2001
 LOCUS 602442068F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4557761 5',
 DEFINITION mRNA sequence.
 ACCESSION BC400012 GI:13293460
 VERSION BC400012.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE 1 (bases 1 to 919)
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1CM1262 row: h column: 18
 High quality sequence stop: 614.

FEATURES

source
 1. 919
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4557761"
 /clone_lib="NIH_MGC_75"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgccctcgcc); Site_2: SfiI (ggccattagcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

BASE COUNT 300 a 181 c 144 g 294 t
 ORIGIN

Query Match 5.5%; Score 574.2; DB 10; Length 919;
 Best Local Similarity 93.9%; Pred. No. 1.1e-52;
 Matches 651; Conservative 0; Mismatches 32; Indels 10; Gaps 5;

QY 9374 gaagaacacagacattttaaagaattgaaggacctcttgaagctagaacaatc 9433
 Db 1 GAAGAAACACACATTTTAAATACAGATTTGAAGACCTCTTGAAGCTAGAAACAATC 60
 QY 9434 tataattatatacttcaataactggtgtactctttaaataatgatttttactt 9493
 Db 61 TATATTTATACATCTTCAATTAATCTGTGTACTTTTAAATATGTAATTTTACATTT 120
 QY 9494 tcttgttaaacctaatgtgtgtagaaattttaaacaactatatactcaalcaagcaaaa 9553
 Db 121 TCCGTGTAAACCTAATTTGTGTAAGAAATTTTTCACCACTCTATATACATCAAGCAAAA 180
 QY 9554 ttctgttatatccctgtggaagtactatgtagtgttgaagaattctcaataatgctg 9613
 Db 181 TTTCTGTATATTTCCCTGTGGAATGTACTATGATGAGTTTCAGAAATTTCTCAAAATACGTG 240
 QY 9614 ttcaaaatttctgcttttgatcttgggacacctcagaacatttaacaactgtga 9673

Db	241	TTCAAAAAATTCCTGCTTTTGGCATCTTTGGGACACCTCAGAAAACTATTATTAACACGTGA	300
OY	9674	atatagaagaatacagaagaanaataataagccctctatacataaataatgcccagcacaaattca	9733
Db	301	AAATAGAGAAATACAGACAGAAATAATATAAGCCCTCTATACATATAATGCCACGACAATTCA	360
OY	9734	ttgttaaaaaaacaacaacccctcacactactgtatttattctatctgtactgtaagaacaat	9793
Db	361	TTGTTAAAAAACAACCAACCTCCACACACTACGTATTTCATTCTGTCGATCGTAACCAAAAT	420
OY	9794	gcttctgactacttaaatctgtgcacatcatcattccactgtaagtagtaatacatctgactaa	9853
Db	421	GC-TTGTGACTATTAAAGTTGCAACATCATTTATTTCACCTGTAAGTAACTATTGACTTAA	479
OY	9854	gccatttg-cctgtgtttctctctctgtgntgnatata-tcaggttaaaatattttccaag	9911
Db	480	GCCATTGTGCTGTGTTTCTTCTGTGGTGTATATATTACAGTAAATAATTTCACAAG	539
OY	9912	agccatctgtctaatctaactgaacccttgatalttgagaacaattaattggaacctgg-	9970
Db	540	AGCCATGTGTCATGTAAATCACTGAACACATTTGATTTGAGACATTAATTGTACCCCTGGT	599
OY	9971	tattatctactagaataatgtata-----ctgnagaacaattgtcctcaattcttcaa	10024
Db	600	TATTATCTACTAGATGTAATGTAAATGTAAATACTGTACGAGAACATATGGTCTATATCTTTTCA	659
OY	10025	aatgtgtcatccccccttaanaangtctctatcc	10057
Db	660	AAATTGTCGCTCCCTTTTAGAATGTTCTATTTCC	692

RESULT	11
LOCUS	AL048638
DEFINITION	AL048638 631 bp mRNA linear EST 29-FEB-2000
ACCESSION	DK22P564A1364_r1_564 (synonymy: hdbir2) Homo sapiens cDNA clone DK22P564A1364, mRNA sequence.
VERSION	AL048638
KEYWORDS	AL048638.3 GI:5927971
SOURCE	EST. human.
ORGANISM	Homo sapiens <i>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo;</i>
REFERENCE	1 (bases 1 to 631)
AUTHORS	Duesterhoft,A., Labber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE	EST (Duesterhoeft, et al.) Unpublished (1999) On Apr 30, 1999 this sequence version replaced gi:586636.
JOURNAL	
COMMENT	

FEATURES
SOURCE
 1..631

```

/cclone_lib="564 (synonym: hfbt2)"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="xl-zhblue"
/notes="Vector: pAMP1. Site1: NotI. Site2: SalI"
BASE COUNT      229 a      93 c      86 g      220 t      3 others

```

ORIGIN

Query Match	5.4%	Score 567.8;	DB 9;	Length 631;
Best Local Similarity	99.0%;	Pred. No. 6.4e-52;		
Matches 591;	Conservative 0;	Mismatches 4;	Indels 2;	Gaps 2;

OY	8525	tttttttttttttttaattgcaacaatgcaaaagccaaagaatgaaggttcaag	8584
DB	28	TTTTTTTTTTTTTTTAATTGGCAAAATGCCAAAGCCAAAGATATAGGCTCACAGT	87
OY	8585	ttaacaatgaattcttcacagggaaaaacagctagctgtgaaaactctgtaaaaaaca	8644
DB	88	CTAAACAAATGAATCTTCTACAGGAAAAACACCTAGCTTGAATCTGCTGAAAAACACA	147
OY	8645	acttggtttatgacatttagtaccttaaaatattgctctgcagatatgtatacccc	8704
DB	148	ACTTGTTGTTTAGGCAATTAGTACCTTCGAAATTAATTTGGCTTGGCAATATGGAAATACCC	207
OY	8705	attaatcgcagacgtcctaattttctatctcttcataactcagtcagaagaatataa	8764
DB	208	ATTAATCTGCACAGCTCTCAATTTTTCATCTTTAAATCATTAGTCAGAAATAATATA	267
OY	8765	aacacaataactccatatgagcagcatittcagaatttctaacocagctctatttc	8824
DB	268	AACACAATATCTTCATATGAGCATTTTTCAGAGTTTTCACGCCAGCTTATTTTTC	327
OY	8825	tagtcaagtaacaattctgtaaaaaatacctgtttcactaatactactggttaactgtcttgag	8884
DB	328	TAGTAGTAATAACTTTGTAATAATCTGTTTCACATAACTTACCTGTTAACTGCTTGAG	387
OY	8885	agaaaagaaaataatgagagaaactatgttttgaggaaagtcaagacattcaataca	8944
DB	388	AGAAAAGAAAAATATGAGAGAACTATTGTTTGGAAGTTCAAGTGATCTTCAATATCA	447
OY	8945	ttactaactctctccacttttccaaaatltgaatattlaacgtlaaaggtgaagacttc	9004
DB	448	TTACTAAGCTCTCTCCACTTTTCCAAAATTGAATATATAAGCTAAGGTGAAGAC-TC	506
OY	9005	agattccaataatccttctctatatlttttlaaattacagaatataataaaccacgtgc	9064
DB	507	AGATTCCAATTAATAC-TCCTATTATTTTAAATTACAGAAATATATATAACCAACACGTC	565
OY	9065	tgaaaaagaaaaatgattgttttgaagaagttaagtcgaatcttgatttlaaata	9121
DB	566	TGAAAAGAAAAATGATGTTTAGAAGTTAAAGTCATATTTGATTAATATA 622	

RESULT	12
BEB79545	
LOCUS	784 bp mRNA linear EST-20-OCT--2000
DEFINITION	G01491738B1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893912 5' , mRNA sequence.
ACCESSION	BEB79545
VERSION	BEB79545
KEYWORDS	BEB79545.1 GI:10328425
SOURCE	EST..
ORGANISM	human.. Homo sapiens

REFERENCE	1 (bases 1 to 784)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: DCTD/DPF/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: L1AM9682 row: 1 column: 09
High quality sequence stop: 573.

FEATURES

source

Location/Qualifiers
1..784
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3893912"
/clone_lib="NHG MGC 69"
/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."

BASE COUNT 223 a 164 c 145 g 252 t
ORIGIN

Query Match 5.4%; Score 562.8; DB 10; Length 784;
Best Local Similarity 90.0%; Pred. No. 2e-51;
Matches 648; Conservative 0; Mismatches 67; Indels 5; Gaps 4;

```

OY 8179 gaacctgtgtatagagagatagccactgcccactatttatttctatgtaag 8238
    |||
Db 1 GAACCTGTGTATAGAGAGATAGCCACCTGCTATTTTATTTATGTATAG 60
OY 8239 ttgcatatcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 8298
    |||
Db 61 TTTGCATATCATCATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
OY 8299 ttaatttgaatttcttcaagatcatttgaagatcatttcaattcattcattca 8358
    |||
Db 121 TTAATATTGAGTTTCTTTCAGATCATTTAGATCTTTAATCTCATTTCATCATCA 180
OY 8359 tatlttttgagtgatgtctgtgagcgaagatgctgtaagcgtatgaagcaga 8418
    |||
Db 181 TATTTTGTGAGTGTGCTGTAGTGAAGATATGATGATGATGATGATGATGATGATG 240
OY 8419 tattaagctcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 8478
    |||
Db 241 TATTAAGCTCTGACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
OY 8479 gtgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8538
    |||
Db 301 GTTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
OY 8539 ttaattgcaaatgcaaaagcgaagaaag--tataaggtcacaagtttaacaatgat 8597
    |||
Db 361 TAAATGGCAACATGCAAAAGCAAGAAAGTTATGAGGCTCAACAGTCTAACAATGAT 420
OY 8598 tctcaacaggaagaacagctagcttgaaaactgtcgaaaacacacactgtgttatg 8657
    |||
Db 421 TCTTACCGGGGAAACAGCTAGCTTGAAGCTTCTGTAAGCAACCTGCTGTTTATG 480
OY 8658 gcaattagtaacctcaaatatgtgcttgagatattgtatccccatlaaactgtgaca 8717
    |||
Db 481 GCATTATGACTTCAAAATATGAGGCT--TTGCAAGATATGGATACCCCATTAATCTGACA 539
OY 8718 gtcataaatttctc--atctctcaactcagtcagtcagtcagtcagtcagtcagtcag 8775
    |||
Db 540 GTCCTAATTTTTCATCTCTTCAATCAGTATGCAAAATTTTAAACCCACCAATTA 599
OY 8776 ctt--ccataagagcatlctcaagatttctcaaccagcttatttcttcaagtcag 8834
    |||
Db 600 CTTCCCTTGTGGAGATTCTCAACAGTTTCTAACCAGCTTATTTCTAGTCGCGCA 659
OY 8835 acattgttaaaatactgttcaactaactactgttaactgttctgtgagaagaaga 8894
    |||
Db 660 CACCTTGTCAAAATCTGGCTCCCTTAATATGCTCAAGTGGCGGCTCTGAGACAACGAAA 719

```

RESULT 13
BE177793/c

LOCUS BE177793 608 bp mRNA linear EST 22-JUN-2000
DEFINITION R1-HT0598-120400-022-a12 HT0598 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE177793
VERSION BE177793.1 GI:8656945
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-R1-HT0598-120400-022-a12&ts=2000-04-12&tl=1)
Seq primer: puc 18 forward
High quality sequence start: 40
High quality sequence stop: 572.
Location/Qualifiers
1..608

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0598"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; site_1: SmaI; site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196/716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 203 a 94 c 91 g 220 t
ORIGIN

Query Match 5.3%; Score 549.6; DB 9; Length 608;
Best Local Similarity 95.1%; Pred. No. 5.7e-50;
Matches 578; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

```

OY 8532 tttttttaaattgcaacaatgcaaaagccaagaagatataaaggtcacaagtttaaca 8591
    |||
Db 608 TTTTGTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549
OY 8592 atgaattctcaacaggaagaacagctagcttgaaaactgtcgaaaacacacactgtg 8651
    |||
Db 548 ATGAATTTGGTCAACAGGAAACAGCTAGCTTGGAACCTGTGGAATACACTGATTGG 489
OY 8652 ttatgtgcatlgtlacttcaaatatgtgcttgcagatattgtatccccatlaaat 8711
    |||
Db 488 TTTATGGCAATTTATGATCTTCAATTAATTTGCGCTTGCAAGTATTTGGAATACCCCATTAAT 429
OY 8712 ctgacagctccaatttctcaatccttcaactcagtcagtcagtcagtcagtcagtcagtcag 8771
    |||
Db 428 CTGACACTCTCAAAATTTTATCTCTTCAATCATCACTACCCCAAGAAAATATTAACACA 369
OY 8772 aatactcatalgagacatttctcagagtttctcaaccagcttatttctcagtcag 8831

```

Db 368 AATACCTTCATATGAGCATTTTTCAGATTTTCTAACCCAGTCTTATTTTCTAGTCAG 309
 Qy 8832 taacatttgtaaaatctgcttccactaaactactactgtaactgctctgagagaagaag 8891
 Db 308 TAAACATTTTGAATACAGTGTCTACTAATFACTACTGTAACTGTCTGAGAGAAAG 249
 Qy 8892 aaaaatgagagagactatgcttggggaagttcaagtgatcttccatactactaa 8951
 Db 248 AAAAATATGAGAGACATTTGTTGGGAGGTTCAAGTATCTTTCAATATCATTTACTAA 189
 Qy 8952 ctcttcacactttcccaaaatgtaatatlaaagcgaagtgtaagacttccagattc 9011
 Db 188 CTCTCTCCACTTTTCTCTAATTTGAATATTAAACGCTAAAGGCTAAGACTTTCAGATTTC 129
 Qy 9012 aaatlaacttctcatalattttaaattcaagaatattatataaaccactgctgaaaa 9071
 Db 128 AATTAATCTTTCTATATTGTTAAATGTACAG-ATATTATTAATACCCACTGCTGAAAAA 70
 Qy 9072 gaaaaaatgattgctttagaagtaagtcataatgattttaaataatgaatgaag 9131
 Db 69 GAAGAAATGATGTTGTTAGAGTAAGTCAATCAGTATTTTAAATATATAGTAATCAAG 10
 Qy 9132 gcatatt 9139
 Db 9 GAGATATG 2

RESULT 14
 BF574391 771 bp mRNA linear EST 12-DEC-2000
 LOCUS 602131601F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270752 5',
 DEFINITION mRNA sequence.
 ACCESSION BF574391
 VERSION BF574391.1 GI:11648103
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 771)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgrabs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 http://image.llnl.gov
 Plate: L10M1082 row: b column: 01
 High quality sequence stop: 637.
 Location/Qualifiers

FEATURES
 source
 1. 771
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="4270752"
 /clone_id="NIH_MGC_81"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: muscle (skeletal); Vector: pDNR-LIB
 (Clontech); Site: 1: SfiI (ggcgccctggcgc); Site 2: SfiI
 (ggccatcagcc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGGCATTTATGGCC-3'
 and 3' adaptor sequence:
 5'-ATCTAGAGCGAGCGGCGGCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size
 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
 inserts by PCR. This library was enriched for full-length
 clones and was constructed by Clontech Laboratories (Palo
 Alto, CA)."

BASE COUNT 271 a 115 c 121 g 264 t
 ORIGIN

Query Match 5.3%; Score 549.4; DB 10; Length 771;
 Best Local Similarity 94.4%; Pred. No. 5.4e-50;
 Matches 658; Conservative 0; Mismatches 26; Indels 13; Caps 8;

Qy 9050 tatataccactgctgtaaaagaaaaaagatgctttagaagttgaatcaatattg 9109
 Db 1 TATATTAACCCACTGCTGAAAAAGAAAAAATGATTGTTTGAAGTTTAAGTCAATATTG 60
 Qy 9110 atttaaatatagtaagtaagcatttcccaactagtgatgcatgctgtaa 9169
 Db 61 ATTTTAATATATAGTAATGAGGATATTTCATTAATAGTATGTCATG-TCGAT 119
 Qy 9170 ttacagtaattcccaaaaatataagaattatagaataattccctcaattaaattt 9229
 Db 120 TTACAGTATCTTCAAAAATACAGAAATTATAGAAATATTCTCTCATTTAATATTTT 179
 Qy 9230 caaatcaagttatgcttccatatttactaaatcgtatctcattctcattag 9289
 Db 180 CAAATCAAAAGTTATGTTCTCATTTTACTAAATGATATCTTCAATTTATG 239
 Qy 9290 taactatagagaaactccttactcgtctcctgatttcaaggcattttaaaaa 9349
 Db 240 TAAATCTATGAGCAACTCTTACTTCGGTCTCTCGATTTCAGGCCATTTTAAAAA 299
 Qy 9350 tcaaaaggacgtgtaactatttgaagaacacagacatttaacagattgaagga 9409
 Db 300 TCAAAAAGCAGCTGTGAACTA-TTGAAGAAAAACACACATTTTAAATACAGATTGAAAA 358
 Qy 9410 cctctctgaactgaaacaaactatagttatcatcttcaacttcaacttctgtaact 9469
 Db 359 CCTCTTCTGAGCTGAAACCAATCTATGATTATCATCTTTAATCTGTGTTACTT 418
 Qy 9470 ttaaatatgaatttcttcaacttccctgltgaacctaattgltgtaaatcttacc 9529
 Db 419 TTAATATATATTTTTCATATTTCCTGCTGAACCTAA-TGSGTGAATTTTAAAC 477
 Qy 9530 aactatactcaatcaagaacaaattctgtatattccctgtggaatgactatgtag 9589
 Db 478 AA-TCTATCTCAATCAACCAAAATTTCTGTAATTTCCCTGGAATGTACTAATGAG 536
 Qy 9590 ttccagaattctcaaaatagctgttcaaaaattctcgtttgattcttggagacct 9649
 Db 537 TTTCAGAAATTTCTCAAAATACGTGTTCAAAAATTTCTGCTT-GATCTTGGACACCT 594
 Qy 9650 cagaaacttatacaaacactgtgaatagagaataacagaagaataataagccctta 9709
 Db 595 CAGAAATATATT--AAATGGGAATATGAGAAAT-CAGAGAAAAATATATAGGGTCTATA 650
 Qy 9710 tacataatgcccagcagcaatcattgtaaaaaa 9746
 Db 651 ---ATTAAATGCGCGCAAAATCTTGTTTAAAAACAAA 684

RESULT 15
 BG567118 648 bp mRNA linear EST 10-APR-2001
 LOCUS 60289265F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4723121 5',
 DEFINITION mRNA sequence.
 ACCESSION BG567118
 VERSION BG567118.1 GI:13574771
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 648)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM1582 row: b column: 18
 High quality sequence stop: 639.
 Location/Qualifiers

FEATURES

source

```

1..648
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:472121"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Liver; Vector: pDNR-LIB (Clontech); Site:1:
SfiI (ggccgcttggcc); Site:2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-GACGGCCATTATG6CC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGGCGCGACATG-dr(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

```

BASE COUNT 207 a 120 c 84 g 237 t
 ORIGIN

Query Match 5.2%; Score 545.8; DB:10; Length 648;

Best Local Similarity 96.1%; Pred. No. 1.4e-49;
 Matches 622; Conservative 0; Mismatches 16; Indels 9; Gaps 6;

```

QY 9457 actgtgtacacctttaaataagtaattttacattccctgtgtgaacctaatgtgt 9516
DB 1 ACTGTGTACCTTTAAATAGTATTTTTCATTTCCTGTGAACCTAATTGTGT 60
QY 9517 agaaattttaccacactatactcaatcaagaagaaattctgtatattccctgtgaat 9576
DB 61 AGAAATTTTACCAACTCTACTCAATCAACGAACAAATTCGTATATTCCTGTGAAT 120
QY 9577 gtacctatgtgtgttcagaaattctcaaatctgtgtcaaaaattctgtctttgcat 9636
DB 121 GTACCTATGTGAGTTTCAGAAATTTCTCAAAATACGTGTTCAAAAATTTCTGCTTTTGCAT 180
QY 9637 ctlttggaacacctcagaactatatacaactgtgaatatgaagaataacagaagaat 9696
DB 181 CTTTGGGACACCTCAGAAAACCTTATTACAACTGTGATATGAGAAATACAGAGAAAT 240
QY 9697 aataagccctatacaataatgcccagacaattcattgttaaaaaaaccaaacctc 9756
DB 241 AATAAGCCCTATATACATAAATGCCCACACATTCATTGTACAAACCAACCAACCTC 300
QY 9757 aacactactgtatattatattctgtactcgaagaatcttltgtactataataatgtgc 9816
DB 301 ACACACTACTGTATTTATTTCTGTACTGAAGCAAAATGCTTTGTACATTTAAATGTTGC 360
QY 9817 acatcatcatcatcatgatactatcatctgaactaaagccattg-ctgtgttttctct 9875
DB 361 ACATCATTCATTCATGTATATGTATCATGTGCTAAAGCCATTTCCTGTGTTCTTCT 420
QY 9876 tgtgtgtatataatcaaggtataaatttccaaagagcaatgtgtcatgtactgtaa 9935
DB 421 TGTGTGTATATATACAGTAAATATTTTCCAAAGAGCCATGTGTCAATGTAATCTGAA 480
QY 9936 cc-cttltatattgacataatttggacccttgtatattactactag-ataatgttaa 9993
DB 481 CCACCTTGTATTTGAGACATTTATTTGATCCCTGTGTATTTACTACTAGTAAATGTA 540
QY 9994 tacttgaagaatatgtcttaattctt--caaaatgtgcatcccccttaaaangt-tc 10050

```

```

DB 541 TACTGTAGAAATATTGCTCTATATTCTTTTCAAAATTTGTGATCCCTTAGAATGTCTC 600
QY 10051 tattccataaggaattagct---tgctatcccttcttatacccta 10094
DB 601 TATTTCATATAGATCTAGATATGCTATTTATTCCTTCTTATACCCCTA 647

```

Search completed: September 14, 2002, 01:19:31
 Job time: 54654 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2002, 07:01:42 ; Search time 277.92 Seconds
(Without alignments) 6013.566 Million cell updates/sec

Title:

US-09-595-526b-1_COPY_291_7094

Perfect score:

6804

Sequence:

1 atgctgtgtggtcctcagc.....gaagaatcctgtcatacag 6804

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/pdata/2/lna/5A.COMB.seq:*
2: /cgn2_6/pdata/2/lna/5B.COMB.seq:*
3: /cgn2_6/pdata/2/lna/6A.COMB.seq:*
4: /cgn2_6/pdata/2/lna/6B.COMB.seq:*
5: /cgn2_6/pdata/2/lna/PCRTUS.COMB.seq:*
6: /cgn2_6/pdata/2/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	430.8	6.3	5894	3	US-08-665-259-24
2	430.8	6.3	5894	3	US-08-762-500-24
3	430.8	6.3	5894	3	US-08-762-500-24
4	56	0.8	7218	1	US-08-232-463-14
5	52.4	0.8	2726	1	US-08-461-823-1
6	52.4	0.8	4646	1	US-08-181-471-2
7	52.4	0.8	4669	2	US-08-583-276-18
8	52.4	0.8	4669	2	US-08-583-276-18
9	52.4	0.8	6505	2	US-08-793-610-5
10	52.4	0.8	9318	2	US-08-793-610-5
11	52.4	0.8	4403765	4	US-09-103-840A-2
12	52.4	0.8	4411529	2	US-09-103-840A-1
13	50.8	0.7	4264	2	US-08-784-649A-1
14	50.8	0.7	4264	2	US-08-784-649A-5
15	50	0.7	4233	3	US-09-120-513-1
16	49.4	0.7	4233	3	US-09-120-513-1
17	49.4	0.7	4233	3	US-09-120-513-1
18	49.2	0.7	4669	2	US-08-752-447-1
19	49	0.7	5045	4	US-09-390-721-3
20	49	0.7	5045	4	US-09-390-721-3
21	46.2	0.7	7218	1	US-08-232-463-14
22	45.2	0.7	23673	4	US-09-773-816-1
23	44.2	0.6	1526	4	US-08-858-207A-34
24	43	0.6	15367	2	US-09-627-376-3
25	42.4	0.6	1518	2	US-08-997-080-88
26	42.4	0.6	1518	2	US-08-997-362-88
27	42.4	0.6	1518	3	US-08-873-970-88

28	42.4	0.6	1518	4	US-09-095-855-88	Sequence 88, Appl
29	42.4	0.6	1518	4	US-09-324-542-88	Sequence 88, Appl
30	40.8	0.6	1971	4	US-08-858-207A-72	Sequence 72, Appl
31	38.8	0.6	1260	2	US-08-578-158-1	Sequence 1, Appl
32	38.8	0.6	1815	4	US-09-042-785A-24	Sequence 24, Appl
33	38.8	0.6	2186	3	US-08-959-382-1	Sequence 1, Appl
34	38.8	0.6	2612	4	US-09-042-785A-3	Sequence 3, Appl
35	38.8	0.6	2638	4	US-09-042-785A-22	Sequence 22, Appl
36	38.8	0.6	3474	4	US-09-527-236A-1	Sequence 1, Appl
37	38.6	0.6	6909	4	US-09-199-637A-111	Sequence 111, App
38	38.2	0.6	3924	2	US-08-996-644-3	Sequence 3, Appl
39	38.2	0.6	3924	3	US-09-352-552-3	Sequence 3, Appl
40	38.2	0.6	3927	2	US-08-996-644-1	Sequence 1, Appl
41	38.2	0.6	3927	3	US-09-352-552-1	Sequence 1, Appl
42	38	0.6	1209	4	US-08-936-165A-55	Sequence 55, Appl
43	37.8	0.6	732	4	US-08-919-573-3	Sequence 3, Appl
44	37.8	0.6	735	4	US-08-919-573-1	Sequence 1, Appl
45	37	0.5	6688	4	US-09-381-862-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-665-259-24
Sequence 24, Application US/08665259
Patent No. 6028173
GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy C.
APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Klinger, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: One Mountain Road
CITY: Framingham
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,259
FILING DATE: 17-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 5894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..5053
US-08-665-259-24


```

OY 2915 ggcgaacccgggggggtctgtgcccccaacataaagtgctgttbaactgtagctgtcgaag 2974
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2386 GGAAGACCTTG6GGGCTGTGCCCCCAGCAGCAAGATCTCTGTTTACAACTTGACAGTCGCAG 2445
OY 2975 aacacatctgtctctatgtcccgctltgaagggtctctctgtagaagcaactgaaggcggaga 3034
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2446 AGCACTTTATTTCTTAAGCCCACTGAAGGGCTGTCAAGTCAAGATGCGCCTGAAGAG 2505
OY 3035 tggagcagatgtgccccttgaatgttgttctgtcattcaagcaagctgaaagcaaaacaaacc 3094
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2506 TCAAGCAGAGATG---CTGCACATCATGTGGCCTGAGAGACAAGTGAACACGAGAGCCGCT 2562
OY 3095 agctgtcaagtgtgaatgaagcaagaagactatctgtgaccttgaccttcttgaggatcta 3154
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2563 TCTCGATCGGGGGGATGAAGCGCAGACCTTCATCGGCATCGCCCTCATCGCAAGCTTCCA 2622
OY 3155 aggtgtcattcttgatgaaccaccacagctggtgtgaaccttactcccgagggggaatat 3214
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2623 AGGTGCTGATTACTTGAGAGACCCACTCTCGGCATGTGAGCCATCTTCCAGAGAGGCGCATCT 2682
OY 3215 gggagctgtctgtgtgaatatcgaacaaggccgacacattatctctctacaacacacatlg 3274
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2683 GGGATCTTCTTCAAGCGGCAGAAAAGTGAACCGCACCATCTGCTGTACACACCCACTTCAATG 2742
OY 3275 atgaagcggagcgtctctggggggaagaagattgcattcatctccatgtggaagctgtgtcgtg 3334
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2743 ACGAGGTGACCTGTGCGGAGACCGCATGCGCATATGCGCCAAAGGGGAGGTGAGTGGACT 2802
OY 3345 tggagctctccctgtcttcttgaagaacagcgtgtggaacagctactactgagcttggtga 3394
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2803 GCGGGTCTCTGCTGCTGTCTTAAGCAAGAAATACGGTGTCCGGCTATATCATATGACCTGTGTA 2862
OY 3395 agaa 3398
      ||| |||
Db 2863 AGGA 2866

RESULT 4
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F
; APPLICANT: SCHEFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:

```

```

      1 TELEPHONE: (703)836-9300
      2 TELEFAX: (703)683-4109
      3
      4 TELEX: 899149
      5
      6 INFORMATION FOR SEQ ID NO: 14:
      7
      8 SEQUENCE CHARACTERISTICS:
      9
     10 LENGTH: 7218 base pairs
     11
     12 TYPE: nucleic acid
     13
     14 STRANDEDNESS: single
     15
     16 TOPOLOGY: linear
     17
     18 IMMEDIATE SOURCE:
     19
     20 CLONE: pTZgpt-F1s
     21
     22 US-08-232-463-14
     23
     24
     25
     26
     27
     28
     29
     30
     31
     32
     33
     34
     35
     36
     37
     38
     39
     40
     41
     42
     43
     44
     45
     46
     47
     48
     49
     50
     51
     52
     53
     54
     55
     56
     57
     58
     59
     60
     61
     62
     63
     64
     65
     66
     67
     68
     69
     70
     71
     72
     73
     74
     75
     76
     77
     78
     79
     80
     81
     82
     83
     84
     85
     86
     87
     88
     89
     90
     91
     92
     93
     94
     95
     96
     97
     98
     99
    100
    101
    102
    103
    104
    105
    106
    107
    108
    109
    110
    111
    112
    113
    114
    115
    116
    117
    118
    119
    120
    121
    122
    123
    124
    125
    126
    127
    128
    129
    130
    131
    132
    133
    134
    135
    136
    137
    138
    139
    140
    141
    142
    143
    144
    145
    146
    147
    148
    149
    150
    151
    152
    153
    154
    155
    156
    157
    158
    159
    160
    161
    162
    163
    164
    165
    166
    167
    168
    169
    170
    171
    172
    173
    174
    175
    176
    177
    178
    179
    180
    181
    182
    183
    184
    185
    186
    187
    188
    189
    190
    191
    192
    193
    194
    195
    196
    197
    198
    199
    200
    201
    202
    203
    204
    205
    206
    207
    208
    209
    210
    211
    212
    213
    214
    215
    216
    217
    218
    219
    220
    221
    222
    223
    224
    225
    226
    227
    228
    229
    230
    231
    232
    233
    234
    235
    236
    237
    238
    239
    240
    241
    242
    243
    244
    245
    246
    247
    248
    249
    250
    251
    252
    253
    254
    255
    256
    257
    258
    259
    260
    261
    262
    263
    264
    265
    266
    267
    268
    269
    270
    271
    272
    273
    274
    275
    276
    277
    278
    279
    280
    281
    282
    283
    284
    285
    286
    287
    288
    289
    290
    291
    292
    293
    294
    295
    296
    297
    298
    299
    300
    301
    302
    303
    304
    305
    306
    307
    308
    309
    310
    311
    312
    313
    314
    315
    316
    317
    318
    319
    320
    321
    322
    323
    324
    325
    326
    327
    328
    329
    330
    331
    332
    333
    334
    335
    336
    337
    338
    339
    340
    341
    342
    343
    344
    345
    346
    347
    348
    349
    350
    351
    352
    353
    354
    355
    356
    357
    358
    359
    360
    361
    362
    363
    364
    365
    366
    367
    368
    369
    370
    371
    372
    373
    374
    375
    376
    377
    378
    379
    380
    381
    382
    383
    384
    385
    386
    387
    388
    389
    390
    391
    392
    393
    394
    395
    396
    397
    398
    399
    400
    401
    402
    403
    404
    405
    406
    407
    408
    409
    410
    411
    412
    413
    414
    415
    416
    417
    418
    419
    420
    421
    422
    423
    424
    425
    426
    427
    428
    429
    430
    431
    432
    433
    434
    435
    436
    437
    438
    439
    440
    441
    442
    443
    444
    445
    446
    447
    448
    449
    450
    451
    452
    453
    454
    455
    456
    457
    458
    459
    460
    461
    462
    463
    464
    465
    466
    467
    468
    469
    470
    471
    472
    473
    474
    475
    476
    477
    478
    479
    480
    481
    482
    483
    484
    485
    486
    487
    488
    489
    490
    491
    492
    493
    494
    495
    496
    497
    498
    499
    500
    501
    502
    503
    504
    505
    506
    507
    508
    509
    510
    511
    512
    513
    514
    515
    516
    517
    518
    519
    520
    521
    522
    523
    524
    525
    526
    527
    528
    529
    530
    531
    532
    533
    534
    535
    536
    537
    538
    539
    540
    541
    542
    543
    544
    545
    546
    547
    548
    549
    550
    551
    552
    553
    554
    555
    556
    557
    558
    559
    560
    561
    562
    563
    564
    565
    566
    567
    568
    569
    570
    571
    572
    573
    574
    575
    576
    577
    578
    579
    580
    581
    582
    583
    584
    585
    586
    587
    588
    589
    590
    591
    592
    593
    594
    595
    596
    597
    598
    599
    600
    601
    602
    603
    604
    605
    606
    607
    608
    609
    610
    611
    612
    613
    614
    615
    616
    617
    618
    619
    620
    621
    622
    623
    624
    625
    626
    627
    628
    629
    630
    631
    632
    633
    634
    635
    636
    637
    638
    639
    640
    641
    642
    643
    644
    645
    646
    647
    648
    649
    650
    651
    652
    653
    654
    655
    656
    657
    658
    659
    660
    661
    662
    663
    664
    665
    666
    667
    668
    669
    670
    671
    672
    673
    674
    675
    676
    677
    678
    679
    680
    681
    6
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/168,621
; FILING DATE: 16-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010,433
; FILING DATE: 27-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Karta, Glenn E.
; REGISTRATION NUMBER: 30,649
; REFERENCE/DOCKET NUMBER: PA-0012 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301 208-6997
; TELEFAX: 301 527-2058
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2726 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-461-823-1

```

Query Match 0.8%; Score 52.4; DB 1; Length 2726;

Best Local Similarity 46.7%; Pred. No. 3e-05;

Matches 253; Conservative 0; Mismatches 271; Indels 18; Gaps 2;

```

QY 2750 atgagctgacgaatatttataagggccagatcacctcctctgagccacaatgag 2809
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1665 AGGAGCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1724
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2810 cggggaagagagagagagagagagagagagagagagagagagagagagag 2869
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1725 GTGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1784
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2870 cctacatcctggaagagagagagagagagagagagagagagagagagag 2926
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1785 TGCTGCTTGAATGGAAGAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1844
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2927 gggctgtcccaagacatacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2986
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1845 GCATCGTGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1904
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2987 tctatgcccgttgaagagagagagagagagagagagagagagagagagag 3046
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1905 GAGACAAACAGCCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1964
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3047 ccttgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3091
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1965 TACATGCTTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2024
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3092 gccagcgttgaatgagagagagagagagagagagagagagagagagagag 3151
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2025 CTGAGCTCTGTGGGCGCAAAACAGCAATTCATTCATTCATTCATTCATTCAT 2084
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3152 ctaaggtgtcatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3211
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2085 CTGATATTGCTTTGGTGAAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2144
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3212 taaggagagagagagagagagagagagagagagagagagagagagagag 3271
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2145 TCCAAAGAGCCCTGAGAAAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2204
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3272 tg 3273
   ||
Db 2205 TG 2206

```

RESULT 6
US-08-181-471-2
; Sequence 2, Application US/08181471

```

; Patent No. 5641508
; GENERAL INFORMATION:
; APPLICANT: Li, Lingna
; APPLICANT: Ishiko, Valeryl K.
; TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL
; TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas Fitting
; STREET: 12526 High Bluff Drive, Suite 300
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92130
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/181,471
; FILING DATE: 13-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,553
; FILING DATE: 02-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: ANT0029P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-792-3680
; TELEFAX: 619-792-8477
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4646 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 425..4267
; US-08-181-471-2

```

Query Match 0.8%; Score 52.4; DB 1; Length 4646;

Best Local Similarity 46.7%; Pred. No. 4.5e-05;

Matches 253; Conservative 0; Mismatches 271; Indels 18; Gaps 2;

```

QY 2750 atgagctgacgaatatttataagggccagatcacctcctctgagccacaatgag 2809
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3585 AGGAGCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3644
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2810 cggggaagagagagagagagagagagagagagagagagagagagagagag 2869
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3645 GTGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3704
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2870 cctacatcctggaagagagagagagagagagagagagagagagagagag 2926
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3705 TGCTGCTTGAATGGAAGAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3764
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2927 gggctgtcccaagacatacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2986
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3765 GCATCGTGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3824
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2987 tctatgcccgttgaagagagagagagagagagagagagagagagagagag 3046
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3825 GAGACAAACAGCCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3884
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3047 ccttgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3091
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Accession	Sequence	Position
Db	3885 TACATGCTTCATCGAGTACTGCTCTAAATAATATATGACACTAAAGTAGACAGCAAAAGGAA	39444
Oy	3092 gccagcgcgtcaagctgtaagatccagaagaagctatcgttgccctgagccttctgcggggat	31514
Db	3945 CTCAGCTCTCTGGTGGCCAGAAACGATTCGATTCGATTCGTCCTCTTTGTATAGACAGC	40044
Oy	3152 ctaaggttgcaatctcgtatgtaaacccacaagctggtgtgtgacccctactccgcagaaggaa	32114
Db	4005 CTCATATTTTGGCTTTTGGATGAAGCCACGCTCAGTCACTCTGGATTCAGAAAGTGAAGGTTG	40644
Oy	3212 tatggagcgcctgcgtgaaataccgacaagagccgacacattctctctaacacacaca	32714
Db	4065 TCCAAGAGAGCCCTGGACAAAGCCAGAGAGAGGCCCGCACCTGCAATTGTGATGTCTACGCC	41244
Oy	3272 tg 3273	
Db	4125 TG 4126	

```

RESULT 7
US-08-583-276-18
? Sequence 18, Application US/08583276
? Patient No. 5837536
?
? GENERAL INFORMATION:
?
? APPLICANT: Mcdonagh, Kevin T.
? APPLICANT: Niemhuis, Paul
? TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
? TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
? NUMBER OF SEQUENCES: 19
? CORRESPONDENCE ADDRESS:
?
? ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
? ADDRESSEE: Cecchi & Stewart
? STREET: 6 Becker Farm Road
? City: Roseland
? STATE: New Jersey
? COUNTRY: USA
? ZIP: 07068
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 inch diskette
? COMPUTER: IBM PS/2
? OPERATING SYSTEM: PC-DOS
? SOFTWARE: DM4.V2
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/583,276
? FILING DATE: 05-JAN-1996
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/332,444
? FILING DATE: 31-OCT-1994
? APPLICATION NUMBER: 07/887,712
? FILING DATE: 22-MAY-1992
? INFORMATION FOR SEQ ID NO: 18:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 4669 bases
? TYPE: nucleic acid
? STRANDEDNESS: singular
? TOPOLOGY: linear
?
? MOLECULE TYPE:
? DESCRIPTION: Genomic DNA
US-08-583-276-18

```

	Query Match	Score	DB	length
	Best Local Similarity	46.7%	Pred. No. 4, 5e-05	
	Matches	253; Conservative	0; Mismatches	271; Indels 18; Gaps 2
Qy	2750	atgcgcctgcactgaatttttatggagggccagatacaactctcttctctggagccacaatgag	2809	
Db	3585	atggactgagccttgagaggtggaagaaggcccaacgcctgctctgtggggccaccacatggcgt	3644	

QY	2810	cggggaagaagaccacatctcaactctcaacgggtgtgtgtcccccgaactctggagcagc	2865
Db	3645	GTGGGAAGAGACAGTGTCTCAGCTCTCTGGAGCGGTTTACAGACCCCTTGCGAGGGAAAG	3704
QY	2870	cctacatccctgggaagaagacat---tcgctctgagatgtagcaacatccgcgagaactcgg	2928
Db	3705	TGCTGCTTGATGGCAAAATAAGCCGACTGAATGTTACGTGCTCCGAGCACACTGG	3764
QY	2927	gggtctgtccccagacataaagctgtgtcttgacatgtgtatctgaaagaacatctggt	2986
Db	3765	GCATCGTGTCCGAGAGACCCATCTCTGTTTACTCGACAGCATTTGCTGAGAAATGGCTTATG	3824
QY	2987	tctatgccgccttgaaaggcctctctgtagaagcagctgaaaggcggagatgtagcagatcg	3046
Db	3825	GACACAAACAGCCGGGTGGTGTCTCAGAGAAAGATCTGTGAGGCGACAAAGAGCCCAACA	3884
QY	3047	ccctgagatgtgtgttctgtcccaatgaagaagctgaaag-----caaaaca	3091
Db	3885	TACATGCCCTTACGACTCCTCCTTAATTAATATATGACTAAAGTAGAGACAAAGGA	3944
QY	3092	gccacgcttcaagtgtaaatgcagagaagaactatctctgtgcttgccttgtctgcggggat	3150
Db	3945	CTCAGCTCTCTGGTGGCCCAAAACAAGCATTCCTCCATCTGTCGCCCTGTTTAACAGC	4004
QY	3152	ctaaggtgtgcatctctggaatgaaacccaacgctgtgtgtggaaccttactccgcagggaa	3211
Db	4005	CTCATATTTTGGCTTTGGATGGAAAGCCAGCTCACTGTGATATCAGAAATGATAAAGTTTG	4064
QY	3212	tatgagagctctgtctgtaaataccgaagaaggccgacacattatctcttaacacacca	3270
Db	4065	TCCAAAGAAGCCCTGAGCAAAACCCAGAGAGAGCGGCACCTGCATTTGATTTGCTCACGCC	4124
QY	3272	tg 3273	
Db	4125	TG 4126	

RESULT 8
5206352-3
PATENT NO. 5206352
APPLICANT: Kohninson, Igor B.; Pastan Ira H.; Gottsman,
Michael M.
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/622,836
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
SEQ ID NO.:3
LENGTH: 4669
5206352-3

Query Match	0.8%	Score 52.4	DB 6	Length 4669
Best Local Similarity	46.7%	Pred. No. 4.5e-05		
Matches 253	Conservative	0	Mismatches 271	Indels 18
			Gaps	2
QY	2750	atgacgcgcgcactgaatttltatgagggccaataactctcttccttgsgccacatgag	2809	
Db	3565	aggagcgcgaccccgsggfggaagaagggccaaagcgtctgctctggtgycgacgagtgct	3644	
OY	2810	cggggaagacgacccaacatgtcaatccttgcacccgggtgttcccccgaactcgggacacg	2869	
Db	3645	gtgggaagacacacagtcggtccagctcctctgagcggtcttaacgaccttgcgaggaag	3704	
OY	2870	cctacacccctgggaanaagcat---tgctctgagatgagacacatccgcgagaactcg	2926	
Db	3705	tgctgcctgtgattggccaagaataaagcgcagcttgaatgttcagtcgtctccggacacacttg	3764	

OY	2927	gggtctgtcccgacgaataacgtgctgtgttgatctgctgtaagaaacacatctggt	2986
OY	2927		
Db	3765	gcatctgtcccgagagccacatctgtttgactgcagatctgtcgaacaatlgcctatg	3824
OY	2987	tctatgccccttgaaaggctctctcgtagaagcagctgtgaagccgagatgtagagacatg	3046
OY	2987		
Db	3825	gagacaacagccgggvggtgctacaggaagagatctgttagggcagcaaggaagccaca	3884
OY	3047	ccctgtatgtgtgttgccatcaagcaagctgaaag-----caaaaca	3091
OY	3047		
Db	3885	tacatgccttcacgcagtcactgccttaataatatagactaaagtaagagacaaagaa	3944
OY	3092	gcacagctgaagttggaatgcagagaaagctactgtgacctgtgacctgtcggggat	3151
OY	3092		
Db	3945	ctcagctctctgtgtgcccagaacaacagatgcatatgcctgcgtgacctgttagacgc	4004
OY	3152	ctaagttgtcatctcgtatgaaccacacagctgtgtgtgacctactccgcagggaa	3211
OY	3152		
Db	4005	ctcatatttgccttcttgatgtagccacgctgcagctcctgtalatagaaagtgaagtgtg	4064
OY	3212	tatggagcgcgtgcctggaatcccaagaagccgcacattatctctctcacaccaca	3271
OY	3212		
Db	4065	tccaagaagcccgagacaacagagagaagccgcacctgcattgtgtgattgtccacgcc	4124
OY	3272	tg 3273	
OY	3272		
Db	4125	tg 4126	
RESULT 9			
US-08-793-610-5			
Sequence 5, Application US/08793610			
Patent No. 5858744			
GENERAL INFORMATION:			
APPLICANT: BAUM, Christopher			
APPLICANT: STOCKING-HARBERS, Carol			
APPLICANT: OSTERTAG, Wolfram			
TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF			
TITLE OF INVENTION: FOR GENE TRANSFER			
NUMBER OF SEQUENCES: 6			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP			
STREET: 655 Fifteenth Street N.W. Suite 330			
CITY: Washington			
STATE: D.C.			
COUNTRY: U.S.A.			
ZIP: 20005-5701			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/793,610			
FILING DATE: 07-MAR-1997			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: DE P 44 31 973.8			
FILING DATE: 08-SEP-1994			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: DE 195 03 952.1			
FILING DATE: 07-FEB-1995			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: PCT/EP95/03175			
FILING DATE: 10-AUG-1995			
ATTORNEY/AGENT INFORMATION:			
NAME: Berman, Richard J.			
REGISTRATION NUMBER: 39,105			
REFERENCE/DOCKET NUMBER: P1614-7007			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (202)638-5000			
TELEFAX: (202)638-4810			
INFORMATION FOR SEQ ID NO: 5:			

```

: SEQUENCE CHARACTERISTICS:
:     LENGTH: 6505 base pairs
:     type: nucleic acid
:     STRANDEDNESS: double
:     TOPOLOGY: circular
:     MOLECULE TYPE: DNA
US-08-793-610-5

Query Matchh              0.8%; Score 52.4; DB 2; Length 6505;
Best Local Similarity 46.7%; Pred. No. 5.8e-05;
Matches 253; Conservative 0; Mismatches 271; Indels 18; Gaps 2;

QY 2750 atggcctgagcactgaattttatagaggccagatatacctcctctctctggccacacatggag 2809
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4977 AGGAGACTGAGCCTGGGAGGTGAAGAAAGGGCCAGACCGCTGGCTCTGTGTGGGACGATGGCT 5036

QY 2810 cgggagaagacgaccaccatgcatcactctgcagcgggtgtgtctcccccgaactcggagaccg 2869
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5037 GTGGGAAGACACACAGTGTGTCCAGCTCTCTGGAGCGGTTCTTACGACCCTTGGCAGGGGAAG 5096

QY 2870 cctacatcctcgggaaaagacat---tcgctctgagatgagacacatccgcgcgaacctgg 2926
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5097 TCGCTGCTTGAATGCGCAAGAAATAAAGCGACATGTAATGTTCACGTGGCTCCGAGCACACCTGG 5156

QY 2927 gggtctgtcccccagacataacgtgctgtgttgcatactgcatctgcgtgcgaagaacacatcgtg 2986
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5157 GCATCGTGTCACAGGAGGCCATCTCTTTTGACTGCAGATTGCTGAGAACATTTGCTATG 5216

QY 2987 tctatgccgcttgaaagggtctctctgagaagcagctgaaagcggagatggaatggaatgag 3046
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5217 GAGCAACAACACCCGGGTGGTGTCACAGGAAGATGCTGAGGGGACGAAAGAGAGCCCAAGA 5276

QY 3047 ccccgatagtgtgttgcgcatacaagcctgaaag-----caaaaaga 3091
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5277 TACATGECCTTCATCGAGTCACTGCTCTTAATTAATATAGCATTAAGATGAGACAAAGAA 5336

QY 3092 agcagcctgtcaggtggaatgcagagaagaagctatctgtgaccttgccttgcctgtcggggag 3151
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5337 CTCAGCTCTCTGTGGTGGCCAGAAACAACGATTCGATAGCTCGNCCCTGTGTAACACAG 5396

QY 3152 ctaagctgtgtcatctcgtgtgaaccacagaagctgtgtgtgagaccttactcccgaggagaa 3211
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5397 CTCATATTATTGCTTTGGATGTAAGCCACAGCTCAAGCTGTGGATACAGAAAGTGAAGAGTTTG 5456

QY 3212 tatggagagctcgtcgtcgaatataccgacagaagccgcgacatattctctctacacacaa 3271
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5457 TCCAAAGAGAGCCCTCGACAAAGCCAGCAAGAGGCGGACCTGCATTGTGATGTCACCGCC 5516

QY 3272 tgg 3273
      ||
Db 5517 TG 5518

RESULT 10
US-08-793-610-6
: Sequence 6, Application US/08793610
: Patent No. 5858744
: GENERAL INFORMATION:
:     APPLICANT: BAUM, Christopher
:     APPLICANT: STOCKING-HARBERS, Carol
:     APPLICANT: OSTERTAG, Wolfram
:     TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF
:     TITLE OF INVENTION: FOR GENE TRANSFER
:     NUMBER OF SEQUENCES: 6
:     CORRESPONDENCE ADDRESSES:
:     ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
:     STREET: 655 Fifteenth Street N.W. Suite 330
:     CITY: Washington
:     STATE: D.C.
:     COUNTRY: U.S.A.
:     ZIP: 20005-5701
: COMPUTER READABLE FORM:

```


MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,610
FILING DATE: 07-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 31 973.8
FILING DATE: 08-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 07-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03175
FILING DATE: 10-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berman, Richard J.
REGISTRATION NUMBER: 39,105
REFERENCE/DOCKET NUMBER: P1614-7007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9318 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-08-793-610-6

Query Match 0.8%; Score 52.4; DB 2; Length 9318;
Best Local Similarity 46.7%; Pred. No. 7.7e-05;
Matches 253; Conservative 0; Mismatches 271; Indels 18; Gaps 2;
QY 2750 atggcctgacacgaattttatgaaggccacataccctccctccgacacatgag 2809
DB 4936 agggactgacacctggagtgagaaaggccacacgctgcttggtggcagcagtgct 4995
QY 2810 cggggaagacgacacacatgacacacacacacacacacacacacacacacac 2869
DB 4996 gtgggaagacgac 5055
QY 2870 cctac 2926
DB 5056 tgcctgctgac 5115
QY 2927 gggctgctgac 2986
DB 5116 gcatgctgctgac 5175
QY 2987 tcatgctgctgac 3046
DB 5176 gaagac 5235
QY 3047 cctgac 3091
DB 5236 tacatgctgctgac 5295
QY 3092 gccagctgctgac 3151
DB 5296 ctgac 5355
QY 3152 ctgac 3211
DB 5356 ctgac 5415
QY 3212 tatggagctgctgac 3271
DB 5416 tcacagac 5475

QY 3272 tg 3273
DB 5476 TG 5477
RESULT 11
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Query Match 0.8%; Score 52.4; DB 4; Length 4403765;
Best Local Similarity 47.6%; Pred. No. 0.008;
Matches 280; Conservative 0; Mismatches 290; Indels 18; Gaps 2;
QY 2776 ggcac 2835
DB 3000421 ggcac 3000362
QY 2836 ctgac 2895
DB 3000361 ctgac 3000302
QY 2896 ctgac 2955
DB 3000301 gactgggac 3000242
QY 2956 gac 3015
DB 3000241 caaaagctgac 3000182
QY 3016 aagcagctgac 3075
DB 3000181 gccac 3000131
QY 3076 ctgac 3135
DB 3000132 ctgac 3195
QY 3136 gcttctgac 3255
DB 3000076 tgcctgac 3315
QY 3196 taccctgac 3375
DB 3000076 gtcac 3435
QY 3235 attctctac 3495
DB 2999956 ttctctac 3555
QY 3313 tccac 3615

Dd	3599	TACATGCCCTTCATGAGTACACTGACTGCTAAATPAATATATGCACTAAAGTAGGAGACAAAGAA	3658
Qy	3092	gccagcgcgtcagctggtgaatcgcagaagaagctactcgtgaccttgagccttctgcggggat	3151
Dd	3659	CTCAGCTCTCTGCTGGTGGCCAAACAAACGCATTGCCATTAGCTCGTCCCTTGTTAAGACAGC	3718
Qy	3152	ctaagtgatgcattctgcatgaaaccaacagctgctgtgagcccttactccgcaggagaa	3211
Dd	3719	CTCATATTTCCTTTGATGTGATGAGGCCACGTCAGCTCTGGATATCAGAAATGAAAGGTTG	3778
Qy	3212	tatgagagctgctgctgcgaaataccgaagaagggccgacacattctctctacacaca	3271
Dd	3779	TCCAAGAGGCCCTGGACAAAGCCAGAGAGGCCGCACTGCATTGGATTGCTCACCGCC	3838
Qy	3272	tg 3273	
Dd	3839	TG 3840	

RESULT 14

```

US-08-784-649A-5
: Sequence 5, Application us/08784649A
: Patent No. 5830697
:
: GENERAL INFORMATION:
: APPLICANT: SIKIC, Branislav I
: APPLICANT: Chen, Gang
: TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
: TITLE OF INVENTION: CYCLOSPORIN MODULATION
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson
: STREET: 2200 Sand Hill Road
: CITY: Menlo Park
: STATE: CA
: COUNTRY: USA
: ZIP: 94025
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/784,649A
: FILING DATE:
:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sherwood, Pamela J
: REGISTRATION NUMBER: Reg. No. 5830697 36, 677
: REFERENCE/DOCKET NUMBER: 06037/007001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-322-5070
: TELEFAX: 415-854-0875
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4264 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
:
US-08-784-649A-5

```

Query Match	0.78;	Score 50.8;	DB 2;	Length 4264;
Best Local Similarity	46.58;	Pred. No. 0.00013;		
Matches 252;	Conservative	0;	Mismatches 272;	Indels 18; Gaps 2

QY	2750	atgagcctgcgacctaatttttagagagccagaatacccttcctcgggcccacatgag	2805
Db	3299	AGGACCTAGCCTTGAGGTGAAGAAAGGCCAGACGCTGCTTGtggggcAGCAAGTGGCT	3355
QY	2810	cgggagagacgaccacacatgcaatccctgcagcgggtgtgttccccccgacctcgggacgc	2865
Db	3359	GTGGGAAAGACGACAGGTGTCAGGCTCTCTGGAGGGGTTTACAGACCCCTTGGGAGGGGAAG	3415

[illegible]

RESULT 15

US-09-194-905-7/c
Sequence 7, Application US/09194905
Patent No. 6306627
GENERAL INFORMATION:
APPLICANT: DECKER, Heinrich
TITLE OF INVENTION: ISOLATION OF THE BIOSYNTHESIS GENES FOR
PSEUDO-OLIGOSACCHARIDES FROM STREPTOMYCES GLAUCESCENS
TITLE OF INVENTION: GLA.O AND THEIR USE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/194,905
FILING DATE: 29-JUL-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP97/02826
FILING DATE: 30-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19622783.6
FILING DATE: 07-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 026083/0193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

```

: INFORMATION FOR SEQ ID NO: 7:
:
: SEQUENCE CHARACTERISTICS:
:
:   LENGTH: 6854 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:
:   MOLECULE TYPE: DNA (genomic)
:
: US-09-194-905-7

```

Query Match	0.78;	Score 50;	DB 4;	Length 6854;
Best Local Similarity	51.58;	Pred. No. 0.00034;		
Matches 141;	Conservative 0;	Mismatches 130;	Indels 3;	Gaps 1;

OY	2743	gagcagatggccttgagcactgaattttatgatgggcacaaatcaacttcctctctggcac	2802
Db	612	gccctgcagcagagctctccttcgcagataccgccccggcagcaaaacgcctctacatcgccgc	553
OY	2803	aatgagcggggaaagacagaccacatgtaatcctgaaccgggtctgtctcccccgaactcg	2862
Db	552	aacggagccggcgaaatcgccacgcacgatcaagaatgctgacgcgcgatcatgatgacccccacctcc	493
OY	2863	ggcaccgcctacatcctctggyaaaaga---cattgctctgaatgatagaacattccggcag	2919
Db	432	gccccctgcacgctggccggcgctgagacccctaacccgcacacggcagcagccaccccccacag	433
OY	2920	aacctgggggtctgtctcccgacataacgtgtcgtcttgacatcgtgactgtcgaagaacac	2979
Db	432	atcgcgctgctgttggcgacgacgacccagctctgctgtggagacctgtgcgttaccgcactcc	373
OY	2980	atctggttctatgcccgcttgaagaaggtctctctg	3013
Db	372	tttcgcgattctgcgcgcattctagacacattccccg	339

Search completed: September 14, 2002, 12:09:42
Job time: 93240 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2002, 01:19:31 : Search time 11758.7 Seconds
(without alignments)
7809.816 Million cell updates/sec

Title: US-09-595-526b-1_COPY_291_7094

Perfect score: 6804

Sequence: 1 atgcgtgtgtgctcctacgt.....gaagaatcctgtcctacag 6804

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues 27472414

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estov:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: qb_estl:*
10: qb_estl2:*
11: qb_hlc:*
12: qb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	692.4	10.2	809	10	BI754756 603025477
2	639.8	9.4	854	10	BI854140 603381449
3	543.6	8.0	837	10	BF160011 601768192
4	536.8	7.9	652	9	BB468374 BB468374
5	532.4	7.8	724	10	BG920223 602823304
6	526.6	7.7	720	10	BI248317 602966918
7	523.4	7.7	702	10	BI658600 603284335
8	489.8	7.2	878	10	BI182779 UNL-P-FN-
9	473	7.0	515	10	BE665489 154542 MA
10	459.4	6.8	515	10	BF094524 MR0-UT004
11	447.6	6.6	554	10	BF076332 225856 MA
12	433.2	6.4	518	10	BF042703 BP2500205
13	428.8	6.3	463	10	BE715104 MK3-HT073
14	425.4	6.3	427	10	BM153383 TCBAP2D11
15	424.2	6.2	998	10	BG678861 602624760
16	411	6.0	596	9	AA063753 m179h09.r
17	399.2	5.9	417	9	AM362709 RC6-CT028

18	366.2	5.4	412	9	AM380897
19	365.8	5.4	441	10	BF042938
20	364.6	5.4	662	10	BI468033
21	363.6	5.3	434	9	AM322680
22	362	5.3	422	10	BE329960
23	345.6	5.1	366	10	BF951740
24	340.8	5.0	717	10	BE742059
25	337	5.0	835	9	AM013420
26	327.6	4.8	351	10	BF928185
27	325.8	4.8	623	9	AM421371
28	321.2	4.7	352	10	BF892148
29	320.8	4.7	324	9	AM845151
30	319.8	4.7	736	9	AU135588
31	318.2	4.7	2640	11	U66691
32	315.6	4.6	551	9	A1733552
33	312.2	4.6	591	9	AL588915
34	309.2	4.5	782	10	BG775975
35	308.8	4.5	381	10	BE757461
36	301.4	4.4	786	10	BI736551
37	301.2	4.4	699	10	BI739256
38	299	4.4	363	9	AV647223
39	296.4	4.4	359	9	BB871492
40	286.2	4.2	549	10	BI976880
41	285.4	4.2	529	10	BC883616
42	285.4	4.2	589	10	BC936214
43	283.2	4.2	370	9	BB871749
44	281.2	4.1	353	9	BB871954
45	277.6	4.1	491	10	BF879888

ALIGNMENTS

RESULT 1
BI754756 809 bp mRNA linear EST 25-SEP-2001
603025477F1 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5195995 5',
DEFINITION
LOCUS
BI754756
VERSION
BI754756.1 GI:15746334
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 809)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11490 row: 1 column: 20
High quality sequence stop: 768.
location/Qualifiers
1. 809
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5195995"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1; Not:
Site: 2; Ecorev (destroyed): RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is Oligo-dT
primed and directionally cloned (Ecorev site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH MGC Library."

BASE COUNT 151 a 199 c 220 g 239 t

ORIGIN

Query Match 10.2%; Score 692.4; DB 10; Length 809;
Best Local Similarity 99.6%; Pred. No. 3.1e-180;
Matches 715; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Y 1828 ggcacgagagaagaactggtgtctatataatgcaacatgcccctatccctgttactgtat 1887
Db 1 GGCACCGAGAGAAACTGGTGTATATATCAACAGATGCCCTATCCCTTTACGTTGAT 60

Y 1888 gacatctcttcgagagatgagccgtcaatgccccctctctatgagcgtgacctgatt 1947
Db 61 GACATCTTTCTGGGGGATGAGCCGGTCAATGCCCTCTTCAATGACGCTGGCTGGATT 120

Y 1948 taactagtgctgtatcatcaaggacatcgatglatgagaaggagacaggtgaaagag 2007
Db 121 TACTACATGCTGCTGATCATCAAGGGGATGCTGATGAGAGAGGACAGCGGTGAAGAG 180

Y 2008 accatgagatcatgagccctgagacaacagatactctgtttagctggttcatagtaac 2067
Db 181 ACCATGGGATCATGGGCTGAGACACAGCATCTGCTTACGCTGCTTCAATGATGAC 240

Y 2068 ctaattctctctctgtgagcgtgagcgtgtagtgatcctctgaagttagaagacctg 2127
Db 241 CTCATTCCTCTCTGTGTGAGAGCGCTGCTGCTGATGCTGCTGAAGTAGAAGACCTG 300

Y 2128 ctgcccacagatgacccagcgtggtgtgtgtctctctgctgctggttctgtgtgaga 2187
Db 301 CTGCGCTACAGTATCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

Y 2188 atccgtgagctctcctgattagacacactctctccagagcacaactgagacagctgt 2247
Db 361 ATCTGAGAGTCTCTGATGATGACACACTCTCTCCAGAGCAACTGGGACAGACCTGT 420

Y 2248 gggagagatcatctactcaacagctgtagcctgacctgacctgtgtgtgtgagtagc 2307
Db 421 GGGAGGCTATCTATCTACAGCTGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

Y 2308 taactgagctcaacatcaacatctctgtagcctgtagcctgtagcctgtagcctgtag 2367
Db 481 TAGCTGGGCTTCAACATCAAGATCTTGGTACGCTGCTGCTGCTGCTGCTGCTGCTG 540

Y 2368 ggcctgtagtacttgcctctctttagagagagagagagagagagagagagagagag 2427
Db 541 GGCCTGAGTACTTGGCTCTTTTGAAGAGACAGGAGATGAGAGTGAAGTGAAGTGAAG 600

Y 2428 tttagagagctctgtg aggaagatgagcttcaatccacacactgtagctcagtagtgc 2486
Db 601 TTGAGAGTCTCTGAGAGAGAGATGGCTTCAATCTCACCACCTTGGCTGCTCAATGAT 660

Y 2487 gtttagacacttccctat-999gtatgagcctgtgacattgagagctgtcttccag 2543
Db 661 GTTGTACACCTCTCTCTATGAGGGGTATGACCTGATGAGCTGATGAGCTGCTTCCAG 718

RESULT 2

LOCUS B1854140 854 bp mRNA linear EST 10-OCT-2001

DEFINITION 60338144F1 NIH_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5388972 5', mRNA sequence.

ACCESSION B1854140

VERSION B1854140.1 GI:15994887

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 854)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D.

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: L1AM1191 row: b column: 13
High quality sequence stop: 801.
Location/Qualifiers

FEATURES

1..854
location/Qualifiers

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5388972"
/clone_id="NIH_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; NotI; Site-2: SalI. Cloned unidirectionally. Primer: Oligo dr. Average insert 2.5 kb. Library constructed by Life Technologies, catalog # 12018-016. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996). Note: this is a NCI_CGAP Library."

BASE COUNT 238 a 198 c 227 g 191 t

ORIGIN

Query Match 9.4%; Score 639.8; DB 10; Length 854;
Best Local Similarity 88.1%; Pred. No. 1.3e-165;
Matches 753; Conservative 0; Mismatches 97; Indels 5; Gaps 5;

Y 5750 tgacgaagatatataagaagaagagagagagagagagagagagagagagagagagag 5808
Db 4 TGACCAAGATCTATATGAG 63

Y 5809 cctctgtgtagtgccttctgagcctcctgagagatgagagagagagagagagagagag 5868
Db 64 CCTCCGAG 123

Y 5869 aagatgttaacagagagatcacactgttaccagagagagagagagagagagagagag 5928
Db 124 AAGATGCTGACTGAG 183

Y 5929 atctatcaaacatcatggaagatcatcagagacatgagcactgagcctcagttgagc 5988
Db 184 ATCTTATCAAAATTCATGAGAGTACACAGAACATGAGGCTACTGCTCACTTTGAGGCC 243

Y 5989 atcacagagctgttgcag 6048
Db 244 ATCACAG 303

Y 6049 ccaagagaagaagttggaagagttgtgagtgagtgagtgagtgagtgagtgagtgagtg 6108
Db 304 CCAGAAAAG 363

Y 6109 tatgagagaataatgctgctgatactatgagagagagagagagagagagagagagag 6168
Db 364 TATGAGAGAAAATATGACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 423

Y 6169 atgagcttgatcgagcggcctcctgtgtgttcttgatgagagagagagagagagag 6228
Db 424 ATGCGTTTGAATTTGGCGGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 483

Y 6229 cccaagagcggcgagttcttgatgagagagagagagagagagagagagagagagagag 6288
Db 6229 cccaagagcggcgagttcttgatgagagagagagagagagagagagagagagagagag

Db 484 CCTAAAGCCCGAGATTTCTGTGAATGTCGCCCTAAGCATGTGCAGGAGGAGATCT 543
QY 6289 gtagtgccttaactcctcaagtagtggaagaagtggaagctcttgcaatagatggcaatc 6348
Db 544 GTAGTCCTTACATTCATGATGATGGAAGATGTAAGCTCTTTGACAGGATGCGCATTA 603
QY 6349 atggtcaatggaagtggaagtggtgcttgcaagtgctcagacatcaaaaatagtggttga 6408
Db 604 ATGGTCATAGGAAGGTTACGAGTCCCTTGCCATGTCCACATCTAATAAAGATGCTCGGA 663
QY 6409 gatgtttatataatagtgtagtaacgaagtagtcaaccccgagacttgaaagctgtagcag 6468
Db 664 GATGTTATACAAATAGTTGTACGAATAGAGAGCTCCAAACCTGAGCTGAGGCTGTCCAG 723
QY 6469 gatctcttgagcttgacattcttcggaagtggtcttaaaaagaagaacccggaacatgcta 6528
Db 724 GA-GTCTTGGAGCTTGCGGTACCGGGAAGTGTCTAAAGAGAAA-ATCGACATGCTT 781
QY 6529 caatacacccttcacatctcattatctctctgccaagatatagaactctctccag 6588
Db 782 CAGTCCACAGCTTCACATC-TCTTGTATCTTACGCAAGATA-TCAGCATCTCTCCAGA 839
QY 6589 agcaaaaagcagactc 6603
Db 840 AGCAACAGCGGACTC 854

RESULT 3
BF160011 837 bp mRNA linear EST 30-OCT-2000
LOCUS 601768192P1 NCI_CGAP_Lu29 Mus musculus CDNA clone IMAGE:3987503 5',
DEFINITION mRNA sequence.
ACCESSION BF160011 GI:11040118
VERSION BF160011.1 GI:11040118
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 837)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9194 row: 9 column: 24
High quality sequence stop: 669.
Location/Qualifiers
1. 837
/organism="Mus musculus"
/strain="CZECH II (fetal)"
/db_xref="taxon:10090"
/clone="IMAGE:3987503"
/clone_1db="NCI_CGAP_Lu29"
/tissue.type="spontaneous tumor, metastatic to mammary."
Stem cell origin.
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 226 a 188 c 230 g 193 t
ORIGIN

Query Match 8.0%; Score 543.6; DB 10; Length 837;

Best Local Similarity 88.4%; Pred. No. 6, 1e-139;
Matches 647; Conservative 0; Mismatches 79; Indels 6; Gaps 5;

QY 5363 tgggtactctgcctcagtttgatgcatcaacagcgttgacttggaagaacagtg 6022
Db 13 TGGGCTACTGGCCCTCAGTGTGACGGCATCACAGGCTGCTGACTGGAAGACATGTGG 72
QY 6023 agttcttgccctcttg-agagagagtcaccagagaagaagttgcaagcttgtagtg 6081
Db 73 AGTCTTTGGCCCTCCTGTAGGGAGTCCAGAAAAGAAAGTGGCAAGTTGGTGAAATGG 132
QY 6082 gcaattcggaactgggagctctgtaagtagtagaagaataatgctgtaactatagtaga 6141
Db 133 GCAATTCGCAAACTGGGGCTGTGAAGTATGAGAAAAAATATGCGAATACTACAGTGGC 192
QY 6142 ggcacaaagcgaagctctctacagcaatgcttgcttgccgagctctctggtgtt 6201
Db 193 GGCAAACAAACGAAAGCTTCACAGCATGGCTTGAATTGGCGGCTCTCTGTGGTGT 252
QY 6202 ctgtagtaaccacacagagatgatcccaagcccgagctcttgtagaattgtgc 6261
Db 253 CTGATGACACCAACACAGCATGGCATGACCTTAACCCGGAGATTCTGTGGAA-TGTGCC 311
QY 6262 ctgaagtgtgtcaagagagagatcagtagtgcttacatctcatagtagtagaagatgt 6321
Db 312 CTAAG-CATGTCAAGGAGGAGGAGATCTGTAGTCTCTTACATCTCATAGTAGAAGATGT 370
QY 6322 gaagctcttgcaactagatggaatcatgtagtagaagtgtagtgcttgtagt 6381
Db 371 GAAGCTCTTGTACAAAGATGGCCATATGTCATATGGAAGGTTCAGGTGCTTGGCAGT 430
QY 6382 gtccagcatcttaaaaatagtttgtagatggttatcaatagttgtacgaatagcaggg 6441
Db 431 GTCCAACTCTGAAGAAACAGGTTTGAGATGTTATACATATGTTGTACATATGCGAGC 490
QY 6442 tccaaaccgagactgaaagcctgcagatctcttgacttgacttgacttgagtggt 6501
Db 491 TCCAAACCTGAGACCTGAACCTGTCCAGAGATGTTTGGACTTGGCTTCCAGAAAGTGC 550
QY 6502 ctaaaagaagaacccggaacatgctacataaccagcttccatctcatctctctg 6561
Db 551 CTAAGAGGAACAAACATCGAAGCATGCTTACATGATGATGATGATGATGATGATGAT 610
QY 6562 gccagatattcagatcctctccagagcaaaagcagctccaca-tagaagactctc 6620
Db 611 GCCAGATATTCAGCATCTCTCCAGAGCAAAAAGCAGCTCCACATTAGAAAGCTACTC 670
QY 6621 tgttctcagacaacacttgcaagaagttagtggaacttgccaaggaacaaagttaga 6680
Db 671 TGGTCTTCAGACAACTGACCAAGTAT--GTGAACCTGCCAAGGACCCCAAGTGATGA 728
QY 6681 tgaccacttaaa 6692
Db 729 TTGACCCCTTAA 740

RESULT 4
BB468374 652 bp mRNA linear EST 25-OCT-2001
LOCUS BB468374 RIKEN full-length enriched, 12 days embryo eyeball Mus
DEFINITION musculus CDNA clone D230019D04 3' similar to X75926 M.musculus abc1
RNA, mRNA sequence.
ACCESSION BB468374 GI:16427507
VERSION BB468374.2 GI:16427507
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 652)
Arakawa,T., Carlnet,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Komno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,

TITLE
JOURNAL
COMMENT

Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M., and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arawaka, T., et al. 2001)
 Unpublished (2001)
 On Jul 22, 2000 this sequence version replaced gi:9385563.
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp
 URL: http://genome.gsc.riken.go.jp/
 Carinacci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)
 Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Tameda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed capillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carinacci, P., Sugahara, Y., and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamakawa, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., and Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences *Mamm. Genome* 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
 cDNA library was prepared and sequenced in Mouse genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research contributed to prepare mouse tissues.

FEATURES
Source

Location/Qualifiers
 1. 652
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone_id="D230019D04"
 /clone_lib="RIKEN full-length enriched, 12 days embryo eyeball"
 /tissue_type="eyeball"
 /dev_stage="12 days embryo"
 /lab_host="DH10B"
 /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGCGCGGCACTGAGATTTTGTGTTTATVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGCTTATTAATTAATTCACCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FLX I."
 151 a 182 c 179 g 140 t

Query Match 7.98; Score 536.8; DB 9; Length 652;
 Best Local Similarity 89.04; Pred. No. 4e-13;
 Matches 580; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

3811 aacagagcgagccttcgggagagacagagctgtcttcgcccgttaactgaatgatgtc 3870
 1 AACGACGCGCTTTCGGGGACACACAGCTGTCTGACACCATTTTACGGAAGTATGCT 60
 3871 gctatccaaatgatcttcacatagaccagaaatccagagagagagactgtcagtgg 3930
 61 GTTATCCCAATGACTCTGACATGAGACCCGAATCCAGGAGACCGCTGACATGGG 140
 3931 atgatgtcaaaaggtctctcccaagtgaaggctggaacttccacagcaagattgtg 3990
 121 ATGAGCGCAAGGCTCTTACCACTGAAGGGCTGGAACTCCACGCAACAGTTTGTG 180
 3991 gccctttgtgaagaagactgaatgtccagagagagagctggaagagatttctcag 4050
 181 GCCCTTTGTGGAAGAGAGCTGCTGATTCAGACGAGCCGGAAGGTTTCTTGGTCAG 240
 4051 atgtcttcgaagtgtgtgtgtctgcatgtgctgtgtgtgtgtgtgtgtgtgtgtgt 4110
 241 ATTGTCTCTGCAAGCTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
 4111 ttgtgcaagtaacccagcctggaacttcagccctgagatgtacacagacagacatt 4170
 301 TTGGAAGATGACCCGACCTGAGACTTACGCTCGATATATATAGCATGTATACATT 360
 4171 gtccagcaatgatctctcttgagagacagaggaacccctggaactcttaagccctc 4230
 361 GTCAATATATATGTCTCCGAGAGCATGTGGCAACCCGAACTCTGATGTCTGACAAA 420
 4231 gacctgagcttcggagacccgtgtatgtgaagaaacccatccacagacgacctgca 4290
 421 GATCCAGGCTTTGGGAGACCCGCTGTATGGAAGAAACCAATCCAGATACCCCTTGT 480
 4291 gcaaggagagagagatgtgacacactgcccagttccacagacatcatgagaccttc 4350
 481 GCTGGGAGAGAGAGATGAGACATGACCCGCTCCGACAGACATCGTACCTTCAG 540
 4351 aatggagacttgagaaatgagagacaccccttcacactgcatgagtgtagcagcaaatc 4410
 541 AATGGAACCTGAGACATGAAGAACCCCTCACCTCGGCCAGTGTACATGACGAAATC 600
 4411 aagaagatgctgctgt 4462
 601 AAGAAGATGCTGCTGT 652

RESULT 5
 BG920223 724 bp mRNA linear EST 05-JUN-2001
 LOCUS 602822304F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4951320 5',
 DEFINITION mRNA sequence.
 ACCESSION BG920223
 VERSION BG920223.1 GI:14300699
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 724)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapds-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

QY 6293 tgcatacctcatagtaaggaagatgtggaagctcttgcacatagatgcaatcatg 6352
 Db 246 TCCCTACATCTCATATGATGGAAGATGTGAAGCTCTTTGACAAAGATGGCATATATG 305
 QY 6353 tcaatgaaggtcaggtcccttgaggtgacgacatctaaataaggttggagatg 6412
 Db 306 TCATGGAAGGTTCAGGTGCTTGGCAGTGTCCACATCTGAAAAACAGTTTGGAGATG 365
 QY 6413 gtatacaatagttgtaagaaatagcaggttccaaaccggagctgaagctgtccagat 6472
 Db 366 GTTATACAAATAGTTGACGAATAGCAGCTCCAAACCTGACCTGAGAGCTGTCCAGAGT 425
 QY 6473 tctt-tgagcttgatcttctggaagtgttctaaagaagaaccggagaatgctacaa 6531
 Db 426 TCTTGAGACTTCCGTTCCGGGAAGTGTCTTAAAGAGAAACATCGAAACATGCTTCAG 485
 QY 6532 taccacctccatctcatatcttcttgcgcagagataatca-gcatctctcccaag 6590
 Db 486 TACACAGTTCATCTCCTTGTCTATCTTACGACAGATTTTCAAGCATCTCTCCACAG 545
 QY 6591 caaaaagcagctccacatagaagaactactgttcttcagacaacaactgaccagat 6650
 Db 546 CAAAAAGCGATCCACATGAAACATCTGTCTCTCAGACACACTTGACCAAGTATC 605
 QY 6651 tgtgaac-ttggcagaagcgaagtgatgatgacacttaaaag--acctctcatlaa 6707
 Db 606 TGTGAACCTTTGCCAAGACCAAAAGTATGATGACCATTTTAAAGAGACTGTACATGCC 665
 QY 6708 caaaaaccagacagtagtgagcttgacagttccatctt 6750
 Db 666 AAAAAACACAGACAGTGTGGATGTGCGTCTTCACATCTCTT 708

RESULT 7
 B1658600 702 bp mRNA linear EST 12-SEP-2001
 LOCUS 603284335F1 NIH_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5328392 5',
 DEFINITION mRNA sequence.
 ACCESSION B1658600
 VERSION B1658600.1 GI:15572836
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 702)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgarbs-r@mail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
 Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM1833 row: f column: 09
 High quality sequence stop: 645.
 Location/Qualifiers
 1..702
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:5328392"
 /clone_1ib="NIH_CGAP_Mam4"
 /tissue_type="tumor, gross tissue"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: PCMV-SPORT6; Site:1; NCBI:
 Site:2; Salt: Cloned unidirectionally. Primer: Oligo dT.
 Average insert 2.5 kb. Library constructed by Life
 Technologies, catalog # 12018-016. Investigators providing

BASE COUNT 191 a 166 c 172 g 173 t
 ORIGIN
 Samples: Lothar Hennighausen/Priscilla Furth, NIH
 Reference for transgenic model: Li et al., Cell Growth and
 Differentiation 7, 3-11 (1996). Note: this is a NCI_CGAP
 Library."
 Query Match 7.7%; Score 523.4; DB 10; Length 702;
 Best Local Similarity 91.6%; Pred. No. 2.2e-133;
 Matches 565; Conservative 0; Mismatches 51; Indels 1; Gaps 1;
 QY 6189 tccgtgtgttcttgatgtaacccacagagatgattcccaaacccggagttct 6248
 Db 1 TCTGTGGTGTCTTGATGTAACCAACCAAGCATGAGCTTAAACCCGGAGATCTT 60
 QY 6249 gtgaatgtgcccctaaagtgtgcaaggaaggagatcagtagtgcatactcag 6308
 Db 61 GTGCAATGTGCTCCTTAAGCATTTGCAAGGAGGAGATGTGATCTTACATCTCATAG 120
 QY 6309 tatggaagaatgtgaagctcttgcaactagatgagcaatcatgtgtaagtgaagttcag 6368
 Db 121 TATGGAAGAATGTGAAGCTCTTTTACAGAGATGCCATATGTGTAATGGAAGTTTCAG 180
 QY 6369 gtgccttgaggtgtccagacactaaagaatagglttggagatgtatatacaatgtgt 6428
 Db 181 GTGCCCTTGACAGTGTCCACATCTGAAAMACAGGTTTGGAGATGTTATCATATAGTTGT 240
 QY 6429 acgaatagcaggtgtccaaaccggaactgtgacagattcttggacttgcatt 6488
 Db 241 ACGAATAGCAGGCTCCAAACCTGACCTGAAAGCTGTCCAGAGATCTTGTGAGACTTGGCTT 300
 QY 6489 tctgtgaaggtgtctaaagaagaacacggagaatgtctacaatcagcttccatttc 6548
 Db 301 TCCGGGAAGTGTCTTAAAGAGAAACATGCAAAATCTCTTACATGAGCTTCATCTTC 360
 QY 6549 attatctctctggcagagatattcagatctctctccagagcaaaagagactcagat 6608
 Db 361 CTGTGATCTGTAGCGAGATATTTCAGCATCTCTCCAGAGCAAAAAGGACTCCCAT 420
 QY 6609 agaaactactctgttctcagacaacacttgacaaatatttggacttggcagaaga 6668
 Db 421 AGAAGACTACTCTGTCTCTCAGACAACACTTGACCAAGTATTGTAACCTTGGCAAGGA 480
 QY 6669 ccaagtgatgatgacacttaaaagactctctattacaacaaacagagagatgaga 6728
 Db 481 CCAAGTGATGATGACCACTTAAAGGACCTGTCACTCCACAAAACCAACAGAGTTGTGA 540
 QY 6729 cgtgcagttctcatcttcttctacagagatga-gaaagtgaagaagaagatgataa 6787
 Db 541 TGTGGCGTCTTCATCTCTTTTGGCAGATGACGAAGACGAGCAAGATGATGAA 600
 QY 6788 gaatcctgttcatcagg 6804
 Db 601 GAATCCCGTTCACACAG 617

RESULT 8
 B1182779/c 878 bp mRNA linear EST 10-JUL-2001
 LOCUS B1182779
 DEFINITION UNL-P-FN-bp-c-01-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
 UNL-P-FN-bp-c-01-0-UNL 3', mRNA sequence.
 ACCESSION B1182779
 VERSION B1182779.1 GI:14657188
 KEYWORDS EST.
 SOURCE pig.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 878)
 Celatano,A.R., Johnson,R.K. and Pomp,D.
 Generation and sequence characterization of a normalized cDNA
 library from swine ovarian follicles

JOURNAL
COMMENT

Unpublished (2001)
Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
Email: dpomp@unl.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail.

Seq primer: M13 -29

FEATURES
Source

Location/Qualifiers

1..878
/organism="Sus scrofa"
/strain="University of Nebraska, Lincoln Swine Selection Lines"
/db_xref="taxon:9823"
/clone="UNL-P-FN-bp-c-01-0-0-UNL"
/dev_stage="ADULT"
/lab_host="DHI0B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UNL-P-FN library is a normalized library representing porcine ovarian follicles, ranging between 2.0 to 10.0 mm in diameter, collected during 7 days of the follicular phase of the pig estrous cycle. This library was derived from the library UNL-P-F2. The tag is a string of 5-6 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996."
TAG_SEQ=None found"
BASE COUNT 212 a 219 c 184 g 258 t 5 others
ORIGIN

Query Match 7.2%; Score 489.8; DB 10; Length 878;
Best Local Similarity 89.4%; Pred. No. 5.3e-124;
Matches 550; Conservative 0; Mismatches 62; Indels 3; Gaps 2;

QY 6190 cctgtgtgtgttcttgatgaaccacacagatgatacccaagcccggtcttg 6249
DB 771 CCCGTGTCTTCTTGATGACCCACACAGGCAATGATCCAAAGCCCGGATCT-- 713
QY 6250 tggaaattgtccctaagtgttcaagagagagatcatgattctcatatcatg 6309
DB 714 GTGATTTGTGCCCTTAAGTATGCTCAAGAGAGAAATGATTTCTTACATCTCATACT 655
QY 6310 atggaagaatgtgaagctccttgcactagatgcaatcatgltcaatggaaggttcagg 6369
DB 654 ATGGAAGATGTGAAGCTCTTTGCACACAGATGCAATTAATGTCATGCGAGTTCCAGG 595
QY 6370 tgcctgtgcagtgatcagatcctaaataatggttgagatggttatacatatg 6429
DB 594 TGTCTTGGAGTGTCCACATCTGAATAATAGTTGAGATGTTATACGATAGTTGTA 535
QY 6430 caataagcagaggtccacacccgactgaagcctgtccaggaattcttggacttcattt 6489
DB 534 CGAATATGACAGGTCACACCTGACCTGACACCGGTCAGAGACTTTTGGACATGCCCTTT 475
QY 6490 cctggaagtgttctaaagaagaacacggaacatgltacataatacagcttccatctca 6549
DB 474 CCGGAGAGCGTCTGAAGAGAGACCGGAACATGTCAGTACACAGCTTCCCTGCTCC 415
QY 6550 tatattctctgtccagagatattcagcatcctctccagagacaaaagcagctcacata 6609
DB 414 CTGTCTCTCCCTGGCCAGGATATTAAGCGTCTTCCAGAGCAAAAACGACTCCACATA 355
QY 6610 gaagactactctgttctcagacacacttgacacagatatttgtaacttggccaagagac 6669

DB 354 GAAGACTACTGACGTTTCTTCAGACACACTTGACCAAGTATTGTAACCTTGGCAAGAC 295

QY 6670 caaagtgaatgatgacacacttaaaagacctctcatcacaaaacacagacagatgagc 6729
DB 294 CAAAGTATGATGACCACTTAAGGAGACCTGTCATTAATATAAAGACAGACAGTAGTGAT 235

QY 6730 gtgcagattctcactcttcttctacagagatgagaagtgaaagactatgataaga 6789
DB 234 GTTCTGTTCTCACATCTTTCTTGACGAGATGAGAAAGTGAAGAGTTACGTGAGGA 175

QY 6790 atccgtgtcacaag 6804
DB 174 ATCCTGTTCTCATGG 160

RESULT 9

BE665489 562 bp mRNA linear EST 25-APR-2001
LOCUS BE665489 154542 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BE665489
ACCESSION BE665489 GI:10026080
VERSION
KEYWORDS
SOURCE
ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 562)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Petta,G., Holt,I., Karayancheva,S., Liang,F., Quackenbush,J. and
Keefe,J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013

JOURNAL
MEDLINE

COMMENT

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68333-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred
v0.960904.e. Vector identified by cross-match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: ACGAAGACCTATGACCAT
BACKWARD: GTTTCACGACGACG
Plate: 67 row: B column: 19
Seq primer: ATTATGCTACACTATAG.

FEATURES

Source

Location/Qualifiers
1..562
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
/tissue_type="pooled"
/lab_host="DHI0B"
/note="Vector: PCMV SPORT6; Site 1: XbaI; Site 2: XhoI;
Library made from pooled tissue from day 20 and day 40
embryos."
BASE COUNT 139 a 134 c 159 g 130 t
ORIGIN

Query Match 7.0%; Score 473; DB 10; Length 562;
Best Local Similarity 91.0%; Pred. No. 1.8e-119;
Matches 503; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 3531 catgatgtctctgtactctcacaactcattcagaagaacatgtctgaagcccggtgtgt 3590
DB 10 CATTGATGTCTCTGTATCTCCAAACCTCATCAGGAACATGTCGAGGCCCGGCTGGT 69

QY 3591 ggaagacataggagcagctgacctaagtgtgctgcatatgaagctgcaagagagagc 3650
 |||||||
 Db 70 ggaagacataggagcagctgacctaagtgtgctgcatatgaagctgcaagagagagc 129
 |||||||
 QY 3651 ctgttggaactcttcacagatgatgacggcctcgaagcctggagcattctagta 3710
 |||||||
 Db 130 ctgttggaactcttcacagatgatgacggcctcgaagcctggagcattctagta 189
 |||||||
 QY 3711 tggcattcagagacgacccctggaagaataatctcctcaaggtggccgaagagatgggt 3770
 |||||||
 Db 190 cggcattcagagacgacccctggaagaataatctcctcaaggtggccgaagagatgggt 249
 |||||||
 QY 3771 ggtatgtgagacctaagatggttaccttgcagcagaagaagcggcctgggga 3830
 |||||||
 Db 250 ggtatgtgagacctaagatggttaccttgcagcagaagaagcggcctgggga 309
 |||||||
 QY 3831 caagcagaagctgtctgcgcgcgttcacatgaagatgctgctgcatccaatgattctga 3890
 |||||||
 Db 310 caagcagaagctgtctgcgcgcgttcacatgaagatgctgctgcatccaatgattctga 369
 |||||||
 QY 3891 catagaccagaaatccagagagacgaactgtctcagtgagatgagcgaagagtccta 3950
 |||||||
 Db 370 catagaccagaaatccagagagacgaactgtctcagtgagatgagcgaagagtccta 429
 |||||||
 QY 3951 ccagagtgaaagagctggaagaactacacagaagaagtttggcccttttggaagaagact 4010
 |||||||
 Db 430 ccagagtgaaagagctggaagaactacacagaagaagtttggcccttttggaagaagact 489
 |||||||
 QY 4011 gctaattgcagagagagagctggaagaagattttgtctcagatgtgttgcagctgtgt 4070
 |||||||
 Db 490 gctaattgcagagagagagctggaagaagattttgtctcagatgtgttgcagctgtgt 549
 |||||||
 QY 4071 tgtctgattgtcc 4083
 |||||||
 Db 550 tgtctgattgtcc 562
 |||||||

RESULT 10
 LOCUS BF094524 515 bp mRNA linear EST 19-OCT-2000
 DEFINITION MR0-UT0047-170900-202-f10 UT0047 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF094524
 VERSION BF094524.1 GI:10900234
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 515)
 REFERENCE
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Birones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baiz,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.U.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT
 CONTACT: Simpson A.U.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0-UT0047-170
 900-202-f10&ts=2000-09-17&ft=1)
 Seq primer: puc 18 forward

High quality sequence start: 15
 High quality sequence stop: 515.
 Location/Qualifiers
 1. 515
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="U0047"
 /dev_stage="Adult"
 /note="Organ: uterus-tumor; Vector: puc18; Site_1: Smal;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 143 a 125 c 132 g 115 t
 ORIGIN

Query Match 6.8%; Score 459.4; DB 10; Length 515;
 Best Local Similarity 98.4%; Pred. NO. 1e-115; 6; Indels 2; Gaps 2;
 Matches 485; Conservative 0; Mismatches 6;

QY 1049 ctacacactctactgcaatgatattgataagaatttgagctcagctcctctccgca 1108
 |||||||
 Db 15 ctacacactctcttactgcaatgatattgataagaatttgagctcagctcctctccgca 74
 |||||||
 QY 1109 ttatctgaaagctctgaaagcgcgtgtctgttgggaagatcctgtatcacctgacac 1168
 |||||||
 Db 75 ttatctgaaagcctctgaaagcgcgtgtctgttgggaagatcctgtatcacctgacac 134
 |||||||
 QY 1169 cagccacaagcagatgacatgagctgagtgaaacagacccctcgaagactgctgttc 1228
 |||||||
 Db 135 cagccacaagcagatgacatgagctgagtgaaacagacccctcgaagactgctgttc 194
 |||||||
 QY 1229 atgacttgaaagcagatgagtgaaagcagcccaagatcttgacattatgagagaa 1288
 |||||||
 Db 195 atgacttgaaagcagatgagtgaaagcagcccaagatcttgacattatgagagaa 254
 |||||||
 QY 1289 gccaaagaatgagcctgtctcggagatgctgttgagacagcaggaagaaatgacatttgg 1348
 |||||||
 Db 255 gccaaagaatgagcctgtctcggagatgctgttgagacagcaggaagaaatgacatttgg 314
 |||||||
 QY 1349 aacagcagtgatgagctgagcttgaattggaagcccaagacatcgttgccttttggccaagc 1408
 |||||||
 Db 315 aacagcagtgatgagctgagcttgaattggaagcccaagacatcgttgccttttggccaagc 374
 |||||||
 QY 1409 acccagagatgctcagctcagctaatgttctgtgtacacttgagagagacttcaag 1468
 |||||||
 Db 375 acccagagatgctcagctcagctaatgttctgtgtacacttgagagagacttcaag 434
 |||||||
 QY 1469 agactaa-ccaggaatccgagacatattctgcttcagtgagtgcttcaacctgaacaag 1527
 |||||||
 Db 435 agactaa-ccaggaatccgagacatattctgcttcagtgagtgcttcaacctgaacaag 493
 |||||||
 QY 1528 ctagaaccataag 1540
 |||||||
 Db 494 ctagaaccataag 506
 |||||||

RESULT 11
 LOCUS BF076322 554 bp mRNA linear EST 25-APR-2001
 DEFINITION 225856 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BF076322
 VERSION BF076322.1 GI:10870075
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 554)

AUTHORS

Smith, T.P.L., Grosse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrnenkrug, S.C., Bennett, G.L., Heaton, M.P., Iaegreid, M.W., Rohrer, G.A., Chitto-McKown, C.G., Perle, G., Holt, I., Karameycheva, S., Liang, R., Quakenbush, J. and Keele, J.W.

TITLE

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL MEDLINE
Genome Res. 11 (4), 626-630 (2001)

COMMENT

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGTCAGCAGG

Plate: 86 row: N column: 9
Seq primer: ATTAGTGACACTATAG.

FEATURES

Location/Qualifiers

1..554

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 2BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

BASE COUNT 138 a 146 c 146 g 124 t
ORIGIN

Query Match 6.6%; Score 447.6; DB 10; Length 554;
Best Local Similarity 89.2%; Pred. No. 2e-112; Indels 1; Gaps 1;

Matches 494; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

QY 774 aaaaacattgctcagctcgtgagctcgtgcccagagcgttcagcatgagaagctg 833

DB 1 AAAAGCTTGTGTGATAGTCTTGGAATCTGGCCCAAGAGCTTTAGCATGAGAGCTG 60

QY 834 gactgacatgacagagagagatgcttctgaccaaagtgaacagctccactccac 893

DB 61 GAGTGACATGGCGGAGAGGTGATGTTCTGACCAACGTGAACAGCTCCAGCTCTCCAC 120

QY 894 ccaaatctaccagctgctgtctcgtatctctgctggagcatcccgagagaggggctgaa 953

DB 121 CCGATCTACCGAGCGCGTCCGATCTCCGCCCATCCGAGGCGGGGCGCTGAA 180

QY 954 gatcaagctctcaactggtatgagacaacaactcaagaacccctcttgagagcaatg 1013

DB 181 GATCAAGTCCCTTAATCTGTGAGAGGACAACTCAAGGCCCTTTGGAGGACAGG 240

QY 1014 cactgaggaagatgctgaaacctctatgacaactctacaactcctactgcaatgatt 1073

DB 241 CACGAGAGAGAGCGTGGCAGCTGTATGACACTTACATCTCTTATGCAATGATTT 300

QY 1074 gatgaagaattgagatctcagctcctctccgcatlactctggaagctctgaagcgcgt 1133

DB 301 GATGAAGAATCTGAGATCCAGTCTCTTCTCGCATCATATGAGAAAGCTCAACCCCT 360

QY 1134 gctcgttggaggaagatcctgatacacctgaacactcagccagcagagctgctga 1193

DB 361 TCTTTGTTGAAAGATCTGTATACACTGACACTCCAGTCACAGGCGGCTTATGACTGA 420

QY 1194 ggtgaacaagaacctccagaa-cgtgctgtgtctcatgatctggaagcatgtggagg 1252

DB 421 GGTGAATAAGACCTTCAGAGAACCTGCTGTCTTTCATGATCTAGAAGCATGTGCAAG 480

OY 1253 aactcagcccaagatctgagcttcctgagaaacagcaagaatgagctgtccgga 1312

DB 481 AGCTCAGGCCCAAGATCTGGACCTTTATGGAGACGACCTCAGAAATGAGACTTGTCCGA 540

OY 1313 tgcctgttgagacgc 1326

DB 541 CACTGTTGACAGC 554

RESULT 12

BF042703

LOCUS 518 bp mRNA linear EST 10-OCT-2000

DEFINITION BP250020B10D9 Soares normalized bovine placenta Bos taurus cDNA

ACCESSION BF042703 GI:10759758

VERSION BF042703.1

KEYWORDS EST.

SOURCE cow.

ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 518)
Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson, J.H.

Bovine ESTs
Unpublished (2000)
Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA

Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534

to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trim: g.

Cross-match from Washington University Genome Center PHRAP suite. This sequence is vector free and at least 200 bp in length.

PCR Primers
FORWARD: TAATGACATCACTATGCG
BACKWARD: ATTAACCTCCTCAATGAG

Insert Length: 518 Std Error: 0.00
Plate: BP250020B10 row: D column: 9

Seq primer: AGCGATTAACAATTCACACAGGA
High quality sequence stop: 518.

location/Qualifiers

1..518

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone="BP250020B10D9"

/clone_lib="Soares normalized bovine placenta"

/sex="female"

/lab_host="DH10B"

/note="Organ: Placenta; Vector: pT73Pac; Site_1: EcoRI; Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806."

BASE COUNT 122 a 121 c 153 g 122 t

ORIGIN

Query Match 6.4%; Score 433.2; DB 10; Length 518;
Best Local Similarity 89.8%; Pred. No. 1.9e-108;

Matches 465; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

OY 1468 gagactaacaggaatccggaacatctcgtctcatgagagtgctgaacctgaacaag 1527

DB 1 GAGACCAACAGGCAATCCAGCACATCTCTGTTTCATGAGGTGTCAATCTGAACAAG 60

OY	1528	cttagaaccccatgagcaacagaagctcggcctcatcaacaatccatgagctgctgagtag	1587
Db	61	CTAGAACCAAGTACGCACAGAGGTTCTGCTCATCAACAAAGTCCATGGAGGCTTTGGATGAG	120
OY	1588	aggaagcttcgagctgtagctgtagtctcaatctggaattaccccaagcagcatgagctggcc	1647
Db	121	CGCAAAATTCGGGGCTGGGGTAGTGTTCACTGGGAATTGGCTCCGGGACGGCTGAGTTACGG	180
OY	1648	catcatgtcaagttacaagaatccgaatgagacattgacaatgtagagagagcaataaatc	1707
Db	181	CATCATGTCAATACAAAGATCCGAGATGACATTTGACAAAGTGAGAGGACGATATAAGATC	240
OY	1708	aaggaatggtagctaggagaccctgctccctgagcttgaccctcttgagagacatgctgtagctc	1767
Db	241	AAGGACGGGTACTGGGAGCCCTGCTCGCTGGGCTGACCCCTTTGAACATATGCGGTATGTC	300
OY	1768	tgggggagcttcgcgctaactcagaatgtagtggtagagcaagcaatcaagagtgctgacg	1827
Db	301	TGGGAGGGCTTCGCTTACTTTGCAGGATGTGGTGAGCAGCAATCATCAGSGTGGCTGAGG	360
OY	1828	ggcacccgagaaacaaactggtgtctatatagacaagatgcccataccctgtaacgttgt	1887
Db	361	GGCACAGAGAGAAAACTGGCGCTGTACATGACGCAAGATCCCTTACCCCGTTATGTTGAT	420
OY	1888	gacacctctctgcgggtatagaccggtcaakgcccctctcaatgaagcttgagctggatt	1947
Db	421	GACATCTTCCTCGGGGTATGAGCCGGTCCATGGCCCTCTTCATGACGCTGGCGCTGATC	480
OY	1948	tactcagtgagctgtatataatcaaggacatcggtatatga	1995
Db	481	TACTCGTGAGCTGTGATCATCAAGGAGCAATGTGTACGA	518

RESULT	13
BEST15104	
LOCUS	463 bp mRNA linear EST 12-SEP-2000
DEFINITION	MRA-HU0737-060700-004-B09 HT0737 Homo sapiens CDNA, mRNA sequence.
ACCESSION	BE715104
VERSION	BE715104.1 GI:10103369
KEYWORDS	EST.
SOURCE	human.

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 463)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G.

Ludwig Institute for Cancer Research
Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=6t2-MR3-HT0737-0660>)
700-004-B09a6t3=2000-07-06&ct=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 461.
Location/Qualifiers
1..463

Query Match	Best Local Similarity	Matches	Score	DB	Length
4480	97.3%	436; Conservative	428.8; Pred. No. 2.9e-107;	6	463;
/organism="Homo sapiens"					
/db_xref="taxon:9606"					
/clone_lib="HT0737"					
/dev_stage="Adult"					
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."					
low stringency conditions."					
BASE COUNT 147 a 105 c 111 g 100 t					
ORIGIN					
4480	gcaagatccttcgaagacctgacgaagaacatttcgattatctgtgtgaagcgtat	4539			
6	gtacagatccttcgaagacctgacgaagaacatttcgattatctgtgtgaagcgtat	65			
4540	gtgcagatccttcgaagacctgacgaagaacatttcgattatctgtgtgaagcgtat	4599			
66	gtgcagatccttcgaagacctgacgaagaacatttcgattatctgtgtgaagcgtat	125			
4600	gaccttccttcgagtgatgaatccttcgaagaccttcctgcagatcgaagatgat	4659			
126	ggctcttcccgagggtgtgagatgattctgaagcacttctccgagtcgaagatgat	185			
4660	gccatcaaacaaatgaagaacacctgaagctgtgcgaagacagttctgcagatgat	4719			
186	gccatcaaacaaatgaagaacacctgaagctgtgcgaagacagttctgcagatgat	245			
4720	ctcaacagcttgggaagattatgaagaagcttggaaccacaaataatgtgaagtg	4779			
246	ctcaacagcttgggaagattatgaagaagcttggaaccacaaataatgtgaagtg	305			
4780	ttcaatacaagaagctgtgcatgcaatcagctcttctcgtgaatgtcatcaaatgat	4839			
306	ttcaatacaagaagctgtgcatgcaatcagctcttctcgtgaatgtcatcaaatgat	365			
4840	ctccggggcaaacctgtcaaaagggagagaacctgacattatgtgaattacgcttcaat	4899			
366	ctccggggcaaacctgtcaaaagggagagaacctgacattatgtgaattacgcttcaat	425			
4900	catccctggaatctcaccgaagcagc	4927			
426	catccctggaatctcaccgaagcagc	453			
RESULT 14					
LOCUS	BM153383	427 bp	mrna	linear	EST 30-NOV-2001
DEFINITION	TCAP2PD11628 Pediatric pre-B cell acute lymphoblastic leukemia				
	Baylor-HESC project=TCBA Homo sapiens cDNA clone TCBA1162, mRNA				
	sequence.				
ACCESSION	BM153383				
VERSION	BM153383.1	GI:17178477			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
	1 (bases 1 to 427)				
	Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr.,				
	Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.				
TITLE	Pediatric leukemia cDNA Sequencing Project (2001)				
COMMENT	Unpublished (2001)				
	Contact: Dr. Judith F. Margolin				
	Texas Children's Cancer Center and Human Genome Sequencing Center				
	at Baylor College of Medicine				

RESULT 14	
LOCUS	BM153383
DEFINITION	BM153383 427 bp mRNA linear EST 30-NOV-2001
ACCESSION	TCAP2P11628
VERSION	Pediatric pre-B cell acute lymphoblastic leukemia
KEYWORDS	Baylor-HESC project-TCBA Homo sapiens CDNA clone TCAP1162, mRNA sequence.
SOURCE	BM153383
ORGANISM	BM153383.1 GI:17178477
REFERENCE	EST.
AUTHORS	human.
TITLE	Homo sapiens
JOURNAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
COMMENT	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
	1 (bases 1 to 427)
	Wei, Y., Tsang, Y. T. M., Mei, G., Ku, J. M., Ali-Osman, F. R., Jr.,
	Gunnarntne, P. H., Muzny, D. D., Bouck, J. J., Gibbs, R. A. and Margolin, J. F.
	Pediatric Leukemia CDNA Sequencing Project (2001)
	Unpublished (2001)
	Contact: Dr. Judith F. Margolin
	Texas Children's Cancer Center and Human Genome Sequencing Center
	at Baylor College of Medicine

COMMENT
Completed (2001)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine

1102 Bates, MC3-3320 Houston, TX 77030, USA
 Tel.: 832-824-4536
 Fax: 832-825-4038
 Email: clonesetxxx.org
 Seq primer: M13 primer

FEATURES

source
 1. 427
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="TCBAP162"
 /clone_lib="Pediatric pre-B cell acute lymphoblastic
 leukemia Baylor-HSC project-TCBA"
 /sex="male"
 /tissue_type="Leukophoresis"
 /cell_type="pre-B cell"
 /dev_stage="pediatric 2 years"
 /lab_host="DH10B"
 /note="Vector: lambda psb; Site_1: BamHI; Site_2: EcoRI;
 First strand cDNA was primed with an anchored
 XhoI-oligo(dT) primer [5'GAGAGCTGACGCGCGGAGAG(T)VN
 3'; V-A/C/G; N-A/C/G,T] and then dg tailed. Second strand
 was primed with a BamHI-dC primer
 [5'ACAGAGCTCGGATCCGCGCGCGCATATATATAT(C) 3'].
 Double-stranded cDNA was then digested with BamHI and XhoI
 and directionally cloned into the BamHI and SalI sites of
 lambda psb vector. Library went through one round of
 normalization. Library was constructed by Mei Yu at RIKEN
 Itoh W, Nagaoka S, Sasaki N, Okazaki Y, Ohsumi T,
 Schneider C, Hayashizaki Y, High efficiency selection of
 full-length cDNA by improved biotinylated cap trapper.,
 DNA Res 4: 1, 61-6, Feb 28, 1997"]

BASE COUNT 85 a 104 c 126 g 112 t
 ORIGIN

Query Match 6.3%; Score 425.4; DB 10; Length 427;
 Best Local Similarity 99.8%; Pred. No. 2.4e-106;
 Matches 426; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1740 tgaaccccttgaggacatgctgctgaggggcttcgctacttgagatgtgt 1799
 |||||||
 Db 1 tgaaccccttgaggacatgctgctgaggggcttcgctacttgagatgtgt 60
 QY 1800 ggaagcaggaatcatcagctgctgaggggacccggaagaactggtgtatata 1859
 |||||||
 Db 61 ggaagcaggaatcatcagctgctgaggggacccggaagaactggtgtatata 120
 QY 1860 acagatgcctatccctgttactgtatgacatcttctgcgggtgatatgacat 1919
 |||||||
 Db 121 acagatgcctatccctgttactgtatgacatcttctgcgggtgatatgacat 180
 QY 1920 gccctcttcatgagcgtgctgctgatttaccagtgtgtgatacaaaaggcatgt 1979
 |||||||
 Db 181 gccctcttcatgagcgtgctgctgatttaccagtgtgtgatacaaaaggcatgt 240
 QY 1980 gtaatgaagaagcagcgtctgaagaagacatgcatgagggccttgagaacacat 2039
 |||||||
 Db 241 gtaatgaagaagcagcgtctgaagaagacatgcatgagggccttgagaacacat 300
 QY 2040 actctggtttagctgttcatatagatgacatcttctcttctgtgagcgtgctgt 2099
 |||||||
 Db 301 actctggtttagctgttcatatagatgacatcttctcttctgtgagcgtgctgt 360
 QY 2100 agtgtgtacatccgaagttagaagaactgtgcttaccatagatgctcaggtgtttgt 2159
 |||||||
 Db 361 agtgtgtacatccgaagttagaagaactgtgcttaccatagatgctcaggtgtttgt 420
 QY 2160 cttctctg 2166
 |||||||
 Db 421 cttctctg 427

RESULT 15
 BG678861 998 bp mRNA linear EST 01-MAY-2001
 LOCUS 602624760F1 NCL_CGAP_Skn4 Homo sapiens cDNA IMAGE:4749735 5',
 DEFINITION mRNA sequence.

ACCESSION BG678861 GI:13910258
 VERSION BG678861
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 998)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LHAM10603 row: 9 column: 16
 High quality sequence stop: 860.

FEATURES

source
 1. 998
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4749735"
 /clone_lib="NCL_CGAP_Skn4"
 /tissue_type="squamous cell carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: skin; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCL_CGAP Library."

BASE COUNT 285 a 233 c 244 g 236 t
 ORIGIN

Query Match 6.2%; Score 424.2; DB 10; Length 998;
 Best Local Similarity 93.8%; Pred. No. 9.3e-106;
 Matches 485; Conservative 0; Mismatches 28; Indels 4; Gaps 4;

QY 33 gtggaagaacctcattcagaagaagaacaacatgacgttactggaagtgtcgt 92
 || |||||
 Db 169 gagaagaagacgcaaacacaaagtgaaacagtgacgtgctggaagtgccctg 228
 QY 93 gccctattatcttccgtatccgtatctctgttcggtgagtcacccacatagaca 152
 |||||||
 Db 229 gccctattatcttccgtatccgtatctctgttcggtgagtcacccacatagaca 288
 QY 153 acaatgaatgcatcttccaaataagcattccctcgcaggaacacatctctgttca 212
 |||||||
 Db 289 acaatgaatgcatcttccaaataagcattccctcgcaggaacacatctctgttca 347
 QY 213 ggggaattatctgtatgcaacaacccctgttccgttaccggaatccctgaggagctcc 272
 |||||||
 Db 348 ggggaattatctgtatgcaacaacccctgttccgttaccggaatccctgaggagctcc 407
 QY 273 cggagttgttgaaa-ccttaacaataccatttggctcgcgttctcagaatgctgga 331
 |||||||
 Db 408 cggagttgttgaaa-ccttaacaataccatttggctcgcgttctcagaatgctgga 467
 QY 332 ggtctcttllataagccagaagaacacagcagatggaagacatgcaaaagtcttgaa 391
 |||||||
 Db 468 ggtctcttllataagccagaagaacacagcagatggaagacatgcaaaagtcttgaa 527
 |||||||
 QY 392 cattaagcagatcaagaataccagctc-aaacttgaagctcaagaattccgtgtgac 450
 |||||||

```

Db 528 CATTACGACAGATCAGAAATCCAGCTCAAAACTTGAGCTTCAGATTTCCTGGTGAC 587
QY 451 aa- tgaacctctctggtctcctatatacaaacctctctctcccaagtlactglgga 509
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 588 AATTGAACCTTCTCTGTGGTTCTCTGATCACAACCTCTCTCTCCCAAAGCTTACTGTGGA 647
QY 510 caagatctgagggctgatatcatlctcccaagta 546
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 648 CAAGATGCTGAGGCTGATGTCAATTCACACAAGTA 684

```

Search completed: September 14, 2002, 01:20:00
 Job time: 54603 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2002, 12:54:11 : Search time 20.07 Seconds
(without alignments)
2751.683 Million cell updates/sec

Title: US-09-595-526B-2

Sequence: 1 MACWPQLLLMKMLFFRRR.....VDVAVLTSFLQDEKESYV 2261

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6931	58.8	1375	3	US-08-665-259-26 Sequence 26, Appl
2	6931	58.8	1375	3	US-08-762-500-26 Sequence 26, Appl
3	3129.5	26.5	1457	3	US-08-665-259-27 Sequence 27, Appl
4	3129.5	26.5	1457	3	US-08-762-500-27 Sequence 27, Appl
5	2642.5	22.4	1684	3	US-08-665-259-25 Sequence 25, Appl
6	2642.5	22.4	1684	3	US-08-762-500-25 Sequence 25, Appl
7	2642.5	22.4	1704	3	US-08-762-500-75 Sequence 75, Appl
8	340.5	2.9	1280	2	US-08-583-276-19 Sequence 19, Appl
9	339.5	2.9	1280	6	5206352-4 Patent No. 5206352
10	337	2.9	1279	2	US-08-784-649A-2 Sequence 2, Appl
11	330.5	2.8	1280	2	US-08-752-447-2 Sequence 2, Appl
12	311	2.6	1275	3	US-09-120-513-2 Sequence 2, Appl
13	311	2.6	1275	4	US-09-450-105-2 Sequence 2, Appl
14	301.5	2.6	1302	1	US-08-232-537-2 Sequence 2, Appl
15	288.5	2.4	1349	2	US-08-612-734B-2 Sequence 2, Appl
16	285.5	2.4	233	4	US-09-627-376-12 Sequence 12, Appl
17	283	2.4	1408	1	US-08-612-521-2 Sequence 2, Appl
18	275	2.3	1307	1	US-08-395-246C-2 Sequence 2, Appl
19	261	2.2	1334	2	US-08-996-545-2 Sequence 2, Appl
20	261	2.2	1334	4	US-09-328-320-2 Sequence 2, Appl
21	250	2.1	376	2	US-08-997-080-89 Sequence 89, Appl
22	250	2.1	376	2	US-08-997-362-89 Sequence 89, Appl
23	250	2.1	376	3	US-08-873-970-89 Sequence 89, Appl
24	250	2.1	376	4	US-09-095-855-89 Sequence 89, Appl
25	250	2.1	376	4	US-09-324-542-89 Sequence 89, Appl
26	240	2.0	1528	1	US-08-463-092B-6 Sequence 6, Appl
27	240	2.0	1528	2	US-08-462-109A-6 Sequence 6, Appl

28	240	2.0	1528	2	US-08-460-907B-6 Sequence 6, Appl
29	240	2.0	1528	3	US-08-463-179A-6 Sequence 6, Appl
30	240	2.0	1528	3	US-08-461-384B-6 Sequence 6, Appl
31	230	1.9	711	3	US-08-772-270A-12 Sequence 12, Appl
32	224.5	1.9	1621	4	US-08-972-927-3 Sequence 3, Appl
33	224.5	1.9	1622	4	US-08-972-927-6 Sequence 6, Appl
34	221	1.9	1531	1	US-08-463-092B-4 Sequence 4, Appl
35	221	1.9	1531	2	US-08-463-092B-4 Sequence 4, Appl
36	221	1.9	1531	2	US-08-460-907B-4 Sequence 4, Appl
37	221	1.9	1531	3	US-08-463-179A-4 Sequence 4, Appl
38	221	1.9	1531	3	US-08-461-384B-4 Sequence 4, Appl
39	218	1.8	244	4	US-08-919-573-2 Sequence 2, Appl
40	218	1.8	244	4	US-08-919-573-2 Sequence 2, Appl
41	217.5	1.8	1476	4	US-09-256-703-2 Sequence 2, Appl
42	217.5	1.8	1480	1	US-07-637-621-2 Sequence 2, Appl
43	217.5	1.8	1480	2	US-08-951-912-2 Sequence 2, Appl
44	217.5	1.8	1480	2	US-08-469-461-2 Sequence 2, Appl
45	217.5	1.8	1480	3	US-07-890-609-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-665-259-26
Sequence 26, Application US/08665259
Patent No. 6028173
GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy C.
APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Klinger, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES.
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: One Mountain Road
CITY: Framingham
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,259
FILING DATE: 17-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IGS-9.1
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-665-259-26
Query Match 58.8%; Score 6931; DB 3; Length 1375;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1336; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

QY 887 CMEEPHTHLKLGVSIONLVKYYROGKVAVDCLALNFYEGOTTSLFGNGAGKTTMTSL 946
 DB 1 CMEEPHTHLRIGVSIONLVKYYROGKVAVDCLALNFYEGOTTSLFGNGAGKTTMTSL 60
 QY 947 TGLFPTSTAYILKIDRSEMSITRONLGVCPHONVFLFDMLTVEHMFARLKGJSEK 1006
 DB 61 TGLFPTSTAYILKIDRSEMSITRONLGVCPHONVFLFDMLTVEHMFARLKGJSEK 120
 QY 1007 HVAKEEMOALDVLGPPSKKLKSTQSLSGMOKRLSVALAFVSGKVVLDEPTAGVDPY 1066
 DB 121 HVAKEEMOALDVLGPPSKKLKSTQSLSGMOKRLSVALAFVSGKVVLDEPTAGVDPY 180
 QY 1067 SRGIMELLKXROGRTIILSHHDEADYIGDRITAIISHGKLCVGSGLFLKNOLGXY 1126
 DB 181 SRGIMELLKXROGRTIILSHHDEADYIGDRITAIISHGKLCVGSGLFLKNOLGXY 240
 QY 1127 YLLVKKDVESLSSCRNSSSTVSYLKKEDSVSSDAGLSGSHESDTLIDVSAISNL 1186
 DB 241 YLLVKKDVESLSSCRNSSSTVSYLKKEDSVSSDAGLSGSHESDTLIDVSAISNL 300
 QY 1187 ITRHVSERLVDDIGHELTYYLPEAAKEGAFVLPHEIDRLSDLGISSTGISETTLEE 1246
 DB 301 ITRHVSERLVDDIGHELTYYLPEAAKEGAFVLPHEIDRLSDLGISSTGISETTLEE 360
 QY 1247 IFLKVAESGVDAETSDGTLPARRRRAFGKOSCLRPTEDDAADPDSIDPESRPTD 1306
 DB 361 IFLKVAESGVDAETSDGTLPARRRRAFGKOSCLRPTEDDAADPDSIDPESRPTD 420
 QY 1307 ILSGMDGKSTOVKGWKLTOOQFVALMKRLLIARRSKGFFAQIVLPAVFCIALVPSL 1366
 DB 421 ILSGMDGKSTOVKGWKLTOOQFVALMKRLLIARRSKGFFAQIVLPAVFCIALVPSL 480
 QY 1367 IYPPGKXPSLELOPMWNTNEOYTFVSNDAPEDTGTLNLTDPGSGTCMGE3NPLD 1426
 DB 481 IYPPGKXPSLELOPMWNTNEOYTFVSNDAPEDTGTLNLTDPGSGTCMGE3NPLD 540
 QY 1427 TPCQAGEEMTAPVPOTIMDLFONGNMTMONPSPACOCSSDKIKKMLPVCPPGAGLPP 1486
 DB 541 TPCQAGEEMTAPVPOTIMDLFONGNMTMONPSPACOCSSDKIKKMLPVCPPGAGLPP 600
 QY 1487 PQRKONTADILQDGRNISDIYVKTYYOIIAKSLKKNLWNERPFGFSLGVSNTQALP 1546
 DB 601 PQRKONTADILQDGRNISDIYVKTYYOIIAKSLKKNLWNERPFGFSLGVSNTQALP 660
 QY 1547 PSQEVNDAIKOMKKHLAKDSADRFLNSLGRFMTGLDTRNNKYKVMNNGWHAISSEFL 1606
 DB 661 PSQEVNDAIKOMKKHLAKDSADRFLNSLGRFMTGLDTRNNKYKVMNNGWHAISSEFL 720
 QY 1607 NVINNAIIRANLOKGENSHYGITAFNHPMLTKOOLSEVALMTTSDVLYSICVIFAMS 1666
 DB 721 NVINNAIIRANLOKGENSHYGITAFNHPMLTKOOLSEVALMTTSDVLYSICVIFAMS 780
 QY 1667 FVPASFVVELFOERYSKAKHLOFISGVKPVLYWLSNFWDMCNYVPAITVITFICQOQ 1726
 DB 781 FVPASFVVELFOERYSKAKHLOFISGVKPVLYWLSNFWDMCNYVPAITVITFICQOQ 840
 QY 1727 KSYVSSTMLPVIALILLYGSIPTPLMTPASFVKIPSTAVVLTSVNLFINGSVATF 1786
 DB 841 KSYVSSTMLPVIALILLYGSIPTPLMTPASFVKIPSTAVVLTSVNLFINGSVATF 900
 QY 1787 VLELFTDKLNNDILKSVFLPHFCLGRLIDMYKNQAMADALEFGNRPVSPLSW 1846
 DB 901 VLELFTDKLNNDILKSVFLPHFCLGRLIDMYKNQAMADALEFGNRPVSPLSW 960
 QY 1847 DLYGRNLEPAAVEGVFELVLVLIQYRFFIRPRPVNAKLSPLNDEDEVDREORILDDG 1906
 DB 961 DLYGRNLEPAAVEGVFELVLVLIQYRFFIRPRPVNAKLSPLNDEDEVDREORILDDG 1020
 QY 1907 GONDILELKELTKYRRKRAKAVDRICVGPPEGCGFLGNGAGKSTFKMLTGD7TVT 1966
 DB 1021 GONDILELKELTKYRRKRAKAVDRICVGPPEGCGFLGNGAGKSTFKMLTGD7TVT 1080

QY 1967 RGDAFLKKNLSILSHIHVHONMGYCPQFDAITELLTGREHVEFPALLRGVPEKEVGKE 2026
 DB 1081 RGDAFLKKNLSILSHIHVHONMGYCPQFDAITELLTGREHVEFPALLRGVPEKEVGKE 1140
 QY 2027 WAIKRLGLVYGERKYGANTSGGKRRKLSMTAMALIGGPPVFLDEPTTGMDPKARRFLAMC 2086
 DB 1141 WAIKRLGLVYGERKYGANTSGGKRRKLSMTAMALIGGPPVFLDEPTTGMDPKARRFLAMC 1200
 QY 2087 ALSVYKESRSVLTSHSMECEALCTRMALMVNGREFRCLGSVOHLKNRFGDGYTIVVRIA 2146
 DB 1201 ALSVYKESRSVLTSHSMECEALCTRMALMVNGREFRCLGSVOHLKNRFGDGYTIVVRIA 1260
 QY 2147 GSNPDLKPVQEFGLAPPGSVLKEKHNNMLOVLPSSLSLAFISLISOSKRRHLIEDY 2206
 DB 1261 GSNPDLKPVQEFGLAPPGSVLKEKHNNMLOVLPSSLSLAFISLISOSKRRHLIEDY 1320
 QY 2207 SVSQTTLDQYFVNFPAKQSDDDHLKDLSLKKNQTVVDVAVLTSFLQDEKVESYV 2261
 DB 1321 SVSQTTLDQYFVNFPAKQSDDDHLKDLSLKKNQTVVDVAVLTSFLQDEKVESYV 1375

RESULT 2
 US-08-762-500-26
 : Sequence 26, Application us/08762500
 : Patent No. 6030806
 : GENERAL INFORMATION:
 : APPLICANT: Landes, Gregory M.
 : APPLICANT: Burn, Timothy C.
 : APPLICANT: Connors, Timothy D.
 : APPLICANT: Dackowski, William R.
 : APPLICANT: Van Raay, Terence J.
 : APPLICANT: Klinger, Katherine W.
 : TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
 : NUMBER OF SEQUENCES: 83
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: GENZYME CORPORATION
 : STREET: One Mountain Road
 : CITY: Framingham
 : STATE: Massachusetts
 : COUNTRY: United States of America
 : ZIP: 01701
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/762,500
 : FILING DATE: 09-DEC-1996
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/665,259
 : FILING DATE: 17-JUN-1996
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: PCT/US96/10469
 : FILING DATE: 17-JUN-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Dugan, Deborah A.
 : REGISTRATION NUMBER: 37,315
 : REFERENCE/DOCKET NUMBER: ICS-9.3
 : TELEPHONE: (508) 872-8400
 : TELEFAX: (508) 872-5415
 : INFORMATION FOR SEQ ID NO: 26:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1375 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: not relevant
 : TOPOLOGY: unknown
 : MOLECULE TYPE: protein
 : US-08-762-500-26

Query Match 58.8%; Score 6931; DB 3; Length 1375;
 Best Local Similarity 97.2%; Pred. No. 0;
 Matches 1336; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

QY 887 CMEEPHKLKGVSTQNLKVKYRDGMKVAVDGALNFEYGOITSTFLGHNGACKTTMSIL 946
 DB 1 CMEEPHKLKGVSTQNLKVKYRDGMKVAVDGALNFEYGOITSTFLGHNGACKTTMSIL 60
 QY 947 TGLPPTSGTAIILKDRSEMSITRONLGVCPQHNVLFDMLTVEHIMFVARLKGLSEK 1006
 DB 61 TGLPPTSGTAIILKDRSEMSITRONLGVCPQHNVLFDMLTVEHIMFVARLKGLSEK 120
 QY 1007 HYKAEEMQALDVGLPSSKLSKTSQLSGGMORLSVALAFVGSKSVYILDEPTAGVDPY 1066
 DB 121 HYKAEEMQALDVGLPSSKLSKTSQLSGGMORLSVALAFVGSKSVYILDEPTAGVDPY 180
 QY 1067 SRRGIMELLKTRGRTIILSTHMDADVGLDRIAIISHGKLCVGSSEFLKNOLGTY 1126
 DB 181 SRRGIMELLKTRGRTIILSTHMDADVGLDRIAIISHGKLCVGSSEFLKNOLGTY 240
 QY 1127 YLTIVKDVESLSSGRNSSSTVYSLKREDVSQSSDAGLSDHESDITLTVSAISNL 1186
 DB 241 YLTIVKDVESLSSGRNSSSTVYSLKREDVSQSSDAGLSDHESDITLTVSAISNL 300
 QY 1187 IRKHVSEARLVEDIGHELTVVLPYEAKKGAFVELFHEIDRLSDLGISYISSETTLEE 1246
 DB 301 IRKHVSEARLVEDIGHELTVVLPYEAKKGAFVELFHEIDRLSDLGISYISSETTLEE 360
 QY 1247 IFLKVAESGVDAETSDGTLPARNRRAFGDKOSCLRPETEDDAADPNDSIDPESRETD 1306
 DB 361 IFLKVAESGVDAETSDGTLPARNRRAFGDKOSCLRPETEDDAADPNDSIDPESRETD 420
 QY 1307 LLSGMDKGSYOVKGMKLTQOQFVALLMKRLILARRSRKGFPAQVLPVFCIALVSL 1366
 DB 421 LLSGMDKGSYOVKGMKLTQOQFVALLMKRLILARRSRKGFPAQVLPVFCIALVSL 480
 QY 1367 IYPPFGKYSLLELOPMWYNEQTYFVSNDAEDTGTLELNLATLKPGESTRCEGNIPLD 1426
 DB 481 IYPPFGKYSLLELOPMWYNEQTYFVSNDAEDTGTLELNLATLKPGESTRCEGNIPLD 540
 QY 1427 TPCQAGEEEMTTAPVPOTIMDLFQNGNMTQNPSPACQSSDK IKMLPVCPPGAGLPP 1486
 DB 541 TPCQAGEEEMTTAPVPOTIMDLFQNGNMTQNPSPACQSSDK IKMLPVCPPGAGLPP 600
 QY 1487 PQRKMTADIIIDLGGRNISDLVKTYYOIIAKSLKNITWNEFRYGGSLGVSTQALP 1546
 DB 601 PQRKMTADIIIDLGGRNISDLVKTYYOIIAKSLKNITWNEFRYGGSLGVSTQALP 660
 QY 1547 PSEVNDATIKOKKHLKLAKDSSADREFLNSLGRFMTGLDTRNNVWYFNNKGMHAISSFL 1606
 DB 661 PSEVNDATIKOKKHLKLAKDSSADREFLNSLGRFMTGLDTRNNVWYFNNKGMHAISSFL 720
 QY 1607 NYINNALILRANLOKGENPSHYGITAENHPLNLTKOOLSEVALMTTSVDLVASICYIFAMS 1666
 DB 721 NYINNALILRANLOKGENPSHYGITAENHPLNLTKOOLSEVALMTTSVDLVASICYIFAMS 780
 QY 1667 FVPASVVFVLIQERVSKAHLOFISGVKPYIYWSNFVMDKNNYVVPATLVITITICFOQ 1726
 DB 781 FVPASVVFVLIQERVSKAHLOFISGVKPYIYWSNFVMDKNNYVVPATLVITITICFOQ 840
 QY 1727 KSVYSTNIPVATALLLLLGWSTITPLMYPASVFEKIPSTAYVVLVSVNLFIGINSVATF 1786
 DB 841 KSVYSTNIPVATALLLLLGWSTITPLMYPASVFEKIPSTAYVVLVSVNLFIGINSVATF 900
 QY 1787 VLELFTDNKLNNINILKSVFLIPFHCIGRLIDMKVKNQAMADALEREGENRFPVSPISM 1846
 DB 901 VLELFTDNKLNNINILKSVFLIPFHCIGRLIDMKVKNQAMADALEREGENRFPVSPISM 960
 QY 1847 DLVGRNLFMAAVGVFFLITVLIQYRFTIRRPVNAKSLPDLNDEEDVRRERQRIIDGG 1906
 DB 961 DLVGRNLFMAAVGVFFLITVLIQYRFTIRRPVNAKSLPDLNDEEDVRRERQRIIDGG 1020

QY 1907 GQNDLLEIKELTKLYRRKKRPAYDRICVGPGEFCGLGVNAGKSTFKMLTGDITYT 1966
 DB 1021 GQNDLLEIKELTKLYRRKKRPAYDRICVGPGEFCGLGVNAGKSTFKMLTGDITYT 1080
 QY 1967 RGDAFLKNSILSNIEYHQMNGCPOPDATITELLTRENHEVFPALLRGVPEKEVYGE 2026
 DB 1081 RGDAFLKNSILSNIEYHQMNGCPOPDATITELLTRENHEVFPALLRGVPEKEVYGE 1140
 QY 2027 WAIRKGLVYKGEYAGYAGSGNKRKLTAMALIGPPVFLDEPTTGMPPKARFLMNC 2086
 DB 1141 WAIRKGLVYKGEYAGYAGSGNKRKLTAMALIGPPVFLDEPTTGMPPKARFLMNC 1200
 QY 2087 ALSVYKGRVYVLSHMECEALCTRMALVNGRFRCLGSVOHLKKNRFGDYTIIVRIA 2146
 DB 1201 ALSVYKGRVYVLSHMECEALCTRMALVNGRFRCLGSVOHLKKNRFGDYTIIVRIA 1260
 QY 2147 GSNPDLKPVDFEGLAPPGSVLKKRHRNMLOYOLPSSLSLARIFSLSSSKRLHIEDY 2206
 DB 1261 GSNPDLKPVDFEGLAPPGSVLKKRHRNMLOYOLPSSLSLARIFSLSSSKRLHIEDY 1320
 QY 2207 SVSOTTLDOVFVNFPAKQSDDDHLKDLNKNQTVVAVLTSFLODEKKESTY 2261
 DB 1321 SVSOTTLDOVFVNFPAKQSDDDHLKDLNKNQTVVAVLTSFLODEKKESTY 1375

RESULT 3
 US-08-665-259-27
 : Sequence 27, Application US/08665259
 : Patent No. 6028173
 : GENERAL INFORMATION:
 : APPLICANT: Landes, Gregory M.
 : APPLICANT: Burn, Timothy C.
 : APPLICANT: Connors, Timothy D.
 : APPLICANT: Dackowski, William R.
 : APPLICANT: Van Raay, Terence J.
 : TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
 : NUMBER OF SEQUENCES: 73
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: GENZYME CORPORATION
 : STREET: One Mountain Road
 : CITY: Framingham
 : STATE: Massachusetts
 : COUNTRY: United States of America
 : ZIP: 01701
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/665,259
 : FILING DATE: 17-JUN-1996
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Dugan, Deborah A.
 : REGISTRATION NUMBER: 37,315
 : REFERENCE/DOCKET NUMBER: IG5-9.1
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (508) 872-8400
 : TELEFAX: (508) 872-5415
 : INFORMATION FOR SEQ ID NO: 27:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1457 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: not relevant
 : TOPOLOGY: unknown
 : MOLECULE TYPE: protein
 : US-08-665-259-27

Query Match 26.5%; Score 3129.5; DB 3; Length 1457;

TELEFAX: (508) 872-5415
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1457 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-762-500-27

Query Match 26.5%; Score 3129.5; DB 3; Length 1457;
 Best Local Similarity 46.0%; Pred. No. 1.5e-288;
 Matches 676; Conservative 207; Mismatches 377; Indels 211; Gaps 28;

QY 888 MEPEPHLKGVSIQNLVYVRDGMKVAADGLANFYEQIISFLGHNAGKTTTMSILT 947
 DB 1 MEPEPHLPVLCVVDKLTLYKNDKRLNLKLSLNLVENVVSVFLGHNAGKTTTMSILT 60
 QY 948 GLPEPTSGAYILGDIRSEMTIRONLGVCPQHNVLFDMLVVEEHIMFYARLKGSEKH 1007
 DB 61 GLPEPTSGAYILGDIRSEMTIRONLGVCPQHNVLFDMLVVEEHIMFYARLKGSEKH 120
 QY 1008 VKAEMEDMALDVLGPPSKLKSQTSLSGQMRKLSVALAFVGGSKVYLIDEPTAGVDPYS 1067
 DB 121 IRKETPKMIEDLEL-SNKRSLVQTLGCGMKRKLVAIAFVGGSKRAIILDEPTAGVDPYA 179
 QY 1068 RKRIWELLKYRGRTIILSTHMDADVLGRIATISHGKLCQVSSFLKMOLOTGYT 1127
 DB 180 RRAIMDLILKKYKGRITLSTHMDADVLGRIATISHGKLCQVSSFLKMOLOTGYT 239
 QY 1128 LTVLVKQVESLSSCRNNSSTVSYLKKEDSVSSQSSDAGLGDHESDTLIDVSAISNLI 1187
 DB 240 LTVLVKQVESLSSCRNNSSTVSYLKKEDSVSSQSSDAGLGDHESDTLIDVSAISNLI 279
 QY 1188 RKHVSEARLVEDIGHELYVLYPEAAKEGAFFVLEHIDRLSDLGISSYGISSETTLEBI 1247
 DB 280 RKHVSEARLVEDIGHELYVLYPEAAKEGAFFVLEHIDRLSDLGISSYGISSETTLEBI 339
 QY 1248 ELVVAEE-----SGVDA-ETSDGTLPARNRRAFGDKOSCLRPFE----- 1287
 DB 340 ELVVAEE-----SGVDA-ETSDGTLPARNRRAFGDKOSCLRPFE----- 399
 QY 1288 -----DDAADPNDSDIDESPREDTLLSGMDGSGYQVKGWKL 1324
 DB 400 VGSARBEGETGYSDGYDTRPLEDNLQDPD--NVSLOBAEMELAAY-GQGSKKLEGMWL 456
 QY 1325 TQOQFVALLMKRLILARRSRKGFPAQIVLPAYFVCIALVFSLIVPPGKYPSLELOPMY 1384
 DB 457 KMQOFGILLVKKRPHCARRNKALCSQILLPAFVGVAMTVALSVPETGLDPLVLSPSQY 516
 QY 1385 NEQYT-----FVSNDAPE-----DTGTELLNALTKDGFSTRCM----- 1419
 DB 517 H-NYTOPRGNFIPIYANEEEREYRLRLSPDASPQOLVSTFRLPSCVGATCVLKSPPANGSLG 575
 QY 1420 -----EGNPI-----PD----- 1426
 DB 576 PMLNLSGSESLAARFPDSCLESFTQGLPLSNFYPPSPAPSPSYXPPDDSLQANN 635
 QY 1427 --TPCOAGEEEMTAP-VPOTIMDLFQNGNMTWONPSPACQSSDKIKMLPYCPGAGG 1483
 DB 636 MSLPRTAGPETWTSAPSLPLVHEPVR-----CTCSAQCTGFS--CPSSVGG 680
 QY 1484 LPPOROKNADLIDLTGNTISDYLVKTYVQIIAKSLNKIMVNEFRGSGSLGVSNTQ 1543
 DB 681 -HPQOMVYVGDILTDTGTNVSLEYLFTSDR-----RLHARGALTEG--NVO 726
 QY 1544 ALPPSOEVNDAIKQMKHLKLADSSADRLNLSGFRMTGLDRNNVKKWFFNNKGNHAIS 1603
 DB 727 KSLPAS-----FGARVPPMVKRIANRRAQVLYLNKKKGHSMP 763
 QY 1604 SPLANVNNALIRANLQGE-NPSHYGITAFAHPLNLTQKQOLSEVALMTTSDVLVSIQYI 1662

DB 764 TYLSLNNALIRANLPKSKGNPAAYXITVTHNPNKTSASLS-LDYLTQGTDVVIAIFII 822
 QY 1663 FAMSFPVPAFVVELLOEVRSAKHLQFISGVKPVYWLNSFVDMQCNVPATLVITIFI 1722
 DB 823 VAMSFPVPAFVVELLOEVRSAKHLQFISGVKPNYTYMLANTVMDLANTLVATCCVILLF 882
 QY 1723 CFQOKSVYSSNTLPVIALILLGWSITPLWYPAFVEKIPSTAVVLTSTVNEFIGINS 1782
 DB 883 VEDLPATSPITNEPAVLISFLILGWSITPLWYPAFVEKIPSTAVVLTSTVNEFIGINS 942
 QY 1783 VATEVLELFT-DNKLNNINDILKSVFLIFPHFCGRLGILDMVKQADALERGE-NRF 1840
 DB 943 VATEVLELFT-DNKLNNINDILKSVFLIFPHFCGRLGILDMVKQADALERGE-NRF 1002
 QY 1841 VESLMDLVGRRLFAMAVEGVFEFLITVLIQRFIRPRPNAKLSPLNDEDEVRREBQ 1900
 DB 1003 KSPFEMDVTGRLVAMTVGEFVGFELTLMQCNFKQORLPVSTKPYED-DVDVASEBQ 1061
 QY 1901 RILDGQNDLLEIKELRIYARK--RKPADVRLCVGI-PPGECFGLGVNAGAKSSTF 1956
 DB 1062 RYLRGDADNDWKIENLTKYKSRKIGRIILAVDRCLGVCVPGECFGLGVNAGAKSSTF 1121
 QY 1957 KMLTDTVTGDAFLNKNLSINIEHYHONKGYCPOFDAITELLTGREHVEFALLRCV 2016
 DB 1122 KMLTDESTTGGEAFVNGHSYVLKDLQVQOSIGYCPQDPVVDDELTAHEHQLYTRLCI 1181
 QY 2017 PEKEVKGCEMAIRKLGIVYKGEKAYAGNYSGNKRKLSLTAALLGGPPVFLDEPTGMD 2076
 DB 1182 PKMDEAQQVKKMLELLETKRADKPAQYSGNKRKLSLTAALLGGPPVFLDEPTGMD 1241
 QY 2077 PARRFLLNCALSVKESRVLVTSMSDECEALCTRAIMVNGFRGLGVSQHLKNRFG 2136
 DB 1242 PARRFLLNCALSVKESRVLVTSMSDECEALCTRAIMVNGFRGLGVSQHLKNRFG 1301
 QY 2137 DGYTVVRIAGSNPDLKPYDFFGLAPGGSVYKKEKRNMLQYOLPSSLSIARIPSIISQ 2196
 DB 1302 DGYTVVRIAGSNPDLKPYDFFGLAPGGSVYKKEKRNMLQYOLPSSLSIARIPSIISQ 1360
 QY 2197 SKKRLHIEDYSQTTLDQVFPVNFAKQSD 2227
 DB 1361 VVGVLGIEDYSQTTLDQVFPVNFAKQSDN 1391

RESULT 5
 US-08-665-259-25
 Sequence 25, Application US/08665259
 Patent No. 6028173
 GENERAL INFORMATION:
 APPLICANT: Landes, Gregory M.
 APPLICANT: Burn, Timothy C.
 APPLICANT: Connors, Timothy D.
 APPLICANT: Deckowski, William R.
 APPLICANT: Van Raay, Terence J.
 TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
 TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
 NUMBER OF SEQUENCES: 73
 CORRESPONDENCE ADDRESS:
 ADDRESSES: GENZYME CORPORATION
 STREET: One Mountain Road
 CITY: Framingham
 STATE: Massachusetts
 COUNTRY: United States of America
 ZIP: 01701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/665,259
 FILING DATE: 17-JUN-1996
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Dugan, Deborah A.
 REGISTRATION NUMBER: 37,315
 REFERENCE/DOCKET NUMBER: 1G5-9.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (508) 872-8400
 TELEFAX: (508) 872-5415
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1684 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-665-259-25

Query Match 22.4%; Score 2642.5; DB 3; Length 1684;
 Best Local Similarity 35.7%; Pred. No. 6.8e-242;
 Matches 639; Conservative 300; Mismatches 523; Indels 327; Gaps 48;

QY 534 AGIYFTGTPGSI-LEPHHYKIKRMDIDNVERTN-----KIKGCV----- 574
 DB 111 AAYFEHPHNSKEPLPLAVKYHLRF---SYTRNNYMTQTGSPFLKETEKGWHTTSLPL 167
 QY 575 --DRGPRADPED--MRYVWGFAVLQDVVEQALIRLTGTE-----KKGVYMOQMPY 624
 DB 168 FPNPGRPLTSPDGEPEYIREGFLAVOHAVDRALMEYHADATROLFORLTWTIKRPY 227
 QY 625 PCYVDLIRVMSRMLFMTLAMIYSAVILKIGIVEKEARLKEKTRIMGJDSIMFS 684
 DB 228 PPLIADPLVALIQOLPRLTLLSTYALTALTAARAVOKEKRLKEKYMGLSWMHMSA 287
 QY 685 WFISSLPLVYASGLVYIILKLG-----NLPSDPSVYEVLSVFAVITLQCFILSTL 739
 DB 288 WFLLEFLLEPLAASFMTLLFCVKVKNVAVYLSRSDPSLVLAFLCFAISTISEFVNSTF 347
 QY 740 FSRNIAAAGCGIIFLYLPLVCAVADYVGTLLKIFASLSPVAFSGCEFEALFEE 799
 DB 348 FSKANMAAFGFLFFIYIFPVARRYNMNTLSOKLCSLLSNVAMACQILGFEA 407
 QY 800 QGIGVQMDNLFESPE-EDGEFNLTTSISMLEDTFLYGVMTVYEAVPQYGIIPRPYF 858
 DB 408 KGMGIQWMDLL-SEVNVDDDFCGQVGLMMLLDLVGLVYWEAVFPGQVPGWYF 466
 QY 859 PCTSYWGE-----ESDEKSHPSGNSOKRMEICMEEPHHLKLGSIONLVYVYDGM 912
 DB 467 FIMPSYWGKRAVAGKEEDSDP---EKALRNEYFEAEPRDLVAGIKIKHLSKVFVRGN 523
 QY 913 K--VAVDGLALNFEQQTTSFLGNAGAKTTMSITLGLPPTSGTAYIILKDIRSEMST 970
 DB 524 KDRAAVRDLNINTEYGOITVLGNAGAKTTLSMLTGLPPTSGRAVYISGEISQMVQ 583
 QY 971 IRONLVCPOHNVLFDMITVEBHWFYARLKGISEKHVAKMEOMALDVLPSKILSKYT 1030
 DB 584 IRKSLGICPOHDLIFDNLTAENHLYFAOLKGLSRCKPREVKOMLHIGL-EDKWNRS 642
 QY 1031 SOLSGMOKRSLVLAFAFGSGKVVITDEPTAGVDPYSRGRIWELLTYRGRTITLSTH 1090
 DB 643 RFLSGGMKRIKSTIGIALIAGSKVLLDEPPTSGMAISRRAIWLLOKOSDRITVLTTHF 702
 QY 1091 MDEADVLDRIATISHKLCVCGSSLEFLKNOLGTGYVLLTVKKDVESLSSCRNSSTVS 1150
 DB 703 MDEADVLDRIATIMAKGRLCCGSSLEFLKQYAGYHMTLYKE-----P 746
 QY 1151 YLKEDSVSGSSDAGLCSHESDTLTIVSAISNLIRKHVSEKRLVEDIGHETLYVLPY 1210
 DB 747 HCNEDP-----ISQLVHNVNPAITLSSAGAEISFTLPR 780
 QY 1211 EAKKGAFFELFHEIDRLSDIGTSSYGISSETTEELFIVAAE--ESGVAAETSDGTLPA 1268
 DB 781 ESTHR--FEGFLAKLEKKOKELGTASFGASITTMEEVFLVKGKLVDSMDIQAIO--LPA 836
 QY 1269 ---RRNRRAFG---DKOSCLRPFTEDDAADPND--SDIDPESEETDLLSGMDKGSGYOV 1319

DB 837 LOYHERRASDMAVDSNLC-----GAMPDSDGIGALLIEERTAVKINTGL----- 881
 QY 1320 KGMKLTQOQOFVALLMKRLLIARRSRKGFPAQIVLPAVEVCIALVSLVPPRGKYPSDEL 1379
 DB 882 ---ALHCQOFKAMFLKKAAYSREKMAVAQVVLPLCTTALL----- 922
 QY 1380 QPMWNEYQTVVSNDAPEDTGTLLELINALTKDPGFETRCMEGNPIPDTPCOAGEEWTYA 1439
 DB 923 -----AINVSSELEDDPML--RLTLG-----EYGR 946
 QY 1440 PVPQTIMDLFONGNNTMNPSPACOCSSDKIKKMLPYCPGAGGLPPOGRKONTADIID 1499
 DB 947 VPFVSVPQSQGLQULSEHLKDLQHEG-----QEPREVLD 983
 QY 984 L-----EEFLI-----FRASVEGGFN----- 1000
 QY 1556 KQKKHLKLAKDSSADRFINSIGREMTGIDTRNNKVMFNNKGMHAISFLVINNALLR 1615
 DB 1001 -----ERCL--VAASFVDGERTVYNALENNQAYHSPATALAVDNLLEK 1043
 QY 1616 ANLQKGENPSHYGITAFNRP-----LNLTKQOLSEVALMTTSVDVLSICVIFAMSFPYA 1670
 DB 1044 --LLCG---PHASIVSNFPQPSRSLQAAKQDPNE---GRKFDIALNL--LFAMAFILAS 1093
 QY 1671 SFVFLIQRVSRKAKHLOPISGVKPYIWLNSFWMCMYVVPATLVIIIFCQOKSYV 1730
 DB 1094 TFSITLAVSERAAQAKHVQSGVHVASFWLSALMDLISFLIPSLLLLVFAKAPVRAFT 1153
 QY 1731 SSTNPLVALLLLVKSTPPLTPMTPASFEKIPRNVAVVTVSVNLFIGNSVAFVTEL 1790
 DB 1154 RQGHMADTLLLLLGWALIPLMYLNMFELGAATVATRLTIFNLISG---ATFLWVT 1209
 QY 1791 ---FTDNKNNINDILKSVFLIFPHCLGRGLIDWKN-----QAMADALERG- 1836
 DB 1210 IMRIPAVKLEELSKTLDHFIVLPNCLGMAVSSFEYENETRYCTSSVAAHYCKKNI 1269
 QY 1837 ---ENRFVSPLSMDL--VGRNLFMAAVEGVFEFLTVLIQYFFIRLPRPVNAKL----- 1885
 DB 1270 QYOENFY---AMSAPGVGRFVASMASCAVYLILFLEITMLRLKGLICALRRRTL 1325
 QY 1886 -----SPINDEDEDYRRRORLIDOGGOND---LEIKELKIRYRRKRK--AVDRICV 1934
 DB 1326 TELYTMVPVLPEDQVADERTKILASPDSLHTPLILKELSKYV--EQRVPLANDRLSL 1384
 QY 1935 GIPPGECFGLLVGNAGKSTFKMLTGTDTYRGDAFLNKSTILSNIEVHONMGCYPOF 1994
 DB 1385 AVQKGCFCFGLGNAGAKTTTFKMLTGESLTSGDAFVGHRISSDVCGKVRORIGYCHOE 1444
 QY 1995 DATTELLGREHVEFPALLRGVPEKEVGVGMALRKGLVYVYGGKYAGNSGGKRRLS 2054
 DB 1445 DALIDMTGRENMLVMYARLGRIPERRIGACVENTLRLGLEHNAKLVRKTSYSGKRRKLS 1504
 QY 2055 TAAALIGCPVYFIDEPPTGMDPKARFLMNCALSVYEGKRVNLTSSMECEALCTRM 2114
 DB 1505 TGTALIGBRAVIFLDEPSTGMDPVARRLMDIVARAREGKAIITTSISMCECALCTRL 1564
 QY 2115 AIMVNGFRCLGSVYHLKRNFGDGYTIVRI--AGSNPLKFPVQDFGLAPPGVYLKKEH 2172
 DB 1565 AIMVQOQFCLCSPQLKSKFGSGYSLRAKYQSEGOQEALEBFKAFVDTLFGSVLEDEH 1624
 QY 2173 RNMLQYQLPSSLSLARITSLSQSKRRLIHEDYVSQTTLDQVAVNFA 2221
 DB 1625 QGVVHYHLGRDLISMAKYFGILLEKAKKEYGVDDYVSQISLEQVLSFA 1673

RESULT 6
 US-08-762-500-25
 ; Sequence 25, Application US/08762500
 ; Patent No. 6030806
 ; GENERAL INFORMATION:


```

QY 1332 LMKRLIARRSKGFEAIVLPAVENCIALVESLIVPPGKYPSLEQPMATNEQYEV 1391
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 708 --WPEYFV-----GVFCALINGCLOPAFAIIFSKII-----736
QY 1392 SNDAPEDGTLELLNALTKDPGFCRMEGNPIPDTPCQAGEEWTAAPVQTIMDLFON 1451
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 737 -----GVFTR-----741
QY 1452 GNMWTMONPSPACOCSSDKIKKMLPVCPPGAGLPPQPKONTADILQDITGRNISDYLVK 1511
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 742 -----IDDPETKRQNSNLFSL-----FLAL 762
QY 1512 TYVOIIAKSLKNKIWNDFRFGSLGVSNQALPSPQEVDAIKQKKHKLAKDSS-A 1570
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 763 GIIISFT-----FPLQFTFGKA-----GELITRLKRYMFRSLRQDYSWF 804
QY 1571 DRFLNSLGRFMTGLDTRNNVYVFNKNGHMAISSFLVNNAILRANLOKGENPSHYGT 1630
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 805 DDPKNTTGALTTRL-ANDAAQV-----KG--AIGSRLAVITQNI--ANLGIGI-----II 849
QY 1631 AFNHPPLNTKQOLSEVALMTTSVDVLVSICVIFAMSPVASEVVELIOERYSKAKHLOFI 1690
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 850 SFIFGMOLT-----LLLAIVPIIIAIGVEMK-----MLSGOALKDKELE-- 891
QY 1691 SGVPRVITWLSNFWMQCNVYVPATIVIIIFICFOOK---SYSSINLPVALL--LLY 1745
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 892 GAGKATEALENF-----RTVVSLEQOKFEMHTAOSLOVPRNSLRKAHIF 938
QY 1746 G--WSTPIAMYPASFEKPTSTAYVVLTVSNLFIGNSVATFVLELTNKLININDITL 1803
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 939 GTFSEFQAMMYFSYAGCFREGAYLVA-----HKLSMSEFVL 975
QY 1804 KSVPLIFPHFCLGLIDMVKNOAMADALERFGENRY-----SPLSMDLVGRNLPAMAY 1858
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 976 ---LVESAUVFAGMAVGQVSSFPADYAKAKISAHHIIMIEKPLIDSYSTEGELMNTL 1931
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1859 EGVEFFLTVLLOYREFTRPR-PYNAKLSPLNDEDEVRERORILDGGQNDILEIKEL 1917
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1932 EGNVTFGEVY---FNYPRPDIPVLOGIS-----LEKK- 1962
QY 1918 TKIYRRKRPVADRICVIGIPGECFGLGVNAGKSSTFKMLJGDTTVYTRGDAFLKNESI 1977
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1963 -----GOTLALVSSGSKSTVYOLLEFRYDPLAGKVLDDKEI 1101
QY 1978 LS-NIHEVQNMGYCPQ-----FD-----ATTELLTGREHEFPALLRGV 2016
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1102 KRLVQWLRALHGLVSOEPIPLFDCSIAENIAYGNSRVYSEETIVRAKAKENIHAFIESL 1161
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 2017 PEKEVGKVGEMAIRKRLGLVKYGERYAGNYSGNKRLSTAMALIGPPVFLDEPTTGM 2076
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1162 PNKYSTKVGDKGTQ-----LSGGQKORIAIARALVROPHILLLDEATSLD 1207
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 2077 PKAREFLMNCALSVKRGSRVYLTSHSMECEALCTIRALIMVNRFCISGVQKLRFG 2136
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1208 TESEKVVQD-ALDKARBSRCTIVIAHRLSTIQN-ADLIVFQNGRVKEGHQOLLAQK 1265
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 2137 DGYTIIVARIAGS 2148
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1266 IYFSMVSVQAGT 1277
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

; APPLICATION NUMBER: 892,575
; FILING DATE: 01-AUG-1986
; APPLICATION NUMBER: 845,610
; FILING DATE: 28-MAR-1986
; SEQ ID NO:4
; LENGTH: 1280
5206352-4

Query Match      2.9%; Score 339.5; DB 6; Length 1280;
Best Local Similarity 18.7%; Pred. No. 4.2e-22;
Matches 272; Conservative 201; Mismatches 470; Indels 509; Gaps 56;

QY 776 KIFASLSFVANGFCCEYALFEBOGIGVQWONLESPEVEEDGFULTISIMLFDTL- 834
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 256 EVILAAIRTVIATGGOKLELERYNK-----NLEBA--KRGIKAITANISIGAEFL 305
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 835 ---YGVMTWY-IEAVFPQYGLPR---PWYFPCTKSYFGEES-----870
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 IYASTALAFWYGTTLVLSGEYSIGQVLYVFSVLIGAFSVGQASFSIEAFANRGAAYEI 365
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 871 ---DEKSHPGSNQKRMSEICMEEBEPTHLKGVSTQNLVKKYRDGMKAAV-DGLALNFE 925
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 366 FKTIIDKPSIDYSK-----SGHKPDNIKGNLEFRNHFVSYSRREKVIILGLMLKYQS 419
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 926 GQTSFLGNAGKTTTMSILGFPPTSGTAVIIGKDIRS-EMSTIQNIGVCPQHNL 984
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 420 GQTVALLVNGSGCKSTVYLMQRLYDTEGMVSVSDQDRTINVRLEIIGVSOEPLV 479
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 985 FDMIVVEEHIWFIYARLKGISEKHVKAEQOMALD--VGLP---SSKLKSKTSQLSGMQR 1039
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 480 F-ATTIAENI-RYGRENVAMDEIEKAVKANAYDFIMKLRPHFPTLVGRGAQSLSGGQK 537
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1040 KLSVALAFYGGSKVVLDEPTAGVDPYSKRGIMELLKTRQRTIILSTHND---EADY 1096
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 538 RIAIRALVNRKILLLDATSALDSEAVYQVALDKARKKRTIYIAHRLSTVRNDV 597
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1097 LG--DRITAIISHGKLCVSSSFLKMQLTGYTLVKKQDV---ESSLSCRNSSSTVSY 1151
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 598 IAGFDGVIYKQ-----NHDELIMKER--GIYFKLVYMQTGNVELENADESKS--- 646
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1152 LKREDSVSSSDAGLSPHESDTLTIDVSAISNLIRKIVSEARLVEDIGHELYVLEPE 1211
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 647 --EIDALEMSSNDSR-----SSLIRK-----665
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1212 AAKGAFVELFHEIDRLSDLGISYGISETTLLEIFLKVABESGVDAETSDGTLPARRN 1271
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 666 -----RST 668
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1272 RRAFGDKQCLRFETEDDAAPNDSDIDPESRETDLLSGMDKGSYQVKGWKLQOQFVA 1331
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 669 RRSVRSQAQDRKLSRKAL---DESIRP-----VSFWIRMLKNTLE 707
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1332 LMKRLIARRSKGFEAIVLPAVENCIALVESLIVPPGKYPSLEQPMATNEQYEV 1391
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 708 --WPEYFV-----GVFCALINGCLOPAFAIIFSKII-----736
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1392 SNDAPEDGTLELLNALTKDPGFCRMEGNPIPDTPCQAGEEWTAAPVQTIMDLFON 1451
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 737 -----GVFTR-----741
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1452 GNMWTMONPSPACOCSSDKIKKMLPVCPPGAGLPPQPKONTADILQDITGRNISDYLVK 1511
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 742 -----IDDPETKRQNSNLFSL-----FLAL 762
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1512 TYVOIIAKSLKNKIWNDFRFGSLGVSNQALPSPQEVDAIKQKKHKLAKDSS-A 1570
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 763 GIIISFT-----FPLQFTFGKA-----GELITRLKRYMFRSLRQDYSWF 804
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1571 DRFLNSLGRFMTGLDTRNNVYVFNKNGHMAISSFLVNNAILRANLOKGENPSHYGT 1630
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 805 DDPKNTTGALTTRL-ANDAAQV-----KG--AIGSRLAVITQNI--ANLGIGI-----II 849
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

: TELEFAX: 415-854-0875
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1279 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-784-649A-2

```

Best Local Similarity 18.7%; Pred. No. 7.2e-22;
Matches 272; Conservative 200; Mismatches 471; Indels 508; Gaps 56

Matches	272;	Conservative	200;	Mismatches	4/1;	Indels	200;	Gaps	200;
---------	------	--------------	------	------------	------	--------	------	------	------

776 KIFASLSPVAEGFGCEYFALFEEQGIGVQWDNLFESPVEEDGFNLTTISMMLFDTEL- 834

[illegible]

b 256 EVLAIRTVIAFGGQKLELYNK-----NLEEA--KKIGLKKALINISJONR 22 202

835 -----YGVMTWY-LEAVFPQYGIPR--PWYFPCTKSYWEGEES----- 870

[illegible]

306 IYASYALAFMYGTTLVLSGEYSIGQVLIVFSVLIGAFSVGQASPSLEAFANNAQNMILL 300

871 ---DEKSHPGSNOKRMEIEMEETHLKLGVSIGNLVKVRDGMKVAV-DGLALNFYEG 926

419
 1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524

366 KIIDNKPSIDSYK-----SGHKPDNIKGNLEFRNVHFSYPSKKEVKLLAGLNVAVQSG 417

927 OTTSEI⁶HN⁶GAGKTTTMS⁶ILTGL⁶FPPTSGTAYILGKDIRS-EMSTIRQNLGVC⁶Q⁶HNVL⁶F 985

[illegible]

420 QTVAVGNSGCGKSTTVQLMQRLYDPTGMSVDGQDIRTINVRFLRELIGVVSQEPVLF 4/9

986 DMTVEEHITFYARLKGLSEKHVKAEMEOMALD--VGLP---SSKLKSKTSQLSGGMQRK 1040

[illegible]

480 -ATTIAENI-RYGRENVITMDEIEKAVKEANAYDFIMKLPKREDTLVGERGAQLSGGQKQR 331

1041 I.SVAIAFEVGGSKVYII,DEPTAGVDPPSRRCIWELLKRYRGRTIILSTHMD--EADVL 1097

1071	1072	1073	1074	1075	1076	1077	1078	1079	1080	1081	1082	1083	1084	1085	1086	1087	1088	1089	1090	1091	1092	1093	1094	1095	1096	1097	1098	1099	1100	1101	1102	1103	1104	1105	1106	1107	1108	1109	1110	1111	1112	1113	1114	1115	1116	1117	1118	1119	1120	1121	1122	1123	1124	1125	1126	1127	1128	1129	1130	1131	1132	1133	1134	1135	1136	1137	1138	1139	1140	1141	1142	1143	1144	1145	1146	1147	1148	1149	1150	1151	1152	1153	1154	1155	1156	1157	1158	1159	1160	1161	1162	1163	1164	1165	1166	1167	1168	1169	1170	1171	1172	1173	1174	1175	1176	1177	1178	1179	1180	1181	1182	1183	1184	1185	1186	1187	1188	1189	1190	1191	1192	1193	1194	1195	1196	1197	1198	1199	1200
1071	1072	1073	1074	1075	1076	1077	1078	1079	1080	1081	1082	1083	1084	1085	1086	1087	1088	1089	1090	1091	1092	1093	1094	1095	1096	1097	1098	1099	1100	1101	1102	1103	1104	1105	1106	1107	1108	1109	1110	1111	1112	1113	1114	1115	1116	1117	1118	1119	1120	1121	1122	1123	1124	1125	1126	1127	1128	1129	1130	1131	1132	1133	1134	1135	1136	1137	1138	1139	1140	1141	1142	1143	1144	1145	1146	1147	1148	1149	1150	1151	1152	1153	1154	1155	1156	1157	1158	1159	1160	1161	1162	1163	1164	1165	1166	1167	1168	1169	1170	1171	1172	1173	1174	1175	1176	1177	1178	1179	1180	1181	1182	1183	1184	1185	1186	1187	1188	1189	1190	1191	1192	1193	1194	1195	1196	1197	1198	1199	1200

538 IAIARALVRNPKILLDEATSEAVVQVALDKARKGRTTIVIAHRLSIVRNADV L 39/

1098 G--DRTATSHGKICGVSSLFKNO LGTYLLVKKDV---ESSLSSCRNSSSTVSYL 1152

[illegible]

598 AGFDDGVIVEK-----NHDELMKEK-----GIYFKLVMTAGNEVELENADESKS----- 645

1153 KKDSDVSOSSSDAGT GSDHESDTLTIDVSAISNLIRKHVSEARLVEDIGHELTYPYEA 1212 .

[illegible]

Db 646 -EIDALEMSNDR-----SSLRK----- 004

1313 AKKCAEVEI EHEIDDI SDIGTSSYGISETTLEEFIFKVAEESGVDAETSDGTLPARNR 1272

1213 ANEGRI VILLI NELLO SCALDO DI CANTÙ 11

665 -----RSTR 668

1333 1332

[illegible]

669 RSVRGSAQDRKLTSTKEAL---DESIPP-----VSEWRIMKLNLT- /06

1333 LWRPIIARPSPKGEFAOTVI.PAVEVCTAI.VESLIVPPEGKYPSLELOPMWNEQYFVS 1392

1333 LMNKKLELIMNNKNOVL E N Y A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

| :: | | : | :: | | :

: : | | : | :: | | :

Db 707 -WPYEVV-----GVFCAIINGGLPAPAFALIESKII-----/35

1303 NDAPEDECTETI ETI NAI TKDPGEGBCMEGNPDPDTPCOAGEEEETAPVPOTIMDLFONG 1452

xy 1393 NDAFEDIOI EEEENNNNDNOICNORONRERRE
| |
|

806

Db 736 -----GVFTR----- 740

1453 MTTMNDSPACOCSSDKTKKM.I.PVCPBGAGGT.PPORKONTADILODLTGRNISDYLVKT 1512

1455 NW 10th St, Miami, FL 33136

Db 741 -----IDDPETKRQNSNLFSL-----FLALG / 62

1513 VVOTAKSIKNKTWNEFRYGFESI.GVSNTOAL.PPSOEVNDAIKOMKHLKLAKDSS-AD 1571

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

Db 763 IISFIT-----FFLQGTFGKA-----GEILTKRLRYMVFERSMLRQDVSWFD 804

1573 PEINSGREMTGIDTPBNVVKVFNKQWHAISSEFLVINNAILRANLÖKGENPSHYGITA 1631

```

Db 805 DPKNTGALTTRL-ANDAAOV---KG--AIGSLAVITQNI--ANLGTGI-----IIS 849
QY 1632 FNNPPLNLTQOOLSEVALMTTSVDVLVSICVIFAMSFVPASFVFLIIOERSAKHLQFIS 1691
Db 850 FIVGMOLT-----LLLAIVPILAIAGVEMK-----MLSGQALKKCKEELF--G 891
QY 1692 GVPFVLYMNSNFWMQCNVVPATLVITIFIGIQOK---SYVSTNLPVLAII--LLYG 1746
Db 892 AGAIATEALENF-----RTVSLTQOKFEHMYAQSLQVPRNSIKRAHJFG 938
QY 1747 --WSTPLMYPASEVFKIPSTAVVLTSVNLFIGINGSVATFVLELTQNKLNINIDLIK 1804
Db 939 ITFSFTQAMMYFSYAGCFREFGATLVA-----HKLSFEDVL- 974
QY 1805 SVFLIPPHFCIGGLDMYKKNQAMADALERFGENRFV-----SPLSMDLVGNLPMAMVE 1859
Db 975 ---LVFSANVFQAMAVGQVSSFPADYAKAKISAHIIMIEKTPILDSYSEGLMPTLE 1031
QY 1860 GVAFELITVLIQYREFIRPR-PVNAKLSPINDEDEDVREBQRILDGGQNDILEIKELT 1918
Db 1032 GNVTEGEVY---FNKPTRDIPVLQGLS-----LEVRK-- 1061
QY 1919 KIYRRKRKAVDRICVIGIPGCEPGLLVGNAGKSTFKMLTGDTVTRGDAFLNKNSTL 1978
Db 1062 -----GQTLALVSSGCGKSTVVOLLERFYDPLAGVLLDGEIK 1101
QY 1979 S-NIHEVHONMGCPQ---FD-----AIFELTGREHVEFPALLRGVP 2017
Db 1102 RLNVQMLRLHIGIVSQEPILFDCSIAENLAVGDSNRVSOEIVAAKEANIHAFIESLP 1161
QY 2018 EKEVGKVEPMARIKGLYKYGKTAGNYSNGKRRKLTAMALLGGPVPVLEDEPTGMDP 2077
Db 1162 NKYSKRVGKGTQ---LSGQOKRIATARALVVRPHILLDEATSAIDT 1207
QY 2078 KARFLMNCALSVYEGRSVVLTSHECECALCTRAIMVNGRPRGCSVOHLKNRQGD 2137
Db 1208 ESEKVOE-ALDKAREGTCVIAHRLSTION-ADLIYVFPNGKVKHGHQULLAQGI 1265
QY 2138 GYTIYVRIAGS 2148
Db 1266 YFSMVSVQAGT 1276

RESULT 11
US-08-752-447-2
: Sequence 2, Application US/08752447
: Patent No. 5994088
: GENERAL INFORMATION:
: APPLICANT: Mechmetner, Eugene
: APPLICANT: Roninson, Igor B
: TITLE OF INVENTION: Methods and Reagents for Preparing and
: TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
: STREET: 300 South Wacker Drive, Seventh Floor
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/752,447
: FILING DATE: 15-NOV-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5994088an, Kevin E
: REGISTRATION NUMBER: 35,303
: REFERENCE/DOCKET NUMBER: 95,1121

```

```

: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-913-0001
: TELEFAX: 312-913-9808
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1280 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-752-447-2

```

```

Query Match 2.8%; Score 330.5; DB 2; Length 1280;
Best Local Similarity 18.5%; Pred. No. 3e-21;
Matches 269; Conservative 197; Mismatches 476; Indels 511; Gaps 54;

```

```

QY 776 KIFPSLSPPVAFGCGCEYFALFEEQIGIGVQMDNLFESPEDEGFNTLTSISMALPFTFL- 834
Db 256 EVLAIRTVIAFGQKKELERYNK-----MLEEA--KRIGIKKATFANISGAAPLL 305
QY 835 ---YGVMTWY-IEAVPQGYIPR---PWYFCTKSWMFGES----- 870
Db 306 IYASVAVAFWYGTTLVLSEGEYSIGVYLVFVSLIGAFSGQASPSIEAFANAGAAEYI 365
QY 871 ---DEKSHGCSNOKRMSIEICMEBEPTHLKLVGSIONLVKVVYDGMKAVV-DGLALNFEY 925
Db 366 FKIIDNKPISIDYSK-----SGHKPDNIKGNLEFNHVSYPSSRREVKILKGLNLYQS 419
QY 926 GQITSPFHNGAGKRTYMTSLTGLFPPTSGTAVIILKDIRS-EMSTIRNLGVCCPHNVL 984
Db 420 GQIVVALVNGSGCKSTTVQMLQRYLDPTEGMSVSDQDITRIWRLKREIIVGSOEPLV 479
QY 985 FDMILYEBEHWFYARLKLSEKAVKAEQMALD--VGLP---SSKLKSTQSLSGQMR 1039
Db 480 F-ATTTAENT-RYGRNVMTDEIEKAVKANAVDEIMKLPKHFDFLVGEGRAQLSGGQK 537
QY 1040 KLSVALAFVQGSKVVLIDDEPTAGVDPSRSGIWEILLKXROGRTIILSTHH--HDEADY 1096
Db 538 RIARARALVRNPKIILLDEPATSALDTESEAVVOALDKARKKRTTIVIAHREATVRNADY 597
QY 1097 LG--DRIATISHQKLCQVSSSLFKNQOLGTGYLLLVKKDY--BSSLSCSNSSSTVSY 1151
Db 598 IAGFDDGVIVEKQ---NHDELMKEK--GIYFKLVMTQGTAGNEVELENADSKS--- 646
QY 1152 LKREDSVSSSSDAGISGSHESDITLIDVSALSNLIRKVSARLVEDIGHELYVLPYE 1211
Db 647 ---EIDALEMSSNDSR-----SSLIRK----- 665
QY 1212 AAKGAFVELFHEIDRLSDLGISYGISSETLLEIFLKVAESGVDAETSDGTLPARRN 1271
Db 666 -----RST 668
QY 1272 RRAFGDKQSCLPFTEDDAADPNDSIDIPESRETDLLSGMDKGSYOVKMKLTOQOEVA 1331
Db 669 KRSVRSQAOHQHKSITKEL--DESIPP-----VSFWRIMKLNLE 707
QY 1332 LMKRLILARSRKGFPAQVILPAVEFCIALVESLIYPPGKPSYSLQLPMMYEQTFV 1391
Db 708 --WPFYFV-----GVFCATINGGLQPAFAIIFSKIIISIVFTRI----- 742
QY 1392 SMDAPEDGTLELLNALAKDKPGFTRCMEGNPIDTPQAGEEBMTTAPVPQITMDLFON 1451
Db 743 --DDPE-----TKRONSMLFSLFLALGIIISFTF----- 770
QY 1452 GNVWQNSPACQSSDKIKKMLVPCPGAGGLPPORKONTADILQDLGRNISDYLVK 1511
Db 771 -----FLOGFTFGKAGELITK 786
QY 1512 TYVOLIAKSL--KNKIWNNEFRYGGFSLGVSNTOALPSPQEVNDAIQMKHKLKAKDSS 1569
Db 787 RLRYWVFRSMRLQDVSWFHD-----PKNTGALTTRLANDAAOV----- 825
QY 1570 ADRLNLSIGRPMGLDTRNNYKVFENKGMHAISSFLNVLINNALIRANLQGENPSHYGI 1629

```

```

Db      826  -----KG--AIGSLAVITONI--ANLGTGI-----I 848
QY      1630 TAFNHPDLNLTQOOLSEVALMTTSVDLVISCIYFAMSFPAFVFLIDERSKAKHLOF 1689
Db      849  ISITYWOLT-----LTLAIVPIIAIAGVENKMFAG-----QALTKKELE- 891
QY      1690 ISGKPEVYIWLNSFVDMCNVYPATLVIIIFICFOOK---SYVSTNLPVALLT--LTL 1744
Db      892  -GAGKLTATEIENF-----RTVSLITQOKFEHMYAQSLOQPYRNSLRKAI 937
QY      1745 YG--WSITPLMPASFAVEKIPSTAYVLTSVNLFIGINSVATFVLELFTDKLNINDI 1802
Db      938  FGITFSFTOAMMFYSAGCFRFGAYLVA-----HKMSFEDV 974
QY      1803 LKSVFLIFPHFCLRGILDMYKNQAMADLERGENRFV-----SPLSMDLYGRNLFMAA 1857
Db      975  L-----LVFSAYVFGAMAVQSSSFADYAKAKISAHHIIMIEKPLIDISYSTEGLMPNT 1030
QY      1858 VEGVFFELTVLQYFFFIKPR--PVNAKLSPLNDEDEDEVREORITLDGGQNDILEIKE 1916
Db      1031 LBSNVTFGEVY---FNYPRPDIPVLOGIS-----LEVAK 1062
QY      1917 LFKYRRKRPAVDRIQVGIPEGEFGLGVNGAGKSTFKMLTGDTVTYRGDAFLNKNS 1976
Db      1063  -----GQTLALVSSGCGKSTVQVOLLERYDPLAGKVLIDGKE 1100
QY      1977 ILS-NIHEVHQNMGYCPD---FD-----ATTELLTGEHVEFFALLNG 2015
Db      1101 IKRLNVOUMRAHLGIYSEPILEDCSIAENIAYGDNRSVSOEIVRAKEANIHFIFIS 1160
QY      2016 VPEKEGKVGEMAIRKLGIVYGEKAYAGNYSNGNKRKLSTAAALIGPVPVFLDEPTTM 2075
Db      1161 LPKKYSTKVGDKGTQ-----LSGQKORIAARLVAQPHILLDEATSL 1206
QY      2076 DPRARELNCALISVYKESRVVLTSHSMECEALCTRAIMVNGFRCLGSVOHLKNRF 2135
Db      1207 DTSEKRVQOE-ALDKAREGRTCIIVIAHRLSTION-ADLIVFONGRVKREHGHQOLLAQ 1264
QY      2136 GDGTIVRVLAGS 2148
Db      1265 GIYFSMVSVOAGT 1277

RESULT 12
US-09-120-513-2
; Sequence 2, Application US/09120513
; Patent No. 6025160
; GENERAL INFORMATION:
; APPLICANT: Brun, Kimberly
; APPLICANT: Chenery, Richard
; APPLICANT: Ellens, Harna
; APPLICANT: Field, John
; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE
; TITLE OF INVENTION: SEQUENCES ENCODING RAT MDRLB2 AND
; NUMBER OF INVENTION: SCREENING METHODS THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY:
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,513
; FILING DATE: 22-JUL-1998

```

```

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: GP50008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5015
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1275 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-120-513-2.

```

```

Query Match      2.68; Score 311; DB 3; Length 1275;
Best Local Similarity 19.08; Pred. No. 2.2e-19;
Matches 281; Conservative 180; Mismatches 437; Indels 580; Gaps 62;

```

```

QY      743  ANLAACGGIYFTLYLPYLCVAMQDYVGFLLKIFASILSPVAFGFCCEYALFEQGI 802
Db      293  ANIST---GIAYLVYASYAL-----AFWYGTSLVLSNEYSI 326
QY      803  GVQWQNDLFESPEVEDGFNLTTSISMMLFDITLYGVMTYIEAVPFGQYGIIPRYW---- 857
Db      327  G-----QVLTVFESILGTGFSIGLAPNIEA-PANAGAAVEYEFKIIDN 369
QY      858  PFCSTSYMFGESDEKSHPGSNQKMSFTICMEEPHTLKLGVSIONLYKVY--RDGKVA 915
Db      370  EPSIDSF-----STKGH-----KDSIMGLERKNYFNPSPSEVKI- 407
QY      916  VDGLALNFYEGQITPSLHNGAGKTTMSILTLGLFPPTSGTAYILGKDIRS-EMSTTRON 974
Db      408  LKGLMLKVKSGQVALVNGSGCKSTVOLLRLYDPIEGEVSIDGQIRITINRYLREI 467
QY      975  LGCPQHNVLFDMLTVEEHMFYARLKLSEKHVKAEMQALD--VGLP---SSKLKS 1029
Db      468  IGVYSEPEVLP-ATTIAENI--RYGRENVTMDIEKAAVEANAAYDFIMKLPKFTVLGER 525
QY      1030  TSOLSGMQRLSVLAFVSGSKVYLIDEPYAGVPSRRCIMELLLKRYRGRTIILSTH 1089
Db      526  GAOLSGGOKORIAARLALVRNPKIILLDEATSLDTESEAVYQALDKARSGRTIYIAH 585
QY      1090  HMDADVLDRIALISHGLCCVSSFLKNQOLGTGYLLVKKDVESLSSCRNSSTV 1149
Db      586  R-----LSTVNAVIA 597
QY      1150  SYLKKEDEVSSSSDAGCGSHESDTLTIDVSAISNLIRKRVSEARLYEDIGHLLTYLP 1209
Db      598  GF-----DGVY-----IYEOGNHE----- 611
QY      1210  YEAAKE-GAFVELF-----HEIDRLSDLGISY-----GISETTELEIFLVAESG 1256
Db      612  -ELMKEKGIYFKLVYTGTRNGEIEP-----GNNAVESDGTGASELT----- 652
QY      1257  VDAETSDGTLPARRNRRAFGDKQSCLRPFTEDDADPNDSIDIPESRETTLLSGMDKGS 1316
Db      653  --SEKSKSPILIRSIIRSIHRQDERLSKE-----DVDEDPV----- 690
QY      1317  YQVKGWKLTOQGFVALLMKRLLIARSKKGFADIVLPAYVVCIALVFSLYPPFGKYP 1376
Db      691  -WVSFWOILKLNISE--WPYLV-----GVLCAVINMCIDQVPAIVFSKIVGF----- 736
QY      1377  LELQPMYNEQYTFVSNDAPEDTGTLLELNLATRDPGGTRCMGKNLIPDTPCQAGEEW 1436
Db      737  -----SRDDHET----- 744
QY      1437  TTAVPYQTIMDLFONGNMTQMNPSPACQSSDKIKKMLPVCPGAAGLPPQRKONTADI 1496

```

```

Db 745 -----KORNCNLSL 754
QY 1497 LQDLTGRNISLYKTYVOIIAKSLKNIWNEFRYGGSLGVSNTQALPSPQEVNDAIK 1556
Db 755 L-----FLVGMISFVT-----YFPGFTFGKA-----GELITRRLR 786
QY 1557 QMKHKLAKDS-ADRFNLISLGRFMTGL-DTRNNVYKVFNNKGMHAISFLVNNAIL 1614
Db 787 YWFKSMRLKODISWFDHKNKTGSLTRRLASDASNVK-----GAMGSLAVYTQNV- 837
QY 1615 RANLQKGNPSSHGYTTAFNHPNLTKOOLSEVALMTTSVDLVSLCYTFAMSPVASFV 1674
Db 838 -ANLGTG-----IILSLVGMQTLTLLVLIIPILVIGIIEK-----874
QY 1675 FLIQERSKAKHLOPISGVKPVYIWLSEFVDMCNVVPALVLIITFCPOK---SYVS 1731
Db 875 -LLSQALDKKLEIS-KIATEAIEVF-----RTVSLTRKRETFYMAQ 919
QY 1732 STNLPVALLLLYGMST-----PLMYPAFVEKIPSTAVVLTSLVLFINGSV 1783
Db 920 SLQIPYRNALKKAHVFGLTFATQAMLYFSYACFRF---GATLV-----961
QY 1784 ATFLVLEFTDKNNINDILKSVLIPPHCLGRGLI-----DMKQAMADALERF 1835
Db 962 ---ARELMT-----FENVMLVFSAVVFGAMAAGNTSSFPADYAKAKVSASHIRI 1008
QY 1836 GE-----NRFVSPLSMDLVGRNLFAMAVEGVFELLVLOYRFPRIPR-PVNAKL 1885
Db 1009 IEKPEIDSYSTEGIKP-NW-LEGNVKF---NGVMF-----NYTPRNIPVLQGL 1053
QY 1886 SPLNDEDEVRERORILIDGGGONDILEIKELIKYRRKKRPAYDRICVGPISPECEGL 1945
Db 1054 S-----FEVKK-----GQTLRLV 1066
QY 1946 GYNGAGKSTKMLTGDTTTRGCAFLKNSILS-NIHEVQNNQCYQD---FD-AIT- 1988
Db 1067 GSSGGKSTVQVLLEREFYNPAGVTFIDGKEIKQINVOMLRANHGIYSQEPILDCSITE 1126
QY 1999 -----ELTGRHEVFEFALLRGVPEREKGVEGEMAIRKLGIVKGEKAYGN 2044
Db 1127 NIAYGDNRRVYSHETIYAAREANIHOFIDSLPERKYNTRVADKIQ-----1172
QY 2045 YSGNKRRLSTAMALIGSPVVFLEDEPTTGMDPKARFRLMCAISVYKEGRSVLTJSHM 2104
Db 1173 LSGGQKRIATARALVRQPHILLDEATSAIDTESEKVVQF-AUDKAREGFTCIIVIAHL 1231
QY 2105 EECEALCTRMALINVGRRCLGSVOHLKNRGDTIY 2142
Db 1232 STON-ADLIIVIQNGVKEHGHQOOLAKGIYFSMV 1268

```

RESULT 13

```

US-09-450-105-2
; Sequence 2, Application US/09450105
; Patent No. 6169166
; GENERAL INFORMATION:
; APPLICANT: Kimberly Anne Brun
; APPLICANT: Richard James Chenery
; APPLICANT: Harna Eliens
; APPLICANT: John Anthony Feild
; APPLICANT: Lin Yue
; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: ENCODING RAT MDRI12 AND SCREENING METHODS THEREOF
; FILE REFERENCE: GP-50008-D1
; CURRENT APPLICATION NUMBER: US/09/450,105
; EARLIER FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/120,513
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1275
; TYPE: PRT

```

```

; ORGANISM: HOMO SAPIENS
US-09-450-105-2

```

```

Query Match 2.6%; Score 311; DB 4; Length 1275;
Best Local Similarity 19.0%; Pred. No. 2,2e-19;
Matches 281; Conservative 180; Mismatches 437; Indels 580; Gaps 62;

```

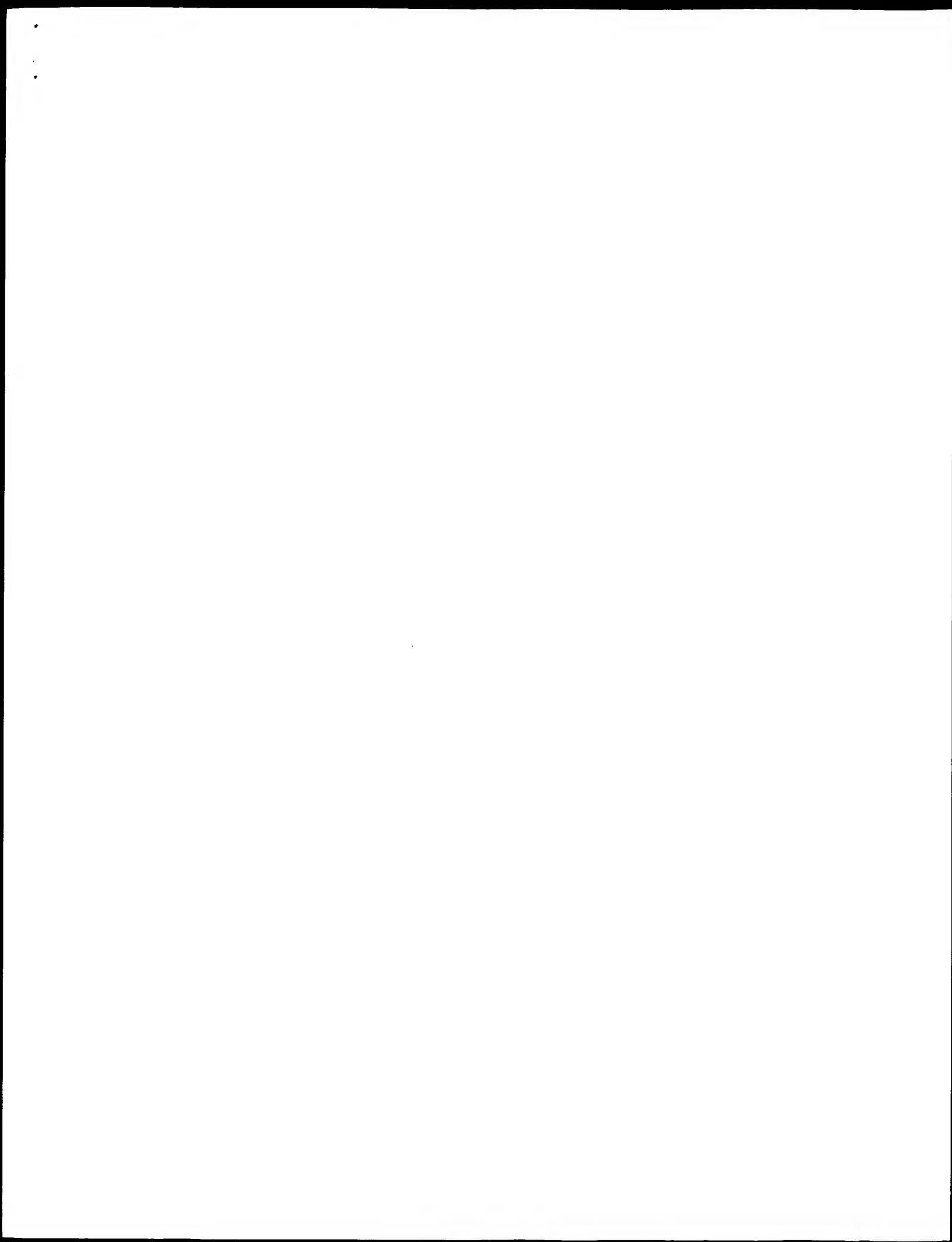
```

QY 743 ANLAAACGGITFTTLYLPVLCVAMODYGFILKIFASLISLVAAFGCEYALPEEGCI 802
Db 293 ANLSI---GIATLVLYASVAL-----ATWYGS-LVLSNESI 326
QY 803 GYQWMDLFSPEVEDGFNLTTSSIMLFDPLFYGVMTWTEAVFPQGXGIPRPWY-----857
Db 327 G-----QVLTFPSTLLGTFSIGLAPIEA-FANARAAEIRKIIDN 369
QY 858 FPCTKSYWFEESDEKSHPGSNOKRMEICEBEPHLKLVSIONLYKVY--RDGMKYA 915
Db 370 EPSIDSF-----STKGH-----KPDISINGNEFKNVFNYPSPREVKI- 407
QY 916 VQGLALNFEYGQTSPLFNGAGKTTMSILGLPEPTGTAVIIGKDIRS-EMSTIRON 974
Db 408 LKGLNLKVSQGVVALVNGSGCKSTVQDLQRLDPIGEVSDIGQDIRITNVYIRI 467
QY 975 LGVCPQHNVLFDMLTVEEHIFEARLKLSEKHVKAEMROMALD--VGLP---SSKLRSK 1029
Db 468 IGVVSOEVLV-FATTAENI-RYGRENVMTDELEKAVKANAYDFIMKLPKHFNTLVGER 525
QY 1030 TQSLSGMOKLSVALAFYGGSKVYLDEPTACVDPYSRKGIWELLKTRQGRTHLSH 1089
Db 526 GAOLSGQKORIAIARALVRNPKILLDEATSAIDTESAVVOALADKAREBRTIYIAH 585
QY 1090 HMEADVLDGRRIAISHGKLCCVSSSLFKNOIGTYLTLVKDVESSLSCRRNSSTV 1149
Db 586 R-----LSTVRNADVIA 597
QY 1150 SYLKEDSVSQSSDAGLSDEHSDTLTIDVSAISNLIRKHVSEARVEDIGHETLYVLP 1209
Db 598 GF-----DCGV-----YVQGNHE-----611
QY 1210 YEAAKE-GAFVLP-----HEIDRLSDLGTSY---GISFTYLEITLKAAEBSG 1256
Db 612 -ELMKRGYIFKLVMTQTRGNETEP-----GNAVESQSDTASSETL-----652
QY 1257 VDLETGDTLPARRNRARFGKOSCLRPTEDDAADPNDSIDPESRETDLSGMDGKS 1316
Db 653 --SEKSKPLIRSTIRSHRQDQERLSKE-----DVDEVP-----690
QY 1317 YQYKGMKLTQOCFVALLMKRLIARRSRKGFPAQIVLPAVFCIALVESLIYPPGKIPS 1376
Db 691 -WVFWQILKLINISE--WPLYLV-----GVLCAVINGCIGQVFAIVFSKIVGF-----736
QY 1377 LELQPMYNNQYTFVSNDAPEDTGTELLNALTKDGFGRMCMEGNPIPDTCQAGBEBW 1436
Db 737 -----SRDDHEH-----744
QY 1437 TTPAPVQTTMDLFEQNGNMTMNPSPACQSSDKIKKMLPVCPPAGGLPPQORKONTADI 1496
Db 745 -----KORNCNLSL 754
QY 1497 LQDLTGRNISLYKTYVOIIAKSLKNIWNEFRYGGSLGVSNTQALPSPQEVNDAIK 1556
Db 755 L-----FLVGMISFVT-----YFPGFTFGKA-----GELITRRLR 786
QY 1557 QMKHKLAKDS-ADRFNLISLGRFMTGL-DTRNNVYKVFNNKGMHAISFLVNNAIL 1614
Db 787 YWFKSMRLKODISWFDHKNKTGSLTRRLASDASNVK-----GAMGSLAVYTQNV- 837
QY 1615 RANLQKGNPSSHGYTTAFNHPNLTKOOLSEVALMTTSVDLVSLCYTFAMSPVASFV 1674
Db 838 -ANLGTG-----IILSLVGMQTLTLLVLIIPILVIGIIEK-----874
QY 1675 FLIQERSKAKHLOPISGVKPVYIWLSEFVDMCNVVPALVLIITFCPOK---SYVS 1731

```


[illegible]

Db 704 -----DFGDE-----GV 710
QY 1240 SETTEEFLLVAESGVDAETSDGTLPARRRRAFGDKOSCLRPFTEDDAADPNDSID 1299
Db 711 T-----RIKTVSSSNSIDA-----VD 727
QY 1300 PESRETDLSGMDGSGYQVQKGMKLTQOQFVALLMKRLIARRSRKGFPAQIVLPAV-EV 1358
Db 728 EKARLEMRKTGTOKSVSAVLSKVPKPEQEKYSIMTLV-----KFIGAFNRPBEGYM 779
QY 1359 CTALVSLIIVPPCKYPSLELOPMWYNBOYTFVNSDAPEDGTLELLNALTKDPGFGTRC 1418
Db 780 LIGTFEFLAG--GGQPT--QAFLYAKAISTLS--LPE-----SMFHKLRIHDANF---- 823
QY 1419 MEGNPIPTPCQAGEEWTAPVOTIMDLFONGNWTQNPSPACQCSKIKKMLPYCP 1478
Db 824 -----WSLM-----827
QY 1479 PGAGLPPPKONTADILDLGTRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLG 1538
Db 828 -----FFVVGIAQFI-----SLS 840
QY 1539 VSNTO-ALPPOEVNDAIKOKKHLKLAKDSSADRFNLSIGRFMTGLDTRNNVQWPNK 1597
Db 841 INGTAFAICSERLIRARRSQAFRSILRODISFFDRENSTG-----881
QY 1598 GMAHISFLNYINNAIILANLOKGNPSHYGITAFAHPLNLTKOOLSEVALMTSVLV 1657
Db 882 --ALTSFLS-----888
QY 1658 SICVIFAMSFVAFVFLIOERVSKAHLOFISGVKPIYWLNFVDMCNVVPATLV 1717
Db 889 -----TETKNLSGVSQV-----TLG 903
QY 1718 IIFIFCFOOKSVSSTNIPVALLLLYGW-----STPLMPASFEVKIPSTAYVL 1770
Db 904 TII-----MTSTTGAMITIALAIGKIALVICISVPIILACGFL-REFYMLAQFOQ 953
QY 1771 TSVNLFIGINSVATFVLETFDNKNLNNINDIKSVFLIFPHFCIGRLIDMVKNOAMAD 1830
Db 954 RKSASIEGSASYACATSAIRTVASLTREODW-----GYTHD 991
QY 1831 ALERGENRFVSPLSMDLVGRNLFMAAVEGVFFLITVIOY-----RFFI- 1876
Db 992 QLOKQGRKSLISVLRSSL-----LYASS-QALVFPCVALGFWYGTLLGHHEYSIFRFVC 1046
QY 1877 -----RPPVNAKLSPLNDEDEDVRRERQRIIDGGGQNDI-----LEI 1914
Db 1047 FSEILFGAOSAGTVFSFAPDMGKAKNAQAQFKLPDSKPTIDWSEGEKLESMEGEIEF 1106
QY 1915 KELTKIY-RRKKRPVADRICVPIPPGECFGLGVNGAKSSTFKKMLJGDTVTRGDAF-- 1971
Db 1107 RDVHRYPTRPQPVLRGINLSVVRKPGOYIALVPGSGCKSTTIALLERFYDALAGVAFVD 1166
QY 1972 -----LNKNSILSNITHEVHQ-----NMGYCPOFDAITE--LITGREHEFPAL 2012
Db 1167 GKDITKILWNSYRSLISVSOEPTLYOGTIKENILLGVDKDVSBEETLIKVCKANITYDF 1226
QY 2013 LRGVDE--KEYGVGEMAIRRLGLVKYGEKAYNGVSGGNRKLISTAMALLIGPPVPELD 2069
Db 1227 VMSLPEGFDTVYVSGK-----GMLSGGQKORVAIARALLJDBPKVLLLD 1269
QY 2070 EPTTGMDPKARFLMNCALSVYKEGRSVVLTSISM 2104
Db 1270 EATSALDSESEKVV-QAALDAAARGRTTIAVAHRL 1303



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2002, 12:54:11 : Search time 42.61 Seconds
(without alignments)
5096.736 Million cell updates/sec

Title: US-09-595-526B-2

Perfect score: 11797

Sequence: 1 MACMPQLRLMKNLTFRRR.....VDVAVLTSFLDEKVKESYV 2261

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_71:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10922	92.6	2201	2	A54774 ATP binding cassette
2	3345.5	28.4	1529	2	A59189 ATP-binding cassette
3	3129.5	26.5	1472	2	B54774 ATP binding cassette
4	2645.5	22.4	1704	2	S71363 probable ATP-bindl
5	2642.5	22.4	1704	2	A59188 ATP-binding cassette
6	2060	17.5	1802	2	T33783 hypothetical prote
7	1984	16.8	1816	2	A84845 probable ABC trans
8	1863.5	15.8	1447	2	T15200 hypothetical prote
9	1792	15.2	1317	2	C88525 protein F35E11.4
10	1542	13.1	1758	2	F88559 protein C48B4.4b
11	1538.5	13.0	1704	2	T42749 ATP-binding cassel
12	1536.5	13.0	1767	2	S60124 transport protein
13	1402	11.9	1246	2	T00826 hypothetical prote
14	1158.5	9.8	1564	2	T27121 hypothetical prote
15	1013.5	8.6	373	2	T47150 hypothetical prote
16	1010.5	8.6	1431	2	T22748 hypothetical prote
17	846	7.2	269	2	T46467 hypothetical prote
18	788.5	6.7	1011	2	T07712 probable ABC-type
19	693	5.9	900	2	T07717 probable ABC-type
20	667	5.7	895	2	T07714 probable ABC-type
21	656.5	5.6	722	2	T07716 probable ABC-type
22	645	5.5	925	2	T07713 probable ABC-type
23	624.5	5.3	1336	2	T18288 ABC transport prot
24	485	4.1	196	2	T12512 hypothetical prote
25	432	3.7	339	2	S74048 probable daunorubi
26	428	3.6	664	2	T07715 probable ABC-type
27	426.5	3.6	324	2	C71081 probable resistanc
28	421	3.6	328	2	E75108 daunorubicin resis
29	411	3.5	330	2	S27707 daunorubicin resis

30	410.5	3.5	310	2	C96929 ABC-type multidrug
31	410.5	3.5	327	2	D72257 hypothetical prote
32	410	3.5	314	2	D97318 ABC-type MDR trans
33	409.5	3.5	398	2	C69485 daunorubicin resis
34	403.5	3.4	297	2	AE1816 ABC transporter (A
35	396.5	3.4	333	2	D72492 probable ABC trans
36	395.5	3.4	246	2	S75436 hypothetical prote
37	390	3.3	301	2	E72384 ABC transporter. A
38	388.5	3.3	310	2	E69920 ABC transporter (A
39	388	3.3	311	2	G69803 ABC transporter (A
40	386.5	3.3	727	2	T07718 probable ABC-type
41	386	3.3	259	2	H97301 ABC-type MDR trans
42	386	3.3	331	2	D70984 probable drpA prot
43	385	3.3	350	2	B69065 ABC transporter (A
44	384	3.3	331	2	E73019 daunorubicin resis
45	380	3.2	312	2	H97342 ABC-type MDR trans

ALIGNMENTS

RESULT 1
A54774
ATP binding cassette transporter ABC1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Apr-1995 #sequence_revision 05-Apr-1995 #text_change 02-Feb-2001
C:Accession: A54774
R:Luciani, M.F.; Denizot, F.; Savary, S.; Mattei, M.G.; Chimini, G.
Genomics 21, 150-159, 1994
A:Title: Cloning of two novel ABC transporters mapping on human chromosome 9.
A:Reference number: A54774; MUID:94375008
A:Accession: A54774
A:Molecule type: mRNA
A:Residues: 1-2201 <LUC>
A:Cross-References: GB:X75926; NID:9495256; PIDN:CAA53530.1; PID:9495257
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
C:Keywords: ATP; duplication; nucleotide binding; P-loop
F:856-1047/Domain: ATP-binding cassette homolog <ABC1>
F:873-880/Region: nucleotide-binding motif A (P-loop)
F:1865-2060/Domain: ATP-binding cassette homolog <ABC2>
F:1886-1893/Region: nucleotide-binding motif A (P-loop)

Query Match	Score	Length	DB 2	Length	DB 1
Best Local Similarity	92.6%	2201	2	2201	2
Matches	2089	Conservative	55	Mismatches	57
				Indels	0
				Gaps	0
QY	61	MPSAGTLPWVGIIICNANNPCFRPTPGEPAGVGNFNKSIYARLSDARRLLYSQKDT	120		
DB	1	MPSAGTLPWVGIIICNANNPCFRPTPGEPAGVGNFNKSIYARLSDARRLLYSQKDT	60		
QY	121	SKDKMKVLRITQOIKKSSNKLQDFLVNDTFFSGFLYHNLSLPSKYVDKMLRADVILH	180		
DB	61	SKDKMKVLRITQOIKKSSNKLQDFLVNDTFFSGFLYHNLSLPSKYVDKMLRADVILH	120		
QY	181	KYFLOGYQHLTSLGKSGSEEMIQGDOEVELGCLPEKXLAARVLRSMQDLKIL	240		
DB	121	KYFLOGYQHLTSLGKSGSEEMIQGDOEVELGCLPEKXLAARVLRSMQDLKIL	180		
QY	241	RLNLTSPFSPSELAETATKLLHSLGTLAQELFSKRSMSDKQEVMTLVNVSSTSSSQI	300		
DB	181	RLNLTSPFSPSELAETATKLLHSLGTLAQELFSKRSMSDKQEVMTLVNVSSTSSSQI	240		
QY	301	YQAVSVIVCGHPEGGLKIKSLNWDNNYKALFSGNGTEDEAEFFYNSSTPYCNDLMK	360		
DB	241	YQAVSVIVCGHPEGGLKIKSLNWDNNYKALFSGNGTEDEAEFFYNSSTPYCNDLMK	300		
QY	361	NLSSPLSRITMKALKPLLVGKILYTPDPATRQVMAEVNKKFQDLAVFHLDEGMEEELS	420		
DB	301	NLSSPLSRITMKALKPLLVGKILYTPDPATRQVMAEVNKKFQDLAVFHLDEGMEEELS	360		
QY	421	PRITWFENSOEMDLVRMLDSDRDHFEWQDLQDLDTADIVAFIAKHPEDVOSSNGS	480		
DB	361	PRITWFENSOEMDLVRMLDSDRDHFEWQDLQDLDTADIVAFIAKHPEDVOSSNGS	420		

Db 361 POLITFMENSQMDLVRTLLDSRGNDQFWEQKLDGIDMTAQDIMAFLAKNPEDVOSPMS 420
 QY 481 VYTRAEAFNETNOAIRTISREMECVNLKLEPIATEVWLINKSMELDERKFMAGIVETG 540
 Db 421 VYTRAEAFNETNOAIRTISREMECVNLKLEPIATEVWLINKSMELDERKFMAGIVETG 480
 QY 541 IIPGSTEIPHHYKXKIRMDIDVERTNKIKDGYNDPGRAPDFEDMRVYWGFAILODY 600
 Db 481 IIPDSVELPHHVKYKIRMDIDVERTNKIKDGYNDPGRAPDFEDMRVYWGFAILODY 540
 QY 601 EQAIIKVLTEKTKGVYQMQMPYCYVDDIFLRVMSRSMPLFMTLAMIYSAVATIKGIV 660
 Db 541 EQAIIKVLTEKTKGVYQMQMPYCYVDDIFLRVMSRSMPLFMTLAMIYSAVATIKGIV 600
 QY 661 YEKEARLKTMTKIGLDSILMFMSFISLPLVLSAGILVYLKGNLPLSDPSVYFV 720
 Db 601 YEKEARLKTMTKIGLDSILMFMSFISLPLVLSAGILVYLKGNLPLSDPSVYFV 660
 QY 721 PLISVFAVVTILLOCFILSTLFSRANLAACGGIIVETIYLYLVCAVMOQDYVGTILKIRAS 780
 Db 661 PLISVFAVVTILLOCFILSTLFSRANLAACGGIIVETIYLYLVCAVMOQDYVGTILKIRAS 720
 QY 781 LLSVAFGCEYFALFEEOGIGVOMDLFESPEDEGFLNLTSTISMLFDTFLGVMTW 840
 Db 721 LLSVAFGCEYFALFEEOGIGVOMDLFESPEDEGFLNLTSTISMLFDTFLGVMTW 780
 QY 841 YLEAVFPGQYGIIPRWYFPCTKSYWFEESDEKSHPGSNOKRMEICMEEBETHIKIGVS 900
 Db 781 YLEAVFPGQYGIIPRWYFPCTKSYWFEESDEKSHPGSNOKRMEICMEEBETHIKIGVS 840
 QY 901 IONLVKVVYDGMKAVVDGALNFYEGOITSEFNGHAGACTTMTSLTGIFPPTSGTAVIL 960
 Db 841 IONLVKVVYDGMKAVVDGALNFYEGOITSEFNGHAGACTTMTSLTGIFPPTSGTAVIL 900
 QY 961 GKDISEKSTIRONLGVCPQHNVLEFDMLTVEEHIMFARLKLSEKHVKAEMEQALDVG 1020
 Db 901 GKDISEKSTIRONLGVCPQHNVLEFDMLTVEEHIMFARLKLSEKHVKAEMEQALDVG 960
 QY 1021 LPSKSKSTKSTOLSGMOKKISVALAFVGSKVYLLDEPTAGVDYSRKGIWELLKTRQ 1080
 Db 961 LPSKSKSTKSTOLSGMOKKISVALAFVGSKVYLLDEPTAGVDYSRKGIWELLKTRQ 1020
 QY 1081 GRTIILSTHHMDEADVLGRIALISHGKLCYSSSLFLKNQLGTYTYTLVKKDVESSLS 1140
 Db 1021 GRTIILSTHHMDEADVLGRIALISHGKLCYSSSLFLKNQLGTYTYTLVKKDVESSLS 1080
 QY 1141 SCRNSSSTYSLKEDSVSQSSDAGLGSDBHSDTLTIDVSAISMLIKRHVSEARLVEDI 1200
 Db 1081 SCRNSSSTYSLKEDSVSQSSDAGLGSDBHSDTLTIDVSAISMLIKRHVSEARLVEDI 1140
 QY 1201 GHELYTVLPEYEAKEGAFVLEFHEIDRLSDIGISSYSETTEIFLKAEBESGVDAE 1260
 Db 1141 GHELYTVLPEYEAKEGAFVLEFHEIDRLSDIGISSYSETTEIFLKAEBESGVDAE 1200
 QY 1261 TSDGTLPARNRRAFQKQSCLRPTEDDAADPNDSIDPESRETDLLSGMDKGSYOKV 1320
 Db 1201 TSDGTLPARNRRAFQKQSCLRPTEDDAADPNDSIDPESRETDLLSGMDKGSYOKV 1260
 QY 1321 GSKLHQOQFVALMKRRLIARSRKGFQAOIYLPVAFVICALVFSLYPPRGKYSLQLQ 1380
 Db 1261 GSKLHQOQFVALMKRRLIARSRKGFQAOIYLPVAFVICALVFSLYPPRGKYSLQLQ 1320
 QY 1381 PMYNDQOQFVNSNDAPEDTGTLELINALTKDPGFGTRCMEGNPJPDTPCOQAGEEBETAP 1440
 Db 1321 PMYNDQOQFVNSNDAPEDTGTLELINALTKDPGFGTRCMEGNPJPDTPCOQAGEEBETAP 1380
 QY 1441 VQOTIMDLFQNGNWTMOPNSPACQSSQKIKMLPYCPGAGGLPPQPKONTADILQDL 1500
 Db 1381 VQOSITVDLFQNGNWTMOPNSPACQSSQKIKMLPYCPGAGGLPPQPKONTADILQDL 1440
 QY 1501 TGRNISTDLYVTKTYOIIKSKLKNKIWNNEFRGGFSLGVSNQOALPPQOEVNDADIKOKK 1560
 Db 1441 TGRNISTDLYVTKTYOIIKSKLKNKIWNNEFRGGFSLGVSNQOALPPQOEVNDADIKOKK 1500

QY 1561 HUKIAKDSADREFLNSGKREMTGLDTRNNVYKWFENNKGMHAISSPLVNIINNALIRANLQK 1620
 Db 1501 LKLTKDTSDADREFLNSGKREMTGLDTRNNVYKWFENNKGMHAISSPLVNIINNALIRANLQK 1560
 QY 1621 GENPSHYGTAFAHNLKLTQOOLSEVALMTSDVLSICVIRFAMSVPASFPVFLIOER 1680
 Db 1561 GENPSHYGTAFAHNLKLTQOOLSEVALMTSDVLSICVIRFAMSVPASFPVFLIOER 1620
 QY 1681 VSKAKHLQFTSGKPVYVYMLSNFVWDMCNVVPATVITITFCQOKSVYSSTNLPVAL 1740
 Db 1621 VSKAKHLQFTSGKPVYVYMLSNFVWDMCNVVPATVITITFCQOKSVYSSTNLPVAL 1680
 QY 1741 LLLTGSSTPLMYPASFPVKIRISTAVVLTSVNLFGLNGSVATVLELFTDNKLNIN 1800
 Db 1681 LLLTGSSTPLMYPASFPVKIRISTAVVLTSVNLFGLNGSVATVLELFTDNKLNIN 1740
 QY 1801 DILKSVFLIPHPCLGRGLIDMYKNQAMADALEFRGNRPVSLSDMLVGRNLFMAVABG 1860
 Db 1741 DILKSVFLIPHPCLGRGLIDMYKNQAMADALEFRGNRPVSLSDMLVGRNLFMAVABG 1800
 QY 1861 VVFFLITVLIOYREFIRPRVYNAKLSPLNDEDEDRERORIIDGGQNDILEIKELTKI 1920
 Db 1801 VVFFLITVLIOYREFIRPRVYNAKLSPLNDEDEDRERORIIDGGQNDILEIKELTKI 1860
 QY 1921 YRRKRKPAVDRIYVGPCEPGLGVNAGAKSSTRKMLTGDTTVRGDAFLKNKSLNS 1980
 Db 1861 YRRKRKPAVDRIYVGPCEPGLGVNAGAKSSTRKMLTGDTTVRGDAFLKNKSLNS 1920
 QY 1981 IHEVHQMNGYCPQPDATTELTGRENHEVFPALLRGVPEKVGAVGMAIYKLGILVYGER 2040
 Db 1921 IHEVHQMNGYCPQPDATTELTGRENHEVFPALLRGVPEKVGAVGMAIYKLGILVYGER 1980
 QY 2041 YAGNYSGNRKRLSTAMALIGPVPVFLDEPTTGMPDKARFLMNCALSVYKGRSVLT 2100
 Db 1981 YAGNYSGNRKRLSTAMALIGPVPVFLDEPTTGMPDKARFLMNCALSVYKGRSVLT 2040
 QY 2101 SHSMECEALCTRAIMVNRFRCLGSVOHLKRFQGGYITVIRIGSNPDILKPYQDFFG 2160
 Db 2041 SHSMECEALCTRAIMVNRFRCLGSVOHLKRFQGGYITVIRIGSNPDILKPYQDFFG 2100
 QY 2161 LAPPQVYKKEKRRNMLQOYQPPSSISLARIFTSILSOSKRLHIEDSVSQTTLDOQVFN 2220
 Db 2101 LAPPQVYKKEKRRNMLQOYQPPSSISLARIFTSILSOSKRLHIEDSVSQTTLDOQVFN 2160
 QY 2221 AKQSDDDHLKDLISLKNQTVVDVAVLTSLQDEKVKESYV 2261
 Db 2161 AKQSDDDHLKDLISLKNQTVVDVAVLTSLQDEKVKESYV 2201

RESULT 2
 A59189
 ATP-binding cassette transporter - human (fragment)
 N:Alternate names: KIAA1062 protein
 C:Species: Homo sapiens (man)
 C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 02-Jun-2000
 C:Accession: A59189
 R:Kikuno, R.; Nagase, T.; Ishikawa, K.; Hirose, M.; Miyajima, N.; Tanaka, A.; Kotan
 DNA Res. 6, 197-205, 1999
 A:Title: Prediction of the coding sequences of unidentified human genes. XIV. The com
 A:Reference number: Z29961; MUID:99397452
 A:Accession: A59189
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-1529 <Kik>
 A:Cross-references: GB:AB028985; NID:95089460; PIDN:BA03014.1; PID:01046841; PID:956
 A:Experimental source: chromosome 9; clone hJ03579; clone lib pBluescriptII SK plus;
 C:Genetics:
 A:Map position: 9
 A:Note: KIAA1062
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

Query Match 28.4%: Score 3345.5; DB 2; Length 1529;
 Best Local Similarity 46.7%; Pred. No. 3.7e-208;
 Matches 721; Conservative 207; Mismatches 381; Indels 235; Gaps 33;

QY 836 GVMNTWYIEAVFPGQYIGPRWYFPCRTKSYWFG-----ESDEKSHPGSNOKRMS-----ETIC 887
 1 GILTWYIEAVHPGMYGLPRWYFPCRTKSYWFGSGTEAWEMSWPMARTRPLSYMEEDQAC 60
 Db 888 -----MEEPFHKLGVSLONLVKYYRDGKKAVADGALNFEGQITSLGN 935
 61 AMBSRREFTRGMEEBEETHLPVAVCDKLTYYKDKDKLANKLSLNLYENQVVSFLGN 120
 QY 936 GAGCTTMSITLGTLPPTSGTAYILGDKIRSEMTIRONLGVCPQHNVLTEHMLTVEHIM 995
 121 GAGCTTMSITLGTLPPTSGTAYILGDKIRSEMTIRONLGVCPQHNVLTEHMLTVEHIM 180
 QY 996 FYARLKLSEKHYAKEMQALDVLGPESSKLKTSQSGMOKLSVALAIVGSKVVI 1055
 181 FYSLKSMAGDEIRREDDKMIEDLEL-SNKRHSIVQTLSSGMRKRLSVAIAFVGGSKRAII 239
 QY 1056 LDEPTAGVDYSRGIMWELLKTYROGRTILSTHMDVAVDRLAIIHGLKCGVSS 1115
 240 LDEPTAGVDYSRGIMWELLKTYROGRTILSTHMDVAVDRLAIIHGLKCGVSS 299
 Db 1116 LFLKQGLGTYLLTVKKDESSLSGCRNSSSTVSYLKKEDVSQSSDAGLSDHESDT 1175
 300 LFLKQGLGTYLLTVKKDESSLSGCRNSSSTVSYLKKEDVSQSSDAGLSDHESDT 337
 QY 1176 LTIDVS--AISNLIRKAVSEARVEDIGHELYVLPYEAKEGAFVLEHIDRLSDLG 1233
 338 PLSSCSLEIYQSFIRKHVACQLVSDTSTELSYLLPSEAKKGAERLFOHLERSIDLALH 397
 QY 1234 ISSYGETSELEEFILVAAE-----SGVDA--ETSDGTP----- 1267
 398 LSSGIMDTLLEEFVFLVSEEDQSLSEADYKESKRDVLPGAEGPSSGCHAGNLARCS 457
 QY 1268 -----ARRNRA--FGDKQSCILPFTEDDADPNSDIDPESRETDLLS 1309
 458 ELTQSQSLQSSASVSGAGDEGAGYIDYGDYRPLF--DNQDPD--NVSLEVEABALS 514
 QY 1310 GMDCKSGYQKGMKLTQOQFVALIMKRLIARSRKGFPAQIYLPANFVCLAVFSLIIV 1369
 515 RV-GQSGRKLDGGLKVKRFGHGLVKKRHCARRSKALFQIILPAFVGVAMVALVSP 573
 QY 1370 PFQGYPSLELOPMYNYBOYT-----FVSNDAPE-----DTGTELLNLTQDGE 1414
 574 ETGLPPLVLSPOYH-NYTOPRGNFIPYANERREYRLRLSPDASQQLVSTRFLPSGV 632
 QY 1415 GTRCM-----EGNPT----- 1424
 633 GATCVLKSANGLSGLPTLNLSSGSRLLARFPDSMCLSEPTQGLPLSNFVPPPPAPS 692
 QY 1425 -----PD-----TPCQAGEEBMTAP--VPOTIMDLFONGWMTMONSPACQSSDK 1469
 693 DSPASPEDLOAMVNSLPRTAGPMMWTSAPSLPRLVREPVK-----CTCSAOG 740
 QY 1470 IKKMLPVCOPGGLPPORRONTADILODLTGRNISDYLVKTYVOJIIASLKIKIWNVE 1529
 741 TGFS-----CPSSVGG--HPPQMRVVTGDLITDITGHANSEYILFTSDR-----RL 785
 QY 1530 FRYGFSIGVSNTOALPPSOEVNDAIKOMKHLKLARDSSADRLNSIGREMTGLDTRNN 1589
 786 HRYGATIFGC--NVLKSTIPASGCTRAPPMVK-----IAVRA 820
 QY 1590 VKVFNKNGHAISSFLVNNALIRANLQGE--NPSHYGTTANHPNLTKOOLSEVAL 1648
 821 AOVFNKNGHAISSFLVNNALIRANLQGE--NPSHYGTTANHPNLTKOOLSEVAL 1648
 QY 1649 MTSVDVAVSLCVIAMSFPVASFVFLIDRVSKAHLQDQISGVKPYIWLISFVWDMC 1708
 880 LLOGTDVAVIATITVANSFVASFVFLIDRVSKAHLQDQISGVKPYIWLISFVWDMC 1708
 QY 1709 NYVVPATLVIIITICFOOKSYVSSNTLVIALLLLLYGSITPLMYPASFEVFKIPSTAYV 1768

Query Match 26.5%: Score 3129.5; DB 2; Length 1472;
 Best Local Similarity 46.0%; Pred. No. 3.7e-194;
 Matches 676; Conservative 207; Mismatches 377; Indels 211; Gaps 28;

QY 888 MEPEPHLKLGVSLONLVKYYRDGKKAVADGALNFEGQITSLGNAGCTTMSITL 947
 16 MEPEPHLKLGVSLONLVKYYRDGKKAVADGALNFEGQITSLGNAGCTTMSITL 75
 QY 948 GLEPPTSGTAYILGDKIRSEMTIRONLGVCPQHNVLTEHMLTVEHIMVYARLKLSEKH 1007
 76 GLEPPTSGTAYILGDKIRSEMTIRONLGVCPQHNVLTEHMLTVEHIMVYARLKLSEKH 135
 QY 1008 VKEMEQMALDVLGPESSKLKTSQSGMOKLSVALAIVGSKVVIIDEPYAGVDYPS 1067
 136 IRRETDKMIEDLEL-SNKRHSIVQTLSSGMRKRLSVAIAFVGGSKRAIIIDEPYAGVDYPS 194

Db 940 NTLVATCCVILLIFVFDLPATYSPINPAVLSTFLYGMSTPLMYPASFEVSSAYV 999
 QY 1769 VLTSVNLFINGSVATVYLELT--DNKLNININDILKSVFLIFPFCGLGRLIDMVKQA 1827
 1000 FIVINLFEGITATVATFLLQLEHDKDKLVNSYLSKSCFLFPYNNIGHGIMEAYNEY 1059
 QY 1828 MADALERGE--NRVPSPLSMDLVGRNLPAMAVEGVFFLITVLIQRFPIPRPVNAKLS 1886
 1060 INEYAKIQOPFKMSPEEMDITVTRGIVAMAVEGVFFLITVLIQRFPIPRPVNAKLS 1119
 QY 1887 PLNDEEDVRRRORLIDOGGNDILEIKELTKYIRK--RKPADRICVGIIPGECFG 1943
 1120 PVED--DVDAVSERORVLRDADNDMWKIENTLKYKSKRIGRILVADRLCLGVRGECFG 1178
 QY 1944 LCVNAGKSSFPKMLTGTTVTRGDAPFNKNSIISNHEVQNNQYCPQPDATIELLTG 2003
 1179 LCVNAGKSSFPKMLTGTTVTRGDAPFNKNSIISNHEVQNNQYCPQPDATIELLTG 1238
 QY 2004 REHVEFFALLRGVPEKEVKGEMAIIRKLGLVYGEKYAGNYSGGNKRRLSTAMALIGCP 2063
 1239 REHVEFFALLRGVPEKEVKGEMAIIRKLGLVYGEKYAGNYSGGNKRRLSTAMALIGCP 1298
 QY 2064 PVFLEDEPTGMDPARRPLMNCALSIVKESGVYLTSHSMECALCTRAIMYNGRFR 2123
 1299 AFIFLEDEPTGMDPARRPLMNCALSIVKESGVYLTSHSMECALCTRAIMYNGRFR 1358
 QY 2124 CIGSVOLTKNRGDDGYTVIRTAGSNPDLKPYODFGLAFPGSVLKEKRNMLQYQLPSS 2183
 1359 CIGSVOLTKNRGDDGYTVIRTAGSNPDLKPYODFGLAFPGSVLKEKRNMLQYQLPSS 1417
 QY 2184 LSLARIFSLSSKRRLEHEDYSQTLTLDQVFNFAKQSD 2227
 1418 HISLAQVFSKMEYSGVLGIEDYSQTLTLDQVFNFAKQSD 1461

Db 1418 HISLAQVFSKMEYSGVLGIEDYSQTLTLDQVFNFAKQSD 1461

RESULT 3
 B54774
 ARP binding cassette transporter ABC2 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 02-Feb-2001
 C:Accession: B54774
 R:Luciani, M.F.; Denizot, F.; Savary, S.; Mattei, M.G.; Chimi, G.
 Genomics 21, 150-159, 1994
 A:Title: Cloning of two novel ABC transporters mapping on human chromosome 9.
 A:Reference number: A54774; MUID:94375008
 A:Accession: B54774
 A:Molecule type: mRNA
 A:Residues: 1-1472 <LOC>
 A:Cross-references: GB:X75927; NID:9495258; PID:CAA53531.1; PID:9495259
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
 C:Keywords: ATP; nucleotide binding; P-loop
 F:44-234/Domain: ATP-binding cassette homolog <ABC1>
 F:61-68/Region: nucleotide-binding motif A (P-loop)
 F:1108-1300/Domain: ATP-binding cassette homolog <ABC2>
 F:1126-1133/Region: nucleotide-binding motif A (P-loop)

```

QY 1068 RRGIMWLLKRYGRTIILSTHMDADVLGDRRIAIIHGKLCVGSSEFLKNOIGTGY 1127
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1195 RRAIMWLIIKYPGRITILSTHMDADVLGDRRIAIIHGKLCVGSSEFLKNOIGTGY 254
QY 1128 LTLVKYDVSSLSGCSNNSSTVYLKKEPVSQSSDAGLSDHSDTLITDVAISNII 1187
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 255 LTLVKYDPAEFTSQEPGLASPSGCRUSSCSEPO-----VSQFI 294
QY 1188 RKNHSEARLVEDIGHLELVVLPYFAKKEGAFVELFHEIDRLSDIGISSYSETLEEI 1247
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 295 RKNHVASLLVSDTSTELSYTLPSBAVKKGAERLQGLEHSDALHLSFGMLDITLLEV 354
QY 1248 ELKVAEE-----SGVDA-ETSDGTLPARNRRAAGDKOSCLRPTE----- 1287
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 355 FLKVESEDSLENSADYVESKRKDLPGAEGTLAAGGAGNLAARSCALASQASLQAS 414
QY 1288 -----DDAADPNDSDIDPESRETDLSGMDKGSYQYKGMKL 1324
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 415 VGSANGEETGYSDGGRPLFDNLQDPD--NVSLOEAKEMFALQV--GQGSRLLEGWML 471
QY 1325 TQOQFVALIKRLLIARSRKGFPAQIVLPAVFCIALVFLVPPFGKYPSELQPMY 1384
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 472 KKRQFGLIYKFRHCAARRSKALCSQILPAFFVCAMVALSVEIGDLPLVLPQY 531
QY 1385 NQOYT-----FVSNDAPR-----DTGTELLMLTDRPGCTKCM----- 1419
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 532 H-NTTQPKGNFIYANEEKQETRLRLSPASFOQLVSTFRPLSGVATGATCLSPANGSLG 590
QY 1420 -----DGNPI-----D----- 1426
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 591 PMLNLSGSRLLAARFEDSMCLESFTQGLPLSNFVPPPPSPAPSDPVXDESLQAMN 650
QY 1427 --TPOAGEEEMTAP-VPOITMDLPQNGNMTMNPSPACQSSSKIKMLPDCPPGAG 1483
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 651 MSLPPLAEPETWTSAPELRLHEPVR-----CQCSAGTGSF--CPSSVGG 695
QY 1484 LPPQKONTADILQDLGRNISIDLVKTYVOIILAKSLKNKIWVEFFGFSLSGVSNTQ 1543
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 696 -HPQMRVVTGDIILDTIGHNVSEYLLFTSDF-----RLHRYCATITG--NVQ 741
QY 1544 ALPPQOEVDATKQKKHKLAKSDASAREFLNSLGRFMTGDLTRNNKAVVFNKNGMAIS 1603
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 742 KSTPAS-----FAARPPMNRKLAIVRVAQVILNNKGYHSP 778
QY 1604 SFLANVINNAIIRANLQKE-NPSHYGITAFNHPNLTKQOLSEVALMTSVDAVLSICVI 1662
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 779 TYLNSLNNAILIRANLPKSGNPAAYXITVTNHPNKTASISL-IDYLLQGDVIAITTI 837
QY 1663 FAMSVPASPVFVLIQERYSKAKHLOFISGVKPVYIWLNFVMDKCNVVPATVILIEI 1722
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 838 VAMSVPASPVFVLIQERYSKAKHLOFISGVKCNVYIWLNFVMDKCNVVPATVILIEI 897
QY 1723 CFQOKSYASTPVLATLILLYGSIPLMYPASFEVKIPSTVYVLTNSLFGINGS 1782
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 898 VEDLPATYSPINTEPAVLSLFLITGMSITPIMYPAFWFEVSSAVFLIVNLGITAT 957
QY 1783 VATEVLELFT-DNKLNINIDILKSVYLFPHFCGLGLIDVKKQAMADALERCE-NRF 1840
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 958 VATEVLELFT-DNKLNINIDILKSVYLFPHFCGLGLIDVKKQAMADALERCE-NRF 1017
QY 1841 VSPLSMDLVGRNLFMAVEGVVFLITVLYRFRIRPRVNAKSLINDEDEVRERQ 1900
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1018 KSPFEMDLYVTGLVAMVEGVEGFLITMCOYNFLRQORLPVSTKPEV-DVVAASERQ 1076
QY 1901 RILDGSGNDILEIKELTKIYRRK---RKPVDRIQVGI-PPGCGFLGVNAGKSKSTF 1956
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1077 RVLREDADNDMVKTIENLKVKYKSRKIGRIILAVDRICGVCPGCGFLGVNAGKSKSTF 1136
QY 1957 KMLTGDITVTGDAFLANKNSLISNHEVHOMGTCPOPDATTEILLTGREHVEFPALLRGV 2016
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1137 KMLTGDISTGGEAFVNGHSHVCLKDLLOVOISIGYCPQFDVAVDELITAREHILQYTLRLCI 1196

```

```

QY 2017 PEKEVGKGEWAIKRLGLVYKGEKYAGNYSGNKRRLSTAMALIGBPVYFLDEPTGMD 2076
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1197 FMKDEADVWVALEKLELTETVADKRPACTYSGGNKRRLSTALIGVPAFLDEPTGMD 1256
QY 2077 PKARFLMNCALSVYKGRSVLTSHEMCEALCTPMALVNGRFRCLASVOHLKNRG 2136
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1257 PKARFLMNLILDLIKTGRSVLTSHEMCEALCTRLALVNGRRLHCLASIOHLKNRG 1316
QY 2137 DGYTIIVRIAGSNPDLKPVODFFGLAPGSLVLEKERNMLOYOLPSLSIARIFSLSQ 2196
    ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1317 DGYTIIVR-IKSSQNVADVVRFFNRNPEAHAGKTPYKQYOLKBSHISLAQVSKMRQ 1375
QY 2197 SKRLHIEDYSVSQTLIDQYVFNKADQSD 2227
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1376 VGVIGIEDYSVSQTLIDVFNKAKKQSDN 1406

RESULT 4
S71363
Probable ATP-binding cassette transporter ABC-3 - human
N:Alternate names: ATP-binding cassette transporter ABC-C
C:Species: Homo sapiens (man)
C>Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 02-Feb-2001
C:Accession: S71363
R:Krugbauer, N., Hofmann, F.
FEBS Lett. 391, 61-65, 1996
A:Title: Primary structure of a novel ABC transporter with a chromosomal localization
A:Reference number: S71363; M0ID:96326608
A:Accession: S71363
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-11704 <KIU>
A:Cross-references: EMBL:X97187; NID:g1514529; PIDD:CA65825.1; PID:e243436; PID:g151
A:Experimental source: cell line medullary thyroid carcinoma
C:Genetics:
A:Gene: GDB:ABC3
A:Cross-references: GDB:3770735; OMIM:601615
A:Map position: 16p13.3-16p13.3
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
C:Keywords: ATP binding, nucleotide binding, P-loop, phosphoprotein, transmembrane pr
F:325-283/Domain: transmembrane #status predicted <TM1>
F:307-329/Domain: transmembrane #status predicted <TM2>
F:345-364/Domain: transmembrane #status predicted <TM3>
F:373-394/Domain: transmembrane #status predicted <TM4>
F:401-422/Domain: transmembrane #status predicted <TM5>
F:452-475/Domain: transmembrane #status predicted <TM6>
F:549-739/Domain: ATP-binding cassette homology <ABC1>
F:566-573/Region: nucleotide-binding motif A (P-loop)
F:605-690/Region: nucleotide-binding motif B
F:1100-1120/Domain: transmembrane #status predicted <TM7>
F:1145-1169/Domain: transmembrane #status predicted <TM8>
F:1181-1207/Domain: transmembrane #status predicted <TM9>
F:1215-1236/Domain: transmembrane #status predicted <TM10>
F:1245-1264/Domain: transmembrane #status predicted <TM11>
F:1299-1324/Domain: transmembrane #status predicted <TM12>
F:1399-1590/Domain: ATP-binding cassette homology <ABC2>
F:1416-1423/Region: nucleotide-binding motif A (P-loop)
F:1535-1540/Region: nucleotide-binding motif B
F:644, 866, 1524/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #s
F:1344/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status pr

Query Match 22.4%; Score 2645.5; DB 2; Length 1704;
Best local Similarity 35.7%; Pred. No. 1.3e-162;
Matches 639; Conservative 300; Mismatches 523; Indels 327; Gaps 48;

QY 534 AGIVTGTIRPGSIE-LPHVYKYYIRDDINVERKN-----KIDGTV----- 574
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 131 AAIVFEHPNHSKEPLVLAQVHLRF---SYTRRNMTQGSFPLKTEGHTTSLEPL 187
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 575 --DPPRADPFED---MRYVWGFAVLQDVQDAIIRVLTGNE-----KKTGVYMQQMPY 624
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 188 FPNRGPREPSPGCGEGRYIRSGFLAVQHAVDRAIMEYHADAATNQLQRLVTITKRPY 247

```



```

Db 168 FPNPBRRLTSPDGEPEYIREGLAVOHAADRAIMEHAADATROLFORLTIVTKRPY 247
QY 625 PCYVDIDFLRVRNSRSMPLFMTLAWISVAJIKGIVEKEARLEETMRIMGLDSIMFS 684
Db 248 PPFIDAPFLVIAIOYOLPRLILSLFYALTITARAAYOKERERLEKYMMLGLSMLHMSA 307
QY 685 WFTSLILPLASAGLIVVILKLG-----NLIPYSDPSVVEFLSVFAVNTLQCEFLISTL 739
Db 308 WFLIFLPLDILASPMILFPCVKKPNVAIVLSRSDPSLVLFILCFALSTISFESMSTF 367
QY 740 FSRANIAACGGIIFLYLPLVLCVAMQDVYGFLLKIFASLISPVAFGCEFAFLFEE 799
Db 368 FSKANMAAAGFGLFELFYIIPFVAPRYRNMNTLSQKCSLLSNVAMAAAOGLIGKEA 427
QY 800 OGIGVONMLESPYE-EDGFNLTTSISMALFDPLFYGVMTVYEAAPROGIGPRMYF 858
Db 428 KGMGIOMBDLL-SPVAVDDDFCGOVLGMLLDVGLVWMEAVPPOGFQOPMYF 486
QY 859 PCTKSYNFE-----ESDEKSHPSGNOKRMSSEICMEEPHMKIGVSIOMLVWYRDM 912
Db 487 FIMPSYWGCKPRAVAGKKEEDSDP---EKALNFEFMEAPEDVAVAGITIKHLSKVFYGN 543
QY 913 K--VAVDGLALNFEYEGQITSPGHNAGKTTMTSLTGLPRTSGTAYILGKDIRSEMST 970
Db 544 KDRAAVRDLNLTLYEGQITVLLGHNAGKTTLSMLTGLPRTSGRAVAYSYEISODMVQ 603
QY 971 IRONLGVCPONHVLFDMLTVEHNTWFAKRLKGLSEKHAKAMDMALDVGIPSKELSKT 1030
Db 604 IRKSLGICLPONDILFDNLTVABHLYTAOLKGLSKOKPREBYKQMLNITGL-ERKWNRS 662
QY 1031 SOLSGMRRKLSVALAFVGSKVYLLDPRAGVDPYSRGIMWELLKXRGORTITLSTNH 1090
Db 663 RFLSGMRRKLSIGITALIAGSKVLLDDEPTSGMDAISRRALIMDLOROKSDRTIVLTJHF 722
QY 1091 MDEAVLDRILALISHGKLCVGSFLKNOGLGTGYLLTKKOVESLSCRSSSTVS 1150
Db 723 MDEAVLDRILALISHGKLCVGSFLKNOGLGTGYLLTKKOVESLSCRSSSTVS 1150
QY 1151 YLKEDSVSSSSDAGLSDHESDPLTIDVSAISNLIRKHVSEARLEVEDIGHEILVYLPY 1210
Db 767 HCNPED-----ISQIVHNHVRNMTLESSACAEISFILPR 800
QY 1211 EAAKGAVALFHEIDDLSDGLISSYIGSETTLEIFLKYAE--ESGVDAETSDGLPA 1268
Db 801 ESTHR--EGFLAKLEKKQKELGIASFASLTTEBEVFLRGKLVDSMDIOAQI--LPA 856
QY 1269 ---RRNRRAFg---DKQSLRPFTEDDAADPND---SQIDSESETDLSGMDKGVSQY 1319
Db 857 LOYQHERASDAVDSNLC-----GAMDSGIGALITEERTAVKLTGL----- 901
QY 1320 KGMKLTQOOFVALLMKRLILARSRKGFPAQIVLPAVFCIALVFSLIVPFGKYPSEL 1379
Db 902 ---ALHCQOFWAMFLKKAAYSREMKVYAQVULVCVLTALL----- 942
QY 1380 QPMWYNEQYTVSNDAPEDTGLTLLNALITDPRGTRCMGANTIPDTPCQAGEEWTTA 1439
Db 943 -----AINYSSELFDDPMI--RLTLG-----EYGR 966
QY 1440 VVPOTIMDLFONGMWTQNPSPACOSSDKIKMLPVCPRPAGGLPPQORKONTADLLOD 1499
Db 967 VVPSVPTSQLGQOOLSHLKDIAQABG-----QPREVLGD 1003
QY 1500 LTGRNISDYLVKTYVQIIAKSLKNIWNERFY---CGFSLGVSNTOALPPSOEVDAI 1555
Db 1004 L-----BEFLI-----FRASVEGGFN----- 1020
QY 1556 KOMKHLKLADSSADRLNSLGRFMGJLDRNNVKKYFENKKNHAISSPLANTVNNALIR 1615
Db 1021 -----ERCL--VAASFRDYGERTVYVNALFNNOAVHSPATALLAVVNDLFLK 1063
QY 1616 ANLKGENDSHYGIATFVHP-----LNLTKOOLSEVALMTTSVIVLSICVIFAMSVPA 1670
Db 1064 ---LLCG---PHASIVSVNFPOPRSAIOAKQDFNE---GRKGFDIALNL--LFMAATLAS 1113

```

```

QY 1671 SPVVELIOERVSQAKHLQFISGVKPIYIWLISNFWDMCNVVPATLVITICFOOKSYV 1730
Db 1114 TFSILAVSERAAVOAKHVOFSGVHVASFMLSALIMLISFLIPSLILVFAFVDRVAT 1173
QY 1731 SSTNPLVALALLLGYMSTPLMTPYASFWKIPSTVYVVLTSNLEFGLINGSVAFVLEL 1790
Db 1174 RCHMADTLLLLLYGMALIPMLTLMNFFLGAAVATYRLITFNLSG---AFLMWT 1229
QY 1791 ---FTDNKLNINDILKSVFLFPHFCISGLIDVKN-----QAMADALREFG- 1836
Db 1230 IMRLPAVKLEELSKTLDHVFVLVPHNCLGMVASSFEYENETRYCSCSSVAHCKYVI 1289
QY 1837 ---ENRVPPLSMDL--VGRNLFMAAVEGVFPLTVLLQYREFIPRYVNAKL----- 1885
Db 1290 QYQENFY---AWSAGQEFVAFMAASCAVALILFLETNLLORLGLICALRRRTL 1345
QY 1886 ---SPLNDEEDVYRERORILDGGONDI---LEIKELTKYRRKRKP--AADRICV 1934
Db 1346 TELYTRMPVLPEDQVADERTRLIARSPDSLHTPLILIKELSVY--EQRVPLVADRSL 1404
QY 1935 GIPPGCEGFLGVNAGKSSFTKMLTGDTTVTRGDAFLKNSTLSNIEVHONMGYPOF 1994
Db 1405 AVOKGCEGFLGFGNAGKTTFTKMLTGESLTSGDAPFVGHRISDPVGRORIGYPOF 1464
QY 1995 DATTELTGREHEVEFALLRGVPEKEVKGEMAIRKGLVWYGEKYAGNYSGGMKRKL 2054
Db 1465 DALDHKTKGEMLVYKARLGRIPERHIGACVENTLGLLEPHANKLVYTSYSGNKRKL 1524
QY 2055 TAMALIGRPVYFLDEPTTGMPKARFLMNCALSVYKGRSVLTSMSMECEALCTRM 2114
Db 1525 TGIALIGEPVAVILDEPSTGMDVARRLLMDTVARARESGKAIITSHSMECEALCTRL 1584
QY 2115 AIVWNGRRCISGVHILKRNPRGDTIVRI--AGSNPLKPYODPFGIAPFGSVLKEKH 2172
Db 1585 AIVWQGFQKLSPPQHLKSFSGISLRAKVOSGQOALDEEKFKAVDLTFPGSVLEDEH 1644
QY 2173 RNMLQYQLPSSLSLARIFSLSQSKRRLHIEDYSVQTTLDQVFNFA 2221
Db 1645 QGVWVYHILPRDLSMAKVFGLLEKAKKGYVDYSQSLDQVFLSFA 1693

```

```

RESULT 6
T33783
hypothetical protein Y39D8C.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Mar-2000
C:Accession: T33783
R:Becker, M.; Graves, T.; Yoakum, M.
submitted to the EMBL Data Library, October 1998
A:Description: The sequence of C. elegans cosmid Y39D8C.
A:Reference number: 221408
A:Accession: T33783
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1802 <BEC>
A:Cross-references: EMBL:AF101313; PTDN:AAC69223.1; GSPDB:GN00023; CESP:Y39D8C.1
A:Experimental source: strain Bristol N2; clone Y39D8C
C:Genetics:
A:Gene: CESP:Y39D8C.1
A:Map position: 5
A:introns: 45/3; 114/1; 195/1; 230/3; 543/3; 794/1; 1036/2; 1099/1; 1132/3; 11
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

```

```

Query Match 17.5%; Score 2060; DB 2; Length 1802;
Best Local Similarity 27.9%; Pred. No. 1,5e+124;
Matches 551; Conservative 338; Mismatches 630; Indels 454; Gaps 52;
QY 385 YPPDPATROVAEVAENKTKQELAVFHLEGMMEEISPKITWFMENSQEMDLVRLMDSRD 444
Db 119 YAPMTATATQIMDKIONKRI-----TANDL-----LNP-VAAVITKGLYNTAVPVLTWMT 167

```

QY 445 NDHEWQOGLDMDTADODIAPLAKHPEDVQSSNGSVYTWREAFNETNOAIRTISRMEC 504
 Db 168 YKGF-----TTEGEMVSMQOFOSS-----EC 189
 QY 505 VNLKLEPATEWMLINKSMELLDERKFMAGIVFTGTPGSIELPHHVKYKIMDIDNVE 564
 Db 190 DN-----PLT-----AGIVFDDSIADKLNPKRDPETTYIRLSNTH 225
 QY 565 RTKIKDGYMDPGPRADPFEDMRYVNG-----GPAV 595
 Db 226 RRSR-----NAGDONSYPMDTSVSAFVAVYVSGPINDDDNGSGPGYMOBGFMT 273
 QY 596 LODVDEQATIRVLTEK-----TGVMQOMPEPCYVDIDFLRVRSMPLFMTLAWY 650
 Db 274 VQRAVDALTEITIGEDAQTLPLDSYVSRFPFGSTKI-TEICAFMPYVIVISPM 332
 QY 651 SVAVITKGYEKEARKETMRIMGJDNSTLWFSPTSSILPILVAGLLVYLKGNLL 710
 Db 333 SVIYIYRAVVEKEDRLKEYMRVWGLSOFINVAHFILINAKLTFPAVITLIMHVAL- 391
 QY 711 PYSDPSVFEVLSVFAVVTILOCELSTLFSRANLAACGIIYFTLYL----- 759
 Db 392 -KDMTLMFEVLTIAFDVYFAFMISFMSNATSATLISVFMMLLYWYAFSSIDOT 450
 QY 760 -PYLVAMODYVFTLKIFASLSP-VAFGCEYFALFEBOGIGVMDNLFESPVED 817
 Db 451 NPYPL-----GYRL-----INCINPDIALNYGLQJLLAVETQADLKKGLFTPPSPN 499
 QY 818 GFLUTISIMLFDTLGYVMYVIAVPPGOYGP-RWVPPCKSYW-GEESDEK 873
 Db 500 NLTFGHALLALIVDGIIMILTWYIEAVIPGEGVPOKEMWF-VLPSPWPNSSGKTVD 558
 QY 874 SHPGSNOKRMESEICMEEPETHLKIGVSIONIVKY-----RDMKAVAVDL 919
 Db 559 SDQFOQIYADAHKLEKEPTDLIPTINAVNLTKYTGTSFKKLPDCKFSKGBKRAVNL 618
 QY 920 ALNFYGOITSLFNGHAGKTTMILTLGTPPTSGTAYILKDKINSESTIRONLGYCP 979
 Db 619 NLKMYPGOCTVLLGHNGACKSTFMSLTGTVASPSSAVVNFDIRTLSPKIRREGLCP 678
 QY 980 OHNVLEDMLEVEHIEFVARKGLS--EKHVAEMQALMDVGLBSSKSKSTSOUSGSM 1037
 Db 679 QYVTLGFMVMEHLEFPAKLEKERTWDPREAREILARLIDF-----KADFNAGALSQGO 733
 QY 1038 ORKLVALAFVSGSVVILDEPTAGVDPYRRIGIWEILLKRYOGRTIILSTHMDADVL 1097
 Db 734 KRRLSLAIALIGSSEVVMDEPTSGMDPGARHETWLLIOREKFRITILTFHMEADLL 793
 QY 1098 GDRIALIISGKLCVGSLLFLKNQJGTGYLLLVKKDVSSLSGCRNSSSTVYLKEDS 1157
 Db 794 GRIALIMAGOLECCGSPMFLKQOYGDGYHLYV----- 827
 QY 1158 VSQSSDAGLGSDESDTLTIDVSAISNLIRKHVSARLVEDIGHELYVLYPEAKBGA 1217
 Db 828 -----IDTITSPVSKTTDITIKETIPBAHVSTYIGOEAYTL--SATHRI 871
 QY 1218 FVELFHEIDRLSDLGISYGISETTELEIFLVAE-----ESGVADETSDTLPAR 1269
 Db 872 FPLFELKEDHQTGCGITSFVGSITTMEEVPLKVGHTADERYNHYGIENDISE----- 925
 QY 1270 RNRRAFGKQSLRPTEDDADDPNDSDIDPRESTDLISGMDGSGVQVKKMLTQOOF 1329
 Db 926 -----MIED--DPLIODI-----BAQVAVTGTLOMOHA 953
 QY 1330 VALLMKRLIARRSRKGFQAVIPLAVFCIALVFLIYPPGKPSLELOQWMTNEQYT 1389
 Db 954 KAMFVKRAIFFRKMTOFLPQVLFVAVIYLVNFSQVLPVSK----- 997
 QY 1390 FVSNDAPEDTGLELINALTKDPGFGTRCMESGNIPDTPCQAGEEEMWTAPVQTIMDLF 1449
 Db 998 -----DPPQITSLA-----PSSDK-KAG-----HLVSD-- 1020
 QY 1450 QNGNMTMGNPSPACCCSSDKIKKMLPVCPFGAGLPPQORKONTADILQDLTGRNISDYL 1509

Db 1021 -SGNYVTL-----LGG-----SOWLSMV 1038
 QY 1510 VYTYOQIILAKSLKNIWNEFRYGGFSLGVSNTQALPPSOEYNDAIKOKMKHLKAKSS 1569
 Db 1039 OGTVTY-----LGVYQT-----VVDITSVEKFINQNTAM 1069
 QY 1570 ADR-----FLNSLGRMTGLDTRNNVYKWFENKMKWHAISSFLANILANILANIK 1620
 Db 1070 GSRFTGLHYALGFVPSMNEST--VSPSLKTFENNFPLYPALAIPTTDSMILISQOKK 1127
 QY 1621 GENPSHYGTAFNHPNLNTKQOLSEVALMTSVDVLSICVIFMSPFASVYVFLIOER 1660
 Db 1128 -----QYSTAVNHPPLPSTODTLKTNBSQCAAFILGVLVSFVAVCAIGQFLITER 1182
 QY 1681 VSKAHLQFISGVKPVIIYWLNSFVMDQCNVYPATLVIIIFICEPOKSVYSTN-LPYLA 1739
 Db 1183 KKSXHMQLSGIRBMMFWLTAFLINDAAMPVIRLCPAIFYIFNITAYTHDFGVMILIT 1242
 QY 1740 LLLILYMSITPLAMPASVFKRIPSTAVVLTLSNLFINGSVATVYLEFTDNKLNNI 1799
 Db 1243 LSFLLYGMALPFTYWFQFFESAPKGFMMYTHILTMIGISIAVPIISOTSSIDAGYL 1302
 QY 1800 NDIKSVFLIPHPCLGGLIDMVKNOAMADALERE-----GENRFS 1842
 Db 1303 WSLIYA--WLPFTYVISOIATVYTONENVRIACKLDCDTIMFRAVYACCTASERLYD 1360
 QY 1843 PLSDMLVGRN-----LEPMAVEGVFELLITVLIOYRPF-----IRRPVNAKLSPLND 1890
 Db 1361 NVLF--VGNRKGLIYVIFLAVOGFIYIWMFEMENDQFTLALIRCKRKNNDNIMDITD 1418
 QY 1891 -----EDEDVARR--QRILDDGGQNDILEIKELTYIRKKRPAYDRICVGIIP 1938
 Db 1419 TDKVDREVEOSDVIAEKSVOQL--ANNKTAVALSNLVWYGNFN--AVKGNFHVNS 1474
 QY 1939 GECEGLILGVNAGKSGSTKMLTGDYTVRGDAFLKNSIILNIEHVHONMGCEPOPAT 1998
 Db 1475 KDCFELLGVNAGKSTOTMLTGEMSSIGAYVNGSVKNNMEAGANTGYCQOYDAIL 1534
 QY 1999 ELLTGRHEVEFPALLRGVPEKVGKVGEMAIKGLVYKYGKAVGNVSGKRLSLTAMA 2058
 Db 1535 KEMSGEETLYMFARLGRIGPEKDIPKVAVIAHIGIGYASROIKTYSGKRRSLGIA 1594
 QY 2059 LIGGPVVELEPTGMPKARFLMNCALSVNEGSRVYLTSSMECEALCTRMIMV 2118
 Db 1535 IYGLPDLVLLEDPISGVDPKARRITIMNLRLDGLTALVLTSSMECEALCTELAIMV 1654
 QY 2119 NGRFCLGSVOHLKNRFGDYTIIVARIAGSNPDLKPYODFFGLAFPGSVLKEKRRMLQY 2178
 Db 1655 YGFRFCYSCQHIKSRVSGYTLLIRLKNR--DAEKTKSTIKQFRGSVIRKEHVADLNF 1713
 QY 2179 QLPSSLALATFSLSSKKRLHIEDYSVSCOTLLDOVFVNFAD--QSDDD 2228
 Db 1714 DIPRCDGSMRLFEKLETVSTSLNMWDYSLSQTLLEOVIEFESRDAGVSSDSE 1766

RESULT 7
 A84845
 Probable Aac transporter [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: A84845
 R:lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MID:20083487
 A:Accession: A84845
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1816 (KSTO)
 A:Cross-references: GB:AE002093; NID:96598351; PIDN:AA02761.2; GSPDB:GN00139

C:Genetics:
A:Gene: A12941700
A:Map position: 2

Query Match 16.8%; Score 1984; DB 2; Length 1816;
Best Local Similarity 28.8%; Pred. No. 13e-119;
Matches 584; Conservative 282; Mismatches 592; Indels 572; Gaps 60;

QY 489 NETNOAIRTIS-REMECVNLNKL--EPIATEVMIINKSMELDERKFWAGIVETGTPGS 545
DB 59 DETNMIDILSLKPELRLVTKIFKDDIELEYITSANHYGVCSSEVRNCSNPKIKGAVFHH 118
QY 546 IELPHNKKYKIRM-----DIDNVERTNKIKOSWMPGRADPE-----DMRY 588
DB 119 EOGHLEFDYSIRLNMHWAFAGFPNVSIMDTN-----GPYINDLENGINTTPTMOT 169
QY 589 VMGGAFLADVDEQALIRVLGTGTEKKTVGMQMPYCYVDIIFLRVMSKSMPLFMILAW 648
DB 170 SFGSEFLRLQOVDSFII-----PASQON-----NDLPLSHSNLSALRFPFLPW 212
QY 649 IYSVAITIKGIYEKARKLKEKRMINGLDSILFESWFISSLPLVLSAGLLVYLKLG 708
DB 213 TLFSPTVIRWVPFPTREYTDDE-----FOSIVKVMGLF-----246
QY 709 LLPEYSDSVFVFLSVFAVYVTLIOCFILITLFSRANLAACGGIYFTLYLPLVLCVAMQ 768
DB 247 LFKISDITLFTYFFELGLSALIMLSFMISTFTFAKTAIVAGILITLGAFFPY--TVND 304
QY 769 DYVGTIKIFASLSPVAFGCEYFALFEEQIGVQWMLFSPVEDEGFTLTTISMM 828
DB 305 ESYSMVLKVVASLSPAFALGSLNFADYERAHGLRMSNIMRA-----SSGVSEFVCLMM 361
QY 829 LFDLFLYGMWYIEANFPQOYGIIPRWYFPCSTYWFGESEDPKSH--TG-----877
DB 362 LLDSILYCALGLYLDKYLPRNENGVYPMNFPFSK--YFGRRKNLQNRIFCFETDMPAD 419
QY 878 -----SNOKRMSET-----CMEEBPTHKLGVSTONIAKVV--RDGMKVAV 916
DB 420 IEVNOGEFDFVFESISLEMKOGLDGR-----IQVNNLKVVASRGNCAV 468
QY 917 DGLALNFEGQITSLFHNGAGKTTTWSILTLGPPTSGTAVYILGKDISEMSTIRONLG 976
DB 469 NSILOLTYENQILSLFHNGAGKSTTSMVGLPPTSCALLIHGNSIITNMEIRKELG 528
QY 977 VCPQHNVLFMDLTYEBEHIMFARLKLSEKKVYKAMEOMALDVGELPSKSKTSKTSOLSG 1036
DB 529 VCPQHDLFPELTYREHLEMFAYLKGVEGSLKSTVDMAMEVGL--SDKINTLVRLALSG 587
QY 1037 MOKRLSVLAFAVGGSKVYIIDEPTAGVDPYRSRGIWELLKTYRGGRTIILSTHIMDEADY 1096
DB 588 MKRRLSGIALIGNSKVIILDEPTSGMDPYSMRLTQOLIKIKKGRILLTLTHSMDABE 647
QY 1097 LGDRITAIISHKLCVGVSSFLKMQILGTGYLLTVKKDVESSLSGCRSSSTVSYLKKED 1156
DB 648 LGDRIGIMANGSLKCCGSSIFLKHGYGYTLTLVK-----TSPT-----687
QY 1157 SVSOGSSDAGLGSDESDTLTIDVSAISNLIRKHVSEARLVEDIGHETLYLPEAKAG 1216
DB 688 -----VSVAHIYHRIIPATCYSEVGNELSPFLP--LASLP 722
QY 1217 AFVELFHEIDRL-----SDL-GISSYGISFTTLEIFLKVAAEESGVDAEWSDTGLPARRN 1271
DB 723 CFENMFREIESCMKNSDSYDGIQSYGISVYTLLEVEFLKVA--GCLNDIE-----770
QY 1272 RRAGDGKSCRLPTEDDAAPNDSIDIPRESRETDLSCMDGKSYQV-----GW 1322
DB 771 -----DKO-----EDIEVSPDKSSILVCIGSSQKSSMOPKLLASGNDGAV 811
QY 1323 KLTQ-----OOQVALLW-----KRLIARSRKGF 1347
DB 812 IITSVAKAFRLIIVAAVWVILIGFISIGCCGCSITISRMFWRRCKALFKRAHSACRDKTY 871

QY 1348 FAQIVLPVAVFCIALVFSILIVPFGKYPSLELOPMWNEQYTFVSNAPADEDTGLELLNA 1407
DB 872 AFQITIPAVFLFGLF-----LQKRP-----HPDQKSTILTATFNP 909
QY 1408 LTRDPFGTRCMENGNPDPDPCQAGEEWTAPYVPTIMDLFONG-----NMTKONSP 1461
DB 910 LLSGKG-----GGGPIPED-----LSVPIAKEVAOYTEGWIOLPRLNTSYKPPNP 954
QY 1462 ACQCSSDKIKKMLPCPPGAGAGLPPRQKONTADLODLOGRNLSIDYLVKTYQIIAKSL 1521
DB 955 -----KEALADNT--DAAGPTIGPILLS-----975
QY 1522 KKKIWNNEFRYGFSLGVSNQALPPSQEYNDALIKOMKHLKLAKDSADRFSLSLGHEW 1561
DB 976 -----MSERLMSFD-----QSYQSRE-----GLSHSDCNHPDGSILG---1009
QY 1582 TGLDRNNKVKVFNKNGKHAISFLNVLNNALIRANLOKGENPISHYGTITANHPLNLTK- 1640
DB 1010 -----YTVLHNGTCHAGPIYINVMHAALLR--LATGN--KMTTQTRNHPLPPTKT 1057
QY 1641 OQLSEVALMTTSVDVLSICVIFAMSPVAFVFLIOLVRSKAKHLQFISGVKRVLYWL 1700
DB 1058 QRIQRHDLDAFSAIITVN-----ASFPIASPAVYIVKEREYKAKHQOLIGSVLSYWL 1113
QY 1701 SNFVDMCNVYVPAVLVLIIFTCFOQKSYVSTNPLVALLLLYGWSITPLMPASFVF 1760
DB 1114 STYVMDIFSLFPSPFAILLFYAFGLIEQFIGRFLPTVLMILEYGLAIASSTVCLTFEF 1173
QY 1761 KIPSTP-----YVVLSTVNLFT-----GINSVAFVFELEF--TDNKLNN 1798
DB 1174 TEHSMQATSSSVLPLISLEVFSPSSNVILMVHFFSGILLMVISFVGLIPATASANSY 1233
QY 1799 INDI-----LKSVELIFPFLCGLGLIDM--VKNOAMADALERFGENFVSPLSWDLVR 1851
DB 1234 LKELLIFRYALQNFRLPSGFCFSDGLASLALRQGMKDSH-----GVFENNVAGA 1286
QY 1852 NLFMAVGEVFPFLTVLIQYFFPIRPVYNAKL-----1886
DB 1287 SICYLGLFRLLEYCRYSMLLSFF--HGIDTKLSIYITIGASRLTELIDRVYSTSEST 1343
QY 1887 PL-----NDEDEDVREORILIDGGGONDILEIKELTYIRKKR---KPAVD 1930
DB 1344 EPLKNDSTGAISTDMDDDIDVOEBRDVYISGIDNTMLYLQMLRKVYTGDKHNGKVAVO 1403
QY 1931 RLCVGIPECEFGILGVNAGKSSFTKMLTGDYTVYRGDAFLNKSLSINIEHVQNMGY 1990
DB 1404 SLTFSVQAGECEGFLGTNGAGKTTLSMLSGEETPTSGTAFIFGKDIVASPKAIRQHIGY 1463
QY 1991 CPOFDAITELLGREHVEFALLRGVPEKEVKGVMGAIKRLGLYKYGKAYAGNSGK 2050
DB 1464 CPOFDALFEYLVYKHELELYARKGVVDHRIIDNVYTEKLVFEDLLKHSKPSFTLSGK 1523
QY 2051 RKSTAMALIGPPVYFLDEPTGMDPKARFLMN--CALSVAKEGRSVLTSHSMECE 2108
DB 1524 KRLSVAIMAGDPPIYIIDEPTSGMDPAKRRMVDYISLSTRSKTAVIILTHSMNEGO 1583
QY 2109 ALCTRNALIVNGRFRCLGVSVOHLKNRG-----2136
DB 1584 ALCTRIGIMVGRICGSPHKLTRYGNHLEVEFPYNGVAPRNEVSNLENEFCOITQ 1643
QY 2137 -----DGYT-----LVVRL-----2146
DB 1644 WLENVPTQPSRLGLLEVCTIGVSDSITPDTASASEISLSPENVOIRAKFLGNEQVSTLY 1703
QY 2147 -----GSPN-----DLKPQDFPGLAFPGSVLKERHR 2173
DB 1704 PPLPEEDVAFDDQLSRQLFRDGIPLPIFAEWMLIRKESALDSFIOGSEFPATFKSCNG 1763
QY 2174 NMLQYLPSSL--SLARISLISQSKRLHLEDVSVOTTTIDQYVAFNA 2221
DB 1764 LSTKYOLPFGEGSLADAFGLHERNRNLGIAEYISISOSTLETTFNHPA 1813

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1758 <SNO>
A:Cross-references: GB:chr_III; PIDN:CAA62384.1; PID:q3757025; GSPDE:GN00021; CESP:C48BA
C:Genetics:
A:Gene: C48B4.4b
A:Map position: 3

Query Match	13.1%;	Score 1542;	DB 2;	Length 1758;
Best Local Similarity	23.8%;	Pred. No. 6.2e-91;		
Matches 520;	Conservative 371;	Mismatches 740;	Indels 558;	Gaps 65

0Y	162	LSLPSYDMLKLRADVILHKVFLQGYOLHLSLONCSGSEMQL--GDEVSFLGCLPPE	220
Dd	7	IPHESTIVRLKRLQLOEKAKKRAKESDIECSSESNESNDSPPLKDGOLAASSRIPPK	66
0Y	221	KLAAER-----VLRSN-----MDILKPLILTLNSTSPFSKEIAEATRTLLHSI	265
Dd	67	KMNRLQFSLLMKMDWLLRNRKKNVTLFELIPLCL-----LL	103
0Y	266	GTIAQELFSMNSWSDMQEYVFLNLNWSSSSQIYAASRIYCGHPDEGGGLKIKSLMY	325
Dd	104	GPLV-----YLVAHAHTSPENITY-----	124
0Y	336	EDNNYKALFGNGTEDEDAETFYDNTSTPYCNDLMLNLESSPLSRII--WKALKPLLVGKI	383
Dd	125	-DN-----FQYKGFYEDY-----FLESNFIKPIYKRMCLRSADVYVG--	159
0Y	384	LYTPPTATROVMAEVKTKPQELAVPHDLBGMBEELSPKLTWTMENSGEHDLYRMLDDR	443
Dd	160	-YTSKDAAKTAYDIDLKKFAE-----RFSAKLKLSVKNESSE-----QLTYVL	204
0Y	444	DNDHEWEOQLDLDMTADIAVFLAKHPEDVOSSNGSVYTRAEAFNTQAIRTSRME	503
Dd	205	RND-----LPLNFTFCAINS-----	220
0Y	504	CYNLKLKEPIATEWMLINKSMHELLDEKKFNAIGYFPGITGSIELPHHVYKTKRMDIDNV	563
Dd	221	-----YAAGVFDEVDVNTNKL-----NYRILLKTPRE	248
0Y	564	EKTNKIKDGYMDPGRADPEEDM-----RYWVGFAFYLDVDVEQALILVLGTKEKTKGVYV	619
Dd	249	EWMLHLETSYMPYGRSSGRYSRISSPPYMTSALTLQHAILESSFLSSVSGAPDLPIYL	308
0Y	620	QMPYPCYVD-----DIFLVNRSMPLEFMTLAWIYSAVAILKGIYVEAKRLKETMR	672
Dd	309	RGLPBPRTKTSVSFAFIDF-----PFIWAFVTEFINVHITREIAENHA--VKPYLT	359
0Y	673	IMGLDNSTLMSWFISSILPLVBSAGLLVTLKGNLLPVSDBSVYVFLSVAVVYIILQ	732
Dd	360	ANGISTFEMFYAHVMAALKEFVY--FLCSTIPLTFEMVEVSPALIVYLMGLGAVIF	417
0Y	733	CELIESTESRANLAAACGIIYFTLYLPYVLCVAMODYVFTLKIFASL--LSLP-----	785
Dd	418	GAFVASPFNNNTNSAIK-----ALIVAMGAMIGISYKLRERLDQISSCFLYGL	464
0Y	786	-----AFGCGEYFALFEQOIGYVOMDLNF--BSPYEEDGFNLUTSISIMLFDTLVLYGMV	840
Dd	465	NINGFALAVASIDSYMRERRELLJLTMFNDSLSH--FSLGALVLMIVDILMMSGAL	521
0Y	841	YIEAV--PGGYGIPRPWFPCTKSVWCGEEDSEKSHG--SNOKRMSFICMEEPHLL--	895
Dd	522	VYDHIRTSADSLKRLPDE-----APEDENOTGCVYRQNTRIEOMNPNASTSLNP	574
0Y	896	-----KLGVSTQNLVKKYVRODMKVAVDGALANFEGQITSFLG	933
Dd	575	PNADSLSLEGSTEADGARDTARADIIYLRNLKYIMTSTGEAVDGLSLRAVRGCSILG	634
0Y	934	HNGACKRTMSTLGLPPTSGTAVIILGKDIRMSMTIROUTLGYCPOHNVLFMLTAYEEN	993
Dd	635	HNGACKSTFSSIAQIRTPMGRITITGYDNGEPEGTRHIGCKPQYNLPYLDYLVSEH	694

Qy	994	IMFARILKGLSEKHVAKEMQMALDVGLPSSKJLKSXTSOLQSGMGRKLSVLAAPVAGSKV	1053
Db	695	LKLYGLGKAREKOPFKODMRLLSDVKL-DKENEKAVNLSCGMGRKLCVCMALIGSEV	753
Qy	1054	VILDEPTAGVDPYPSRRGIMWELLKLYKROGRPIILSTHMDADVLGDRITAIISHKGLCVG	1113
Db	754	VILDEPTAGMDPGARQOVQVLVEREKANRPIILTTMYMEARLELDWVFIMSHGLVASG	813
Qy	1114	SSLEFKNOLGTGYLLTVLKQDVESSLSSCRNSSQVSYLAKEDYSQSSDAGLGDHES	1173
Db	814	TNOYKLKOFEGTGYLLTVV-----LDHNG	836
Qy	1174	DTLITDVSAISNLIRKRVASRLVEDIGHETLVLYEAKGAEVLFHEID-----	1226
Db	837	DKRKMAV-TILDVCTHYVKEERGENHGOOETILPEARKKE--FVPLEQALEAIQDRNY	893
Qy	1227	-----DRLSDLGISSYGISETTLEEIFLKAVEESGVDAETSDGTLPARRRR	1273
Db	894	RSNVEDNMPNLKQGLATLEMRSGISLNTLBEQVFTTIDQ-----YDKIASRQMSR	946
Qy	1274	AFGDKQSLRPFTEDDAADPNDSIDPESRETDLSGMDKGSYOVKGKLTQOQVALL	1333
Db	947	ISHNRNASEPSLTPAGYDTQSSPKASDYOK--LMDSOARGP-EXSGAKVVAQFISIM	1003
Qy	1334	WKRLLIARSKKGFADIVLPAFVVCALAFSLLVPPFKYSLELOPMYNYEQTYFVSN	1393
Db	1004	RKKFLYSRRMAOLFTVOYLP--TILGLVGLSL-----TLKSN	1040
Qy	1394	DAPEDTGTLELNLATFDPDGFTRCMEGNIPPTPCQAGEEEMWTAPVQUTIMDLFQNGN	1453
Db	1041	NMDQ-----FSVNSL-----TP--SGIE-----PSKYVMFENGIT	1068
Qy	1454	WTMONPSPACOSSDKIKKMLPVCPRGAGLPPRQKONTADILDLTGRNISDYLVTY	1513
Db	1069	-----IPEANAEKILRKSGFEVLANTKNP	1096
Qy	1514	VOIKKSLKNIMWNEPFGFSLGVSNTQALPPSQEVDNAIKOMKKHLKAKDSSADR	1573
Db	1097	LPNTIKSL-----IGE-----MPPA-----	1111
Qy	1574	INSLREFMTGDLTRNNKVMFNNGKMHAISSFNIVNMAILRANLOKGNPSHYGITAFN	1633
Db	1112	--TICMTMNS--DNLEAFNMKYHYHVELTLSMLNRARLTGTVDALSSGVFLYKST	1165
Qy	1634	HPNLTKOOLSEVALMTTSDVULVSVICVIFAMSFPVASEVFLIDERSKAKHLOFISG	1693
Db	1166	SNSNLLPSQL-----IDVLLAPMLILIPAMVSTFMEFLIERTCOFAHOOQITGCI	1216
Qy	1694	KVIVTWLSNEFWMDMCNVVPAITVLIIFTCFOOKSYVSSNLPVLAULLILTGNSITPLM	1755
Db	1217	SPITFYSASLLYDGLYSLLCLLEFLFMFLAF---HMVYDHLAIVLFWELVFFSSVPI	1272
Qy	1754	YPASVEFPIPSAAVYLVTSVLFJGINGSATFVLELFTDNKLNINLTKSVFL-----	1808
Db	1273	YAVSFLPSPSKANVLLIMOVVISGALLAVFLFM-----IFNIDEMIKSLIVNIMF	1322
Qy	1809	IFPHCTLRGLIDWKNQAMADALERGENREFSP-----LSMDVGRNLFMAAVGEVYF	1864
Db	1328	LHPSTAFPSAII-----TINTYG--MLPSEELMNDHCGKNMLMGITGVYCSF	1374
Qy	1865	LITVLIOYRFIR-----PRPVNAKLSPLNDE--DEVARREKQRLDGGGONDLE	1913
Db	1375	ALFVLLQKFPARFLSOYWTVRRSSHHNVOPMAGDLPVCESEVSEEBERYHNRVNSOALS	1434
Qy	1914	IKELIKIRRRKRKPAVDICGIRPGBCFGLGVNAGKSSPFKMLTGDTPTVTRBDAPLN	1973
Db	1435	IDKLTKTR--GFTFVNLCLAVDQKCEFGGLGNGAGKTTFNILITGOSFASSEAMIG	1492
Qy	1974	KNSIISNIEHVONMGJPOCFADITTELLTREHVEFFALLRGVPEKGVKVEEMAIRKL	2033
Db	1493	GNDVIEL-----SIGYOPORDALMDLDTRESLEILAQNHGENYKA--KAEILLBECV	1545
Qy	2034	LVKGETAGYAGNSGGRKRLSTAMALLIGRPVVYLDPEPTTGMDPKARRPLMNCALSUYKE	2093

```

Db 1546 MIAHADKIVRYTSGQKRKISVGVALLAPTOITLDEPTAGIDTKARREWEILLWCREH 1605
QY 2094 GRS-VVLISHMECEALCTRMATMVGRRFCGLSVOLHKNREDCGTIIVRIAGSNPD 2152
Db 1606 SNSALMLTSHMDECEALCSRIATVNLNGSLAISSQELKSLVNNNTMTLSLTERPORD 1665
QY 2153 KPYODFGOLAPPGSVLKEKHNMM---LQYQLPSSLSEL-ARISITLSQSKRLHIEDYSV 2208
Db 1666 MVVO-LVOTRLPNSVLKTYTSTNKTLLNKWQIPKREDCWAKFEMOALAKDLGVKDFIL 1724
QY 2209 SQTLLDQVFNFA---KDQSDDDLKDLDS 2234
Db 1725 AQSLEEFRLAGLDDEQDHTSTVELS 1753

RESULT 11
T42749
ATP-binding cassette transport protein homolog - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession: T42749
R:Wu, Y.C.; Horvitz, H.R.
Cell 93, 951-960, 1998
A:Title: The C. elegans cell corpse engulfment gene ced-7 encodes a protein similar to A
A:Reference number: 222559; MUID:98297348
A:Accession: T42749
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1704 <MW>
A:Cross-references: EMBL:AF049142; NID:g3172340; PID:AMC24116.1; PID:g3172341
C:Genetics:
A:Note: ced-7
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 13.0%; Score 1538.5; DB 2; Length 1704;
Best Local Similarity 24.9%; Pred. No. 9.9e-91;
Matches 484; Conservative 347; Mismatches 675; Indels 441; Gaps 59;

QY 458 WTADIV-----AFIAKHREDVQSSNGSV-----TMRFAFNEN----- 492
Db 24 WTLPELLIPCLLGLPLVLYVKKKADHTSSPENITDNFOYGVGVEDVFLSENFITKPIYKRW 83
QY 493 -----QAIRTL---SRFMECVNLKL-----EPATEVWLINKS 523
Db 84 CIRSDDVVGYSKDAAKRIVDDLMKKFAERFQSAKLKLSVKNSSPEQLLT---VLKRD 140
QY 524 MELIDE-----RKFMAIGIVTGTIPGSIELPHHYKYYKIRDDINVEKTNKIKQGYMDPGR 578
Db 141 LPMLETFCAINSTYAGVVEDEVDTNKKL---NRIILGKTPPEETWHLTETSYNBYGP 196
QY 579 RADPEEDM---RYVMGGFAYLDVVDQALIRVLTGTEKKTGYVMOOMPQCYVD----- 629
Db 197 SSGKYSRLSPSPPYWTSAPLIFQHAITSSSFLSSVSGAPDLPTLRKLPERRPKTKTSVSA 256
QY 630 --DIFLVMSRSMPLFMTLAMIYSAVITIGIYEKEARLKETMRIMGLDNLISLHMSWT 667
Db 257 FIDPEF-----PFIWAFYFIVNIHITREIAEENHA--VKPYLTAMGLSTFEMFYAHVY 307
QY 688 SSILPLVSGGLVLIKLGNLLPYSDPSVFEVFLSFYAVATTLQCFILSTLSRANLMA 747
Db 308 MAPLAKFVIT---FLCSIIPLTFWMEVSPALIVTVMGTGAGAVIFGAFVASFNNMTNSAI 365
QY 748 ACGGIITFLYLPYVLCAVADQVYGLTKIPASL--LSPV-----AFGFCGEYFAL 796
Db 366 K-----ALIVAGMAMIGISYKRLPELDQSSCFELGLMNGAFALAYALSD 412
QY 797 FEEDGIGVQMDNLF-ESPVEEDGNLTLSMMLPDTFLYGVNTWYIEAV-FCQYQIDPR 854
Db 413 YMRERELNLTNNFNDSSSLH---FSLGVALVMMIVIDILMWSIGALIVVDHRTSADSLRT 469
QY 855 PWYFPCYSWYFGSEDESKSHPG-----SNOKMSEICMBEER---THL----- 895

```

```

Db 470 LDFDE-----APEDEENQTDGVTAAQNTIRINEOVYRNRVRSDMEIQHNPASTLSNPN 522
QY 896 -----KLGVSTIONLVKYYRQGMKAVAVGGLNLNVEGOITFELGN 935
Db 523 AUSDLSLESTENDAGRDARADIIYRNLYVKIMSTTGEAVDGLSLRAVROCSLILGN 582
QY 936 GAGKTTYSILTGLPEPTSGTAVILGKDIRSEMSTIRONLGVCPQHNVLFDMLVVEHIW 995
Db 583 GAGKSTTFESKIAGITRTNGRITITGVDNGNEPGETRRHIGMCPQNPYDOLTVSEHLK 642
QY 996 FYARKLGSSEKIVKAEEMQALDVGLPSSKLSKTSQSLSGGMORLSVALAFVGSXVYI 1055
Db 643 LYVGLGAREKDFKQDMKLLSDVKL-DFKEKEKAVNISGKKRKLVCYOMALIGDSEVYL 701
QY 1056 LDEPTAGVDPYSRGIWELLKRYROGRTIILSTHMDPADVLDRIATISHGKLCVSS 1115
Db 702 LDEPTAGMDPGARODVOKLVEREKANRTILTTHYMDEERLGDWVFIHSGKILVASTGN 761
QY 1116 LPLKNDLGTGYVLTLYVKRYVSSLSSCRNSSTVSTLYKKEDSVSSSDAGIGSHEDT 1175
Db 762 QYLKQKFGTGYLLTVV-----LDHNDK 784
QY 1176 LTIIDVSAISNLRKHYSEARLEDIGHETLYVLPYEAKEGAFVLEFHEID----- 1226
Db 785 RKMAY-ILTDVCTHYVKEAREGEMHGOEILIPARKKE--FVPLPQALEAIDRNTRS 841
QY 1227 -----DRLSDLGSSYGISSETTLEETLEIKVAEBSGVDAETSDGTLPRARRNRAF 1275
Db 842 NYEDNMPTNLKSQLATLEKRSFGLNLTLEQVFIIGDK-----YDKALASRONSRI 894
QY 1276 GKOSCLRPFETDDAADPNDSDIDPESRETDLSGMDKGSVOYGMKLTQGOFPALMK 1335
Db 895 HNSRNASSESLKPAQVDIQTSSKADSIOK--LMSQARKP-EKSGVAKMWAQFIISIRK 951
QY 1336 RULLIARRSRKGFQAVLPAVFCIALVFSLLVPPFGKYPSELEQPMYINBOYTFVSND 1395
Db 952 KFLYSRRNNAOLFQVLP--LILGLVGSLT-----TLKSNT 988
QY 1396 PBDTGLLELNLNLTQDPGGTFCMEGNLPIDPCOAGEEWTAPVPTINDLQNGWT 1455
Db 989 DQ-----FSVNSL-----TP--SGLE-----PSKVWRRENG-- 1014
QY 1456 MGNPSPACQSSDKIKMLPVCPRGAGGLPPQKQONTADILQDITGNISDYLVKTYVQ 1515
Db 1015 -----IDVLANFEKILIRKSGGEVLYNTKPNLP 1044
QY 1516 IIAKSLKNTIYNERPYGFSIGVSNTOALPPSQEVNDAIQMKKHLKLANDSSADRELN 1575
Db 1045 NITKSL-----IGE-----MPA----- 1057
QY 1576 SLGRPMTGIDTFRNNKVFENNKGWHAISSFLVINNALIRANLQGENPSHYGITAENHP 1635
Db 1058 TIGMIMNS-----DNEALEFNMYHVLPTLLSMIRAKLTGVDAEISSGVFLVSKTSN 1113
QY 1636 LNLTKQQLSEVALMTTSDVLYSICVITFAMSFVPSAFVFLIQRVSKAKLQFISGKP 1695
Db 1114 SNLPSQL-----IDVLAPEMLILIFAMVSTTFMFILIEERTCOFAHQDFTLGISP 1164
QY 1696 VTYWLSNFMDCNVCVVPATVITIFICEQKSVSYSNLVLALLLLLYGMSITPLMYP 1755
Db 1165 ITFYASLILYDILYSLCLLFLFMFLAF-----HMYDHLAIVILFMFLYFSSVPFLYA 1220
QY 1756 ASFEVRIPTAVVLYVNLVFIGINGSVATVLELTDNKLNININDILKSYFL-----IF 1810
Db 1221 VSFLQSPSKANVLLIMQVYISGALLAVFLIF-----IFNIDEMKLSILVINIFELL 1275
QY 1811 PHFCIGRLIIMVKNQAMADALERGENRYSV-----LSMDLVGRNLPAMAABGVVFFLI 1866
Db 1276 PSYAGSAII-----TINTYG--MILPSEELNMMDHCKKNMWLMGTGVCFSFAL 1322
QY 1867 TYLIGYREFIR-----PRVNAKLSPLNDE--DEDVAREGORILIDGGQNDILEIK 1915

```

Db 1323 EVLLQFVKRRRLSQVYIVRRSSHNVPQPMGDLPYCESVSEERERHVRVNSQNSALYIK 1382
 QY 1916 ELTKIRRRKRPADVRICGIPGECFGLGVNAGKSTFPMILGDTVTGRGDAFLNNK 1975
 Db 1383 DLTKTF--GRTAVNMLCVAPOKECFGLGVNAGKSTFTTNILTLGQSPASSGEAALIGR 1440
 QY 1976 SILSINIEVHOMNGYCPQFQDATTETLLTGREHVEFFALLNGVBEKEVKGAEAKRLGLV 2035
 Db 1441 DVTLEI-----SIGYCPQDQALMDLTGTRESLELLAQMGMFENYKA--KAELILECVGMI 1493
 QY 2036 KIGEKYAGNYSGGNKRKISTAMALLGGPPVPLDEPTTGMDFKRRFLMNCALSVYKEGR 2095
 Db 1494 AHADKLVREYSGGQKRIISVGVALLAPTMILDEPTAGIDPKARREVELLMCEHESN 1553
 QY 2096 S-VYLTSHEMECEALCTSMATMVNGFRGICLSVOHLKMRFGDGYTIYVRKINGSPDLKP 2154
 Db 1554 SALMTLSHMDCEALCSRIAYLNRSGLAIIGSQELKSLYGNNTMTLSLEPNORDKV 1613
 QY 2155 VQDFGLAFPGSVLYKEKHNNM--LQYQLPSSLSL-ARIFSLISQSKRLHIEDVSQO 2210
 Db 1614 VQ-LVQTRLPNSVLTKTSTNTKTLNLKQWLPKEKEDCWSAKFEVQVALADLGKDPILLQ 1672
 QY 2211 TPLDQVFVNFPA--KQSDDDLKLDLS 2234
 Db 1673 SSLETFELRLAGIDEDQLDTHSTVEIS 1699

RESULT 12

S60124

transport protein homolog C48B4.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 13-Jan-1996 #sequence revision 12-Apr-1996 #text change 02-Feb-2001

C:Accession: S60124; S40724; S40725

R:Kershaw, J.

submitted to the EMBL Data Library, November 1995

A:Reference number: S60124

A:Accession: S60124

A:Molecule type: DNA

A:Residues: 1-1767 <KER>

A:Cross-references: EMBL:Z29117; NID:9439247; PID:91066912

C:Genetics:

A:Map position: III

A:Intons: 47/1; 112/3; 161/2; 220/2; 543/3; 574/3; 903/2; 1056/1; 1115/3; 1178/3; 1265/3

C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

C:Keywords: ATP; duplication; nucleotide binding; P-loop; transmembrane protein

F:628-818/Domain: ATP-binding cassette homology <ABC1>

F:645-652/Region: nucleotide-binding motif A (P-loop)

F:764-769/Region: nucleotide-binding motif B

F:1457-1642/Domain: ATP-binding cassette homology <ABC2>

F:1474-1481/Region: nucleotide-binding motif A (P-loop)

F:1586-1591/Region: nucleotide-binding motif B

Query Match 13.0%; Score 1536.5; DB 2; Length 1767;

Best local similarity 23.7%; Pred. No. 1.4e-90;

Matches 522; Conservative 370; Mismatches 735; Indels 575; Gaps 66;

QY 162 LSLPKSTVDKMLRADYILKRVFLQYQLHTSLCNGSKSEEMIQ--GDOEVSFLGLPKE 220
 Db 7 IPMHSHIVMLRRLYLONEKAKRAKESDIECSSSENESENDSPTPLDQDLAESSRIPKK 66
 QY 221 KLAAR-----VLRSN-----MDILKPLKTLNSTSPFPSEKLAENKTLHL 265
 Db 67 KMKRLKQFILLMKMDVLLKRNKVVTLFEILITPL-----LL 103
 QY 266 GTLAQELFSMRWSMDKROEYMLPLTNVSSSSSTQIYQAVSRVCGHPREGGLKIKSLMNY 325
 Db 104 GPLV-----YLIVKNDHTSSPENIT----- 124
 QY 326 EDNNYKALPGNGTGEDAEFFYNSTTPPCNDLAKMLDESSPLSRIT--WKALKPLLYGKI 383
 Db 125 -DN-----FOYKGTVEVY-----FLESNFIKPIYKRWCLKSDVYV-- 159

QY 384 LYTPTPATQVMAEVNKTFOELAVFHDLCEGMEELSPKWTWENSOEMDLVBMILDSR 443
 Db 160 -TSDSAAAKRPVDLMMKFAE-----RFSAKIKLSVKNESSSE-----QLTLVL 204
 QY 444 DNDHFWEQDLGLMDTADIVAFIAKHPEDVQSSNGSVYTTWREAFNETNOAIRTISFME 503
 Db 205 RND-----LPMINTEFCALNS----- 220
 QY 504 CVNLKLEPIATEFWLIMKSMELDERKFWAGIVFTGTPGISELPHVVKIKIMIDNV 563
 Db 221 -----YAGVVFDEVDVTKKL-----NYRILGATPE 248
 QY 564 ERTNKKIKDQWDPGRADPFEDM-----RYWVGGAFLYQDVVEQAIIRYLTGTEKKTGVYM 619
 Db 249 EFWHLTEISYNPYGGSSGRYRIIPSPRYWMSAFLLTQHALESFSLSSYGSGARDLITL 308
 QY 620 QOMPYPCTVD-----DIFLRWSKSRPLFMTLAWIYSAVILIKGIYKEEAKLKETMR 672
 Db 309 RLPEPRRYKTSVSFAFIDF-----PFIWAEVTFINVIHITREIAENHA--VKPYLT 359
 QY 673 IMGLDNLIMFMSWIFSLIPLLYSAGLLVYLKIGNLLPYSDPSVVFELSVFAVITLQ 732
 Db 360 AMGLSTFMEYIAHVMAFLKFPVT--FLCSTIPLTFWMEFSPALLVYTLMTGLGAVIF 417
 QY 733 CFLISTLESRLAALAAACGIIYFTLYLPYLCVAMQDVGFTLKIFASL--LSPV----- 785
 Db 418 GAFVASFFNNNTNSAIK-----ALLVAMGAMIGISYLRPRELDISSCFLYGL 464
 QY 786 ---AFGFCGEYFALFEBOGIGVQMDNL-F-ESPVEEDGFNLTTISIMLFTPLGYMTW 840
 Db 465 NINGAFALAVEAISDYMRERELNTNMFNDSSLSH--FSIGMALVMYIVDILMMSIGAL 521
 QY 841 YIEAF-FPGQYQIRPRPWFPCTKSYWFEESDEKSHG-----SNOKRMSRIC 887
 Db 522 VVDHIRTADSLSRTLFDFE-----APEDDENQDQVTAQNRINQVNRVRSD-- 572
 QY 888 MEEP-----THL-----KLQVSTQNLVYKVRDGMKAVVDGLA 920
 Db 573 MEMNMASTSLNPPNADSDSLLEGSTEADGARDARADIIYRNILKWTSTGERAVDGLS 632
 QY 921 LNFYEGQITFLGNHAGKTTMTSLTGLFPPTSGTAVILKQDIRSEKSTIRQNLGVCPO 980
 Db 633 LRAVAGQCSILLGNHAGKSTFESSIAGIIRPTNGRITICGYDVNGEGERRHIGMCPQ 692
 QY 981 HNVFLDMILVEHITFYARLGLSKNHYKAEQMDALDVGCPSSKLSKTSQOLSQGMQRK 1040
 Db 693 YNPLVDOLTVSEHLKLVYGLGARGKDKQDKMRLSDVKL--DEKENKAVNLGGMKRK 751
 QY 1041 LSVLALFVGGSKRVVILDEPTAGVDPSYRSGIWEILLKTRQGRITILSHHMDADVLDGR 1100
 Db 752 LCVCAALLIODSEVYLDELDEPTAGMDGARQDYOQLVERKARKNTILLTHYVDEARLGDW 811
 QY 1101 IAIISHGKLCCVSSSLFLKNQLTGTYVLLVKKQDVSSLSGCRNSSSTVYLLKEDSVSQ 1160
 Db 812 VIMSHGKLVAGTQYQKQFGTGYLLTV----- 842
 QY 1161 SSDPAGLSDHDSPTLITDYSALSLIKKHVSEARLVEDIGHETLYVLPYEAKEGAVVE 1220
 Db 843 -----LDHNGDKRKMAV--LTDVCTHYVKEARGEMHQOQLEIILPEARKKE--FVP 891
 QY 1221 LFEHID-----DRLSDGLSSYSISETTLEELFLKVAEESGVDAE 1260
 Db 892 LFOALEIADQRYRNSVVDNMNPTLAKSLATLLEMSPGLSINTLEQVITIGDK----- 945
 QY 1261 TSDGTLPARRRRRAFGDKQSCLRPTEDDAADPNDSIDIDPSRETDLISGDKGSGIOVK 1320
 Db 946 -VDKAIASRONSRIISHNSRNASEPSLKPAGYDQTSSTKSADSYOK--LMDSQARGP--EKS 1001
 QY 1321 GMLKQOQFVALMLMKRLLIARSRKCFPAQIVLAVFICIALVLSLIVPPGKPSLEIQ 1380
 Db 1002 GVAKNVAQFISIMRKPLYSRRNMAQLFTQVILP--ITLLDVGSLT----- 1046
 QY 1381 PMWYNEQYTFVSNDAPEDTGTLELINALTLKDPGFGTRCMEGNPIPDTPCQAGEEWTPAP 1440

```

Db 1047 -----TKSNNTDQ-----FRSLT-----PSGIE----- 1065
OY 1441 VPOTIMDLFQNGMWMQNPSPACQSSDKTKKMLPVCPPGAGLPPQRQNTADILQDL 1500
Db 1066 -PSKVYKREFNGT-----IPEANERKLLKRS 1092
OY 1501 TGRNISDYLVKTYVOIIAKSLKNKIWNNEFRYSGFSLGVSNTQALPPSGOEVDNAIKOMKK 1560
Db 1093 GGEVLVNYNKNKPLPNITKSL-----IGE-----MPPA----- 1120
OY 1561 HLKAKASSADRLNSGRMTGIDFRNNKYKWNPNKGMHAISFLVNNATLRANLQK 1620
Db 1121 -----TIGMTMNS-----DNLEALFNMYTHVLPFLLSMIRAKLTGTVA 1161
OY 1621 GENSHYGTAFNHPMLNLTQKQSEVALMTTSDVIVLSICVIFAMSEVPASFPVFLIOER 1680
Db 1162 EISSGVFLYKSTSNMLRPSQL-----IDVLLAPMLLIPAMVSTFVMEFLIEER 1212
OY 1681 VSKAKHOFISGVKPYVYIWSNFVDMCNVVPATLVIIIFICFOOKSYVSSINLEVAL 1740
Db 1213 TCQFAHQFPLTGLSPITFEYASLIDGILSLICLIFLMEFLAF-----HMMDHLATVIL 1268
OY 1741 LLLYGSITPLMWPAFSEFKIPSTAVVLTSYNLEFINGSVATFVLELTDKNLNIN 1800
Db 1269 FMFLYESSVPFIYAVSEFLQSPSKANVLLIMQVVISGALLAVFLIFM-----IFNID 1323
OY 1801 DILKSVFL-----IFPEFCIGRGLIDKYNQAMADALERFGENREVS-----LSMDLVGR 1851
Db 1324 EMKSLIVNFMFLPSYAGSAII-----TINUYG-----MLPSEELNMWCHGK 1370
OY 1852 NLFMAVEGVVFLITVLIQYREFIR-----PRVNAKLSPLNDE-----DEVDREERO 1900
Db 1371 NAMLMGFVGCSTALFVLLQFKYRRFLSQWTVKRSSHNNVQPMAGDLPVCSVSDEKE 1430
OY 1901 RILDDGGQNDILEIKELTKTYRRKKRPAYDRICVGIIPGECFGLLVGNAGKSSFTKMLT 1960
Db 1431 RVHVNVSQNSALVYKDLTKTF--GRFTAVNELCLADQKCEFLLVGNAGKKTTFENILT 1488
OY 1961 GDTTVTGDAFLNKNSTLSINHEVHONMGYCPQPDATITELTGREHVEFPALLRGPEKE 2020
Db 1489 GQSAASGEMIGRDYTEL-----SIGCPQPDALMDLTRESIELIAOHNGENRK 1543
OY 2021 VGVAVEMAIRKLGLVYKGEYAGNYSQGNKRKLSTAMALIGBPVFLDEPTTGMPDKAR 2080
Db 1544 A--KAELILRCVGMIAHADKLVRFYSGGGRKISVGVALLAPQMIIDEPFAGIDPKAR 1601
OY 2081 RFLMNCALSVYKESGR--VVLTSMECECALCTRAIMWNGFRCLGSYQHLKNRFGDGY 2139
Db 1602 REVMELLKCRHSNSALMTLSHMDCECALCSRIAVLNGSLIALIGSSQELKSLYGNVY 1661
OY 2140 TIIVRIAGSNPDLKPYODFGLAFPGSVLKEKHRNM-----LOYLPSSLSL--ARIPSILS 2195
Db 1662 TMLTSLTEPNQORDMVVQ--LVQTRLPNSVYLKTTNTKNTLNKMIIPREKEDCSAKTEMVQ 1720
OY 2196 QSKRLHIEDYVSQTTLDQVYVNA-----KDSQSDHLKDL 2234
Db 1721 ALAKDLGVKDFILAOSSLETFPLRGLADEDDLDHTSTVEIS 1762

RESULT 13
T00826
hypothetical protein T326.22 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
C:Accession: T00826
R:Bounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, November 1997
A:Description: Arabidopsis thaliana chromosome II BAC T326 genomic sequence.
A:Reference number: Z14163
A:Accession: T00826
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA

```

```

A:Residues: 1-1246 <R0U>
A:Cross-references: EMBL:AC002510; NID:g2618683; PID:g2618705
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 2
A:Introns: 33/3; 95/2; 113/3; 137/3; 168/3; 361/3; 421/2; 432/3; 493/3; 521/3; 535/3;
A>Note: T326.22

Query Match 11.9%; Score 1402; DB 2; Length 1246;
Best local similarity 28.7%; Pred. No. 4, 1e-82;
Matches 415; Conservative 195; Mismatches 388; Indels 450; Gaps 43;

OY 1019 VGLPSSKLSKTSQLSGGMOKRLSYALAFVGSKVYIIDEPTAGVDPYSRRGIWELLKY 1078
Db 1 VGL-SDKINTLVRAISGMKRLSLGIALIGNSKYIIDEPTSGMDPYSMRLTQWLKIKI 59
OY 1079 RQGTIIISTHMDADVLGDRIALIISHGKLCQVSSSFLKNOLGTGYTLVLYKKDVSS 1138
Db 60 KKGRIILITSHMDAEELGDRIGIMANGSLKCCSSIFLKHGYGVTTLVV----- 113
OY 1139 ISSCRNSSVSYLKKEDSVSSQSSDAGLGSDBESDTLIDVSAISMLRKVSEARLYE 1198
Db 114 -----TSPT-----VSAAHIVHRHIPSACVS 136
OY 1199 DIGHLTYLVPEAKKEGAFVLEHIEDRL-----SDL-GISSGISTETLEELFLKAYE 1253
Db 137 EVGNIEISFRLP--LASLPCFENMFREIESCKMNSDSDPGIQSGIVSTLTLEEVFLVA- 193
OY 1254 ESGVAETSDGTLFARRRRARAFGDKOSCLRFETEDDADPDNDSDIDESRETDLSGMDG 1313
Db 194 GGNLDIE-----DKQ-----EDIVSPDTKSLVCISNQ 223
OY 1314 KSYOVK-----GKKLTQ-----QGFVALLM----- 1334
Db 224 KSMQPKLLASGNDAGVITISVAKAFRLIYAATVLLIGFISIOCCGSIISRSMFNRHC 283
OY 1335 -----KRLIARRSKRGFAQIVLPAVFCIALVFSLVLPFGKYPSELIOPMYVNBQYT 1389
Db 284 KALFLKRRASRCRDKRYAFQFIIPAVFLFLGLF-----LQKLP----- 323
OY 1390 EVSNDAPEDTGTLELLNALTKDQPGFTRCMGEMNPIDTPCOAGEEMVTAPVQTIIDL 1449
Db 324 --HPQKSTITLTAAFNFLLSGKG-----GGGPIPD-----LSVPIAKEVAYI 366
OY 1450 GNG-----NMTMNPSPACQSSDKIKKMLPVCPPGAGLPPQRQNTADILQDLGR 1503
Db 367 EGGWIOPLRNTSYKFPNP-----KDALDAI--DAAGP 397
OY 1504 NISDYLVKTYVOIIAKSLKNKIWNNEFRYSGFSLGVSNTQALPPSGOEVDNAIKOMKKHL 1563
Db 398 TLGPTLLS-----MSEFLMSFD-----GQSQSR-----G 424
OY 1564 LAKSSADRLNSGRMTGIDTRNNKYKWNPNKGMHAISFLVNNATLRANLQKGEN 1623
Db 425 LSHSDSCHMPDGSIG-----YTVLNGTCQAHGPIYIWMHAALR--LARGN- 470
OY 1624 PSHYGTAFNHPMLNLTQKQSEVALMTTSDVIVLSICVIFAMSEVPASFPVFLIOERVS 1682
Db 471 -KNMTIOTRRNHPLEPTKTQRIQRHDLDAFSAIIVNT-----AFSEFIPASFAVPVYKREV 525
OY 1683 KAKHLQFISGVKPYVYIWSNFVDMCNVVPATLVIIIFICFOOKSYVSSINLEVALLL 1742
Db 526 KAKHQLISGVSIVLSYMLSTVYMDPISFLPSTPAIILFVAFGEQFGLIGRFLPVYML 585
OY 1743 LLYGSITPLMWPAFSEFKIPSTAVVLTSYNLEFINGSVATFVLELTDKNLNIN 1800
Db 586 LEYGLAIASSTYCLTFEFTESHMAQANSSVLLPISLFEVSFSSNVILWHPFSSILM 645
OY 1783 VAFVLELF--TDNKLNNINDI-----LKSVFILPHFCIGRLIDM--VKNQAMADALE 1833
Db 646 VISFVMGILPATASANSYKLELILFRYALQNFRLSGFCFSQGLASLALLRQMKKSS 705

```

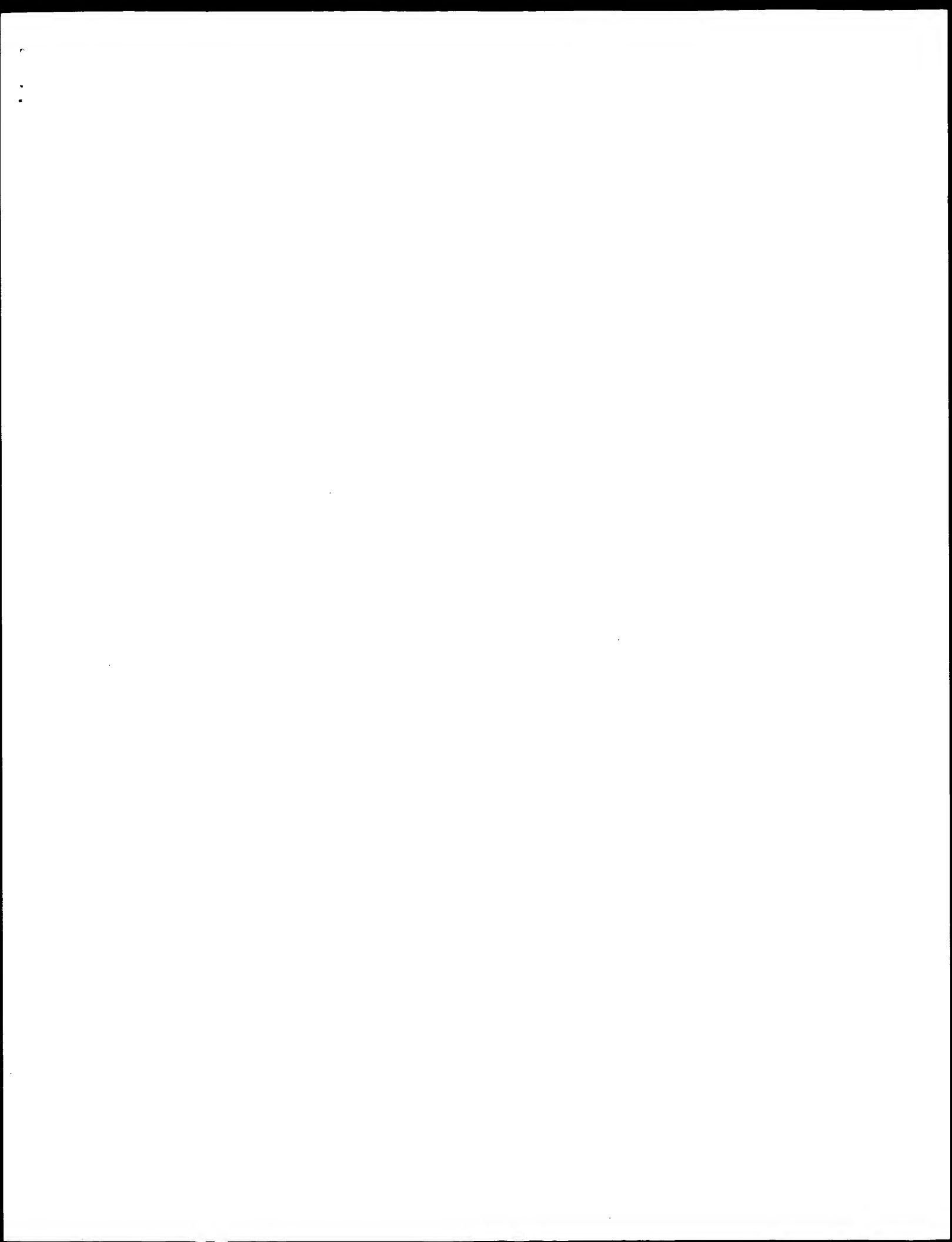

QY 1834 RFGENREVSPLSMDLVGNLFAMAVEGVFELLTLIOYRFFIRPRPVNAKLS----- 1886
 Db 706 H-----GVFENNVATGSIYCLDLVLRLECYRSMILSF-----HGIDTKLSLITTYGA 755
 QY 1887 -----PL-----NDEDEDVRRERORILLDGGGONDILEIKE 1916
 Db 756 SRLTELYDRVYSFSTFEPILKDSGTGAISTDMEDDIDVQEDRDRVISGLSDNTMYLON 815
 QY 1917 LTKIYRRK-----KPADRICVGIPGECRCELLGVNAGKSTFKMLTGDITTVRGDAFL 1972
 Db 816 LRKYVPGDRHGHGPAVVAOSLTFESVQAGCEFCFLGTNAGKTTLSMLSGEETPTSGTAFI 875
 QY 1973 NKNSTLSNHEHVQNMGYCPQFDATITELTGREHVEFFALLRGVPEKEVGAGEMAIKRL 2032
 Db 876 EGDIVASPKAIRQIHGICPPQDALFELYVKEHLELTARIKGVADRIDNVVTEKLEVF 935
 QY 2033 GLVYKGEYKAYNSGNGRKLSTAMALIGPPVFLDEPTTGMDPKARFLMN--CALSV 2090
 Db 936 DLKSHKSPFTLSGNGRKLSTVALIAMIGDPIYLDEPTSGMDPVAKRFMDVYSRLST 995
 QY 2091 VKEGSVYLTSHSMEECALCTRAIMVNGFRCLGSOHLKNRFG----- 2136
 Db 996 RSGKTAVILTTTHSMNEAQLCTRIGIMVGRLCIGSPHLLKTRYGMHLELVFPYNGVK 1055
 QY 2137 -----DGYT-----I 2141
 Db 1056 PNEVSNNLENFCCOITQOMLFNPQPSRLGLDEVCIGVSDSTTPDTASASELSLSPEM 1115
 QY 2142 VVRIA-----GSPN-----DLKPV 2155
 Db 1116 VORIAKFLGNBQVSTLVPPLPEEDVRFDDQLSQFLRDGIPPLPIFAEWMLTKKESFAL 1175
 QY 2156 QDFELAPGVSLEKHNMLQYOLPSSLS--SLARIFSLSSQSKRLHIDYVSQTL 2213
 Db 1176 DSFIQSSFPGATFKNSCLSIKYLQPLFEGGLSLADAGHLERNRNLGIAEYSISOSTL 1235
 QY 2214 DOVEYNFA 2221
 Db 1236 ETIFNHFA 1243

RESULT 14
 127121
 hypochelical protein Y53C10A.9 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence-revision 15-Oct-1999 #text-change 04-Mar-2000
 C:Accession: 127121
 R:White, S.
 submitted to the EMBL Data Library, November 1998
 A:Reference number: Z20314
 A:Accession: 127121
 A:Status: preliminary; translated from GR/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1564 <MIL>
 A:Cross-references: EMBL:AL033536; PIDN:CAA22142.1; CESP:Y53C10A.9
 A:Experimental source: clone Y53C10A
 C:Genetics:
 A:Gene: CESP:Y53C10A.9
 A:Introns: 43/3; 92/2; 148/2; 226/3; 354/1; 712/3; 817/1; 875/1; 916/3; 984/3; 1069/2;
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 9.88; Score 1158.5; DB 2; Length 1564;
 Best Local Similarity 23.08; Pred. No. 4e-66;
 Matches 433; Conservative 324; Mismatches 673; Indels 451; Gaps 60;

QY 458 WTAODI-----VAFLA-----KHPEDVQSSNGSY--YTWRAPENET-----NQ 493
 Db 22 WTGFVVALPLILIAFPAVMYIAKSAQAPEDAKSSGSPSIDMLSTESFHPYVSSTQCDPSY 81
 QY 494 AIRTISRMECVNLKLEPIATEWLINKSMELDERKFMAGIYFTGTGTSIELPHVH- 552
 Db 82 GVQTVNNVENVNYSPPMR-----W--DNTNLSIDLAKNPARKLFIKDVRAACKIIVIVE 133

QY 553 -KTKIRMDIDNVERTNKKIKDGYWDPGRADPFEDMRVWGCFAY-----LDVVEQA 603
 Db 134 DKTKTMVLPAT-----GRRSNFSYIYANKIMFGISQANNTSITENF 180
 QY 604 IIRVLGTE-KRTGVYMOQMPYPCYVDIFLRVMSRSMPLFMTLAMIYSAVAIINKIYVE 662
 Db 181 DIKLSITNEESG-----FGNGFLFVAVCLMDEVISVARALVE 221
 QY 663 KEARLETMAIKMLDMSIIMFSNFIISLPLVLSAGLVIYILKGLULYSDPSYFVL 722
 Db 222 KSS-VKPYLTITIP--LMMFLHEFLFCVINTEFLILTLSTLYIFSDNCPYTVLACI 277
 QY 723 SVRAVYTILOCFILSPLFSRANLAACGGITVETLPLVYCA-----MODY-----CE 773
 Db 278 FMTCHCVSFIICSTLIPPLGKRIYEGMYIITLLIIMHLSLEFFDMLFVWPLINPWT 337
 QY 774 TLKIFASILSPVAFGCECFALFEEOGIGVQMDNLFESFVEDGPNLTTSIMLFDTP 833
 Db 338 SLKLFVDATFLASGPNQTPISALFSSK-----KTLQSAAYVFGIMISCTVYMLVAALF 391
 QY 834 LYGVMTYITAVPFGQYIGPRPWYFCTYSY--FEESDEKS---HPSNQKRMSEIOM 888
 Db 392 MERKLYTFVGHAI-----KRFMRILFSGKGRSKIBERDQVEDRSTILO 436
 QY 889 EEPETHLK-----LGVSIONLVKYYRDMQKAVADGIALNFEQITSLFCHNGCKTTMS 944
 Db 437 CKETVEGRGSAIDIELSGLVKYYONGEK-AVNGSLRALRIGOVSTLLGNGGCKSTTG 495
 QY 945 ILTGLPPTSGTAVYIILKDIRSEMSTLRONLGYCPQHNVLFDMLVVEHIMFYARLGLS 1004
 Db 496 MITGMHQATEGKVMIGSIDANANRAEARRELIGYCPQNPYDELTVMEHLRLVNALKGRS 555
 QY 1005 -EKHYAKEMQALDVLGSPSKLKSSTLSGCMQKRLSALALFVSGKVIILDEPTAGV 1063
 Db 556 GGSDFKMDAESLKLQLEL-TDKRNTLAKNLSCGMKRLCVMAMIGSRVITLIDEPDAGM 614
 QY 1064 DPYSRGIWELLLKYRGQFTIISTHMDADVIGIRATISGKLCVCCSSFLFNOLG 1123
 Db 615 DPSARIDVQNMALVYKADRTILTLTHMDAEKLGIMFYMSHGKMAASGSKYLYLQKYG 674
 QY 1124 TGYVLTLY-----KKDVESLSGCRNSSSTVSYLKEDSVSOSSDAGLGSDES 1173
 Db 675 GGMILLTIVFSYHDPMPKRSYEFAYDVCTVOSTA--LVKDR-----GQMIEI 722
 QY 1174 DTLETIVSAISNLIRKIVSARLAVEDIGHELTIVLYPEAKKBAFVELHEIDRLSDIG 1233
 Db 723 SILETEKSRLLPTLLK--ILESVMEEDYNP-----EFQALBEDIOEKCRTELE 767
 QY 1234 ISSYGISETLLEIFLKVAAE-----SGVDAETSOGTLPARNRRAFGDKOSCLRPPT 1286
 Db 768 LATIGVSMSSLEOVFIYIGECDDIMNGTGYDKT-----ERKEKSTLY 812
 QY 1287 EDDAADPNDSIDIPESKETDLSGMDGKSGYOVKGMKLTOQOEVALLMKRLLIARRSRG 1346
 Db 813 QYKIQCPK-----QGSKLMMVMVALLQKRAYLYLRNPQ 847
 QY 1347 FFAQIVLPANFVICALVSLIVPPFGKYPSLELQPMKYNQYTFVNDAPEDGTIELLN 1406
 Db 848 ITYQIILP-----LTLTLMFAVPELR--LEBKPKLSDIESFDSQYPHSVTLQLEN 898
 QY 1407 ALTKDPGFTRCMEGNIPDTPQAGEEWTAPVQTIMDLFQNGNMTQWNPSPACOS 1466
 Db 899 E-----N 900
 QY 1467 SDKIKKMLPVCPPGAGLPPQKKONTADILLQDLTGRNISDYLVKYVOIIAKSLNKTM 1526
 Db 901 DDLRLANLY-----NSFSNF-----EYVEFTL 921
 QY 1527 VNEFRYGFSGISVNTQALPPSOEVNDATIKOMKHLKLAK--DSADRLFNLISGRFY- 1581
 Db 922 -----GFTVKYVK-----KGSDFKYKISOGDRNAAILMNIITASAMYLND 960



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2002, 12:55:51 : Search time 22.98 Seconds
(without alignments)
3809.613 Million cell updates/sec

Title: US-09-595-526b-2
11797

Perfect score: 11797
Sequence: 1 MACWQGLLLMKNTLFRRR.....VDVAVLTSFLDCKKESYV 2261

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11770	99.8	2261	1 ABC1_HUMAN	O95477 homo sapien
2	11256	95.4	2261	1 ABC1_MOUSE	P41233 homo musc
3	5870.5	49.8	2273	1 ABCR_HUMAN	P78363 homo sapien
4	4230.5	35.9	2436	1 ABC2_HUMAN	O9bzc7 homo sapien
5	4093.5	34.7	2434	1 ABC2_MOUSE	P41234 mus musculu
6	2642.5	22.4	1704	1 ABC3_HUMAN	O99758 homo sapien
7	1537	13.0	1691	1 YLH4_CAEEL	P34358 caenorhabdi
8	411	3.5	330	1 DRRA_STRPE	P32010 streptomyce
9	382.5	3.2	343	1 NOD1_RHISN	P5476 rhizobium s
10	366	3.1	304	1 NOD1_RHIS3	P72335 rhizobium s
11	347	2.9	308	1 YADG_ECOLI	P36879 escherichia
12	344.5	2.9	340	1 NOD1_RHITO	P23703 rhizobium 1
13	343.5	2.9	347	1 NOD1_RHIGA	P50332 rhizobium 9
14	339.5	2.9	1280	1 MDR1_HUMAN	P08183 homo sapien
15	331.5	2.8	355	1 NOD1_RHIME	O52618 rhizobium m
16	329.5	2.8	578	1 YBHE_ECOLI	P75776 escherichia
17	327.5	2.8	1281	1 MDR3_CRIGR	P23174 cricetus
18	327	2.8	894	1 YH1H_ECOLI	P37624 escherichia
19	326	2.8	1276	1 MDR3_MOUSE	P21447 mus musculu
20	325.5	2.8	308	1 NOSF_PSEST	P19844 pseudomonas
21	324.5	2.8	1276	1 MDR2_MOUSE	P21440 mus musculu
22	322.5	2.7	306	1 NOD1_BRNJA	P26050 bradyrhizob
23	321	2.7	1276	1 MDR1_CRIGR	P21448 cricetus
24	317	2.7	1362	1 PMD1_SCHPO	P36619 schizosacch
25	316	2.7	1276	1 MDR2_CRIGR	P21449 cricetus
26	315.5	2.7	311	1 NOD1_RHITV	P08720 rhizobium 1
27	315	2.7	1278	1 MDR1_RAT	P08201 rattus norv
28	314.5	2.7	1277	1 MDR1_RAT	P43245 rattus norv
29	313	2.7	354	1 Y415_STNY3	P22040 synechocyst
30	310.5	2.6	1276	1 MDR1_MOUSE	P06795 mus musculu
31	304.5	2.6	1294	1 YOH5_YEAST	O08234 saccharomyc
32	300	2.5	381	1 OPBA_BACSU	O45460 bacillus su
33	298.5	2.5	262	1 YA23_MERJA	O58429 methanococc

34	297	2.5	380	1 OPBA_BACSU	O34992 bacillus su
35	296	2.5	1335	1 Y719_AMASP	O05067 anabaena sp
36	293.5	2.5	1321	1 AB11_HUMAN	O95342 homo sapien
37	292.5	2.5	305	1 YHCH_BACSU	P54592 bacillus su
38	287.5	2.4	274	1 Y179_MYCPN	O30294 mycoplasma
39	286.5	2.4	274	1 Y179_MYCGE	P21432 mycoplasma
40	285.5	2.4	1279	1 MDR3_HUMAN	P42332 homo sapien
41	284	2.4	306	1 BCRA_BACIL	P42332 bacillus 11
42	284	2.4	1321	1 MDR1_CAEEL	P34712 caenorhabdi
43	284	2.4	1336	1 MAM1_SCHPO	P78966 schizosacch
44	281.5	2.4	308	1 YEHX_ECOLI	P33360 escherichia
45	281.5	2.4	343	1 ABC_ECOLI	P30750 escherichia

ALIGNMENTS

RESULT ID	1	ABCI_HUMAN	STANDARD:	PRT: 2261 AA.
AC	O95477	Q9UN08	Q9UN07	Q9UN06
DT	16-OCT-2001	(Rel. 40)	Created	
DT	16-OCT-2001	(Rel. 40)	Last sequence update	
DT	01-MAR-2002	(Rel. 41)	Last annotation update	
DE	ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette transporter 1) (ATP-binding cassette 1) (ABC-1) (Cholesterol efflux regulatory protein)			
GN	ABCA1 OR ABC1 OR CERP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20345099; PubMed=10884428;			
RA	Santamarina-Fojo S., Peterson K.M., Knapper C.L., Qiu Y., Freeman L.A., Cheng J.F., Osorio J., Remaley A.T., Yang X.-P., Haudenschild C.C., Prades C., Chimini G., Blackmon E.D., Francois T.L., Duveger N., Rubin E.M., Rosier M., Deneffe P., Fredrickson D.S., Brewer H.B. Jr.,			
RA	"Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter."			
RT	Proc. Natl. Acad. Sci. U.S.A. 97:7987-7992(2000).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	TTSUSE-Skin.			
RA	Schwartz K., Lawn R.M., Wade D.P.,			
RT	"ABCA1 gene expression and apoA-I-mediated cholesterol efflux are regulated by LXR."			
RL	Submitted (Jul-2000) to the EMBL/Genbank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=2151004; PubMed=11352567;			
RA	Qiu Y., Cavalleri L., Chiu S., Yang X., Rubin E., Cheng J.-F.,			
RT	"Human and mouse ABCA1 comparative sequencing and transgenesis studies revealing novel regulatory sequences."			
RL	Genomics 73:66-76(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Tanaka A.R., Abe-Dohmae S., Arakawa R., Sadanami K., Kidera A., Roka N., Amachi T., Yokoyama S., Ueda K.,			
RT	"A new topological model of functional human ABCA1-signal peptide cleavage and glycosylation of a large extracellular domain."			
RL	Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 21-2261 FROM N.A.			
RX	MEDLINE=99194549; PubMed=10092505;			
RA	Langmann T., Klucken J., Reil M., Liebisch G., Luciani M.F., Chimini G., Kaminski W.E., Schmitz G.,			
RT	"Molecular cloning of the human ATP-binding cassette transporter 1 (ABCA1): evidence for sterol-dependent regulation in macrophages."			
RL	Biochem. Biophys. Res. Commun. 257:29-33(1999).			
RN	[6]			

- RP SEQUENCE OF 21-2261 FROM N.A.
RX MEDLINE=99364413; PubMed=10431238;
RA Rust S., Rosier M., Funke H., Real J., Amoura Z., Piette J.-C.,
RT Delzeu J.-F., Brewer H.B., Duverger N., Deneffe P., Assmann G.;
RA "Tangier disease is caused by mutations in the gene encoding
RT ATP-binding cassette transporter 1.";
RL Nat. Genet. 22:352-355(1999).
RN [17]
RP VARIANTS FHA THR-1091 AND 1893-GLU-ASP-1894 DEL.
RX MEDLINE=20001430; PubMed=10533863;
RA Marcell M., Brooks-Wilson A., Clee S.M., Roomp K., Zhang L.-H., Yu L.,
RA Collins J.A., van Dam M., Molhuizen H.O.F., Loubser O.,
RA Ouellette B.F.F., Senses C.W., Fichter K., Mott S., Denis M.,
RA Boucher B., Pimstone S., Genest J. Jr., Kastelein J.J.P., Hayden M.R.;
RT "Mutations in the ABCA1 gene in familial HDL deficiency with defective
RT cholesterol efflux.";
RL Lancet 354:1341-1346(1999).
RN [18]
RP VARIANTS TD ARG-597 AND ARG-1477, AND VARIANT FHA LEU-693 DEL.
RX MEDLINE=99364411; PubMed=10431236;
RA Brooks-Wilson A., Marcell M., Clee S.M., Zhang L.-H., Roomp K.,
RA van Dam M., Yu L., Brewer C., Collins J.A., Molhuizen H.O.F.,
RA Loubser O., Ouellette B.F.F., Fichter K., Ashbourne-Excoffon K.J.D.,
RA Senses C.W., Scherer S., Mott S., Denis M., Martindale D.,
RA Frohlich J., Morgan K., Koop B., Pimstone S., Kastelein J.J.P.,
RA Hayden M.R.;
RT "Mutations in ABC1 in Tangier disease and familial high-density
RT lipoprotein deficiency.";
RL Nat. Genet. 22:336-345(1999).
RN [19]
RP VARIANTS TD SER-590; SER-935 AND VAL-937, AND VARIANTS ALA-399 AND
RP MET-883.
RX MEDLINE=99364412; PubMed=10431237;
RA Bodzioch M., Orso E., Klucken J., Langmann T., Boettcher A.,
RA Diederich W., Drobnik W., Barlage S., Buechler C.,
RA Porcch-Oezuerne M., Kaminski W.E., Hahmann H.W., Oette K.,
RA Rother G., Aslanidis C., Lackner K.J., Schmitz G.;
RT "The gene encoding ATP-binding cassette transporter 1 is mutated in
RT Tangier disease.";
RL Nat. Genet. 22:347-351(1999).
RN [110]
RP VARIANTS TD ARG-929; ARG-597 AND ARG-1477, AND VARIANTS FHA LEU-693
RP DEL, THR-1091; 1893-GLU-ASP-1894 DEL AND LEU-2150.
RX MEDLINE=20540002; PubMed=11086027;
RA Clee S.M., Kastelein J.J.P., van Dam M., Marcell M., Roomp K.,
RA Zwarts K., Collins J.A., Koelants R., Tamasaawa N., Stult T.,
RA Suda T., Ceska R., Boucher B., Rondeau C., Desoulh C.,
RA Brooks-Wilson A., Molhuizen H.O.F., Frohlich J., Genest J. Jr.,
RA Hayden M.R.;
RT "Age and residual cholesterol efflux affect HDL cholesterol levels and
RT coronary artery disease in ABCA1 heterozygotes.";
RL J. Clin. Invest. 106:1263-1270(2000).
RN [111]
RP VARIANTS TD ASN-1289 AND HIS-1800.
RX MEDLINE=20171564; PubMed=10706591;
RA Brousseau M.E., Schaefer E.J., Dupuis J., Eustace B.,
RA Van Berdwegh P., Goldkamp A.L., Thurston L.M., Fitzgerald M.G.,
RA Yasek-McKenna D., O'Neill G., Eberhart G.P., Weifendach B.,
RA Ordoas J.M., Freeman M.W., Brown R.H. Jr., Gu J.Z.;
RT "Novel mutations in the gene encoding ATP-binding cassette 1 in four
RT Tangier disease kindreds.";
RL J. Lipid Res. 41:433-441(2000).
RN [112]
RP VARIANT TD ASP-1046, VARIANT FHA CYS-230, AND VARIANTS LYS-219;
RP ILE-825; MET-883 AND LYS-1587.
RX MEDLINE=20396633; PubMed=10938021;
RA Wang J., Burnett J.R., Near S., Young K., Zimman B., Hanley A.J.G.,
RA Connolly P.W., Harris S.B., Hegele R.A.;
RT "Common and rare ABCA1 variants affecting plasma HDL cholesterol.";
RL Arterioscler. Thromb. Vasc. Biol. 20:1983-1989(2000).
RN [113]
RP VARIANT TD TRP-587, AND VARIANT LEU-2168.
RX MEDLINE=21157002; PubMed=11257260;
RA Bertolini S., Pisciotta L., Seri M., Cusano R., Cantafora A.,
RA Calabresi L., Franceschini G., Ravazzolo R., Calandra S.;
RT "A point mutation in ABC1 gene in a patient with severe premature
RT coronary heart disease and mild clinical phenotype of Tangier
RT disease.";
RL Atherosclerosis 154:599-605(2001).
RN [114]
RP VARIANTS LYS-219; MET-883 AND ASP-1172.
RX MEDLINE=21157003; PubMed=11257261;
RA Brousseau M.E., Bodzioch M., Schaefer E.J., Goldkamp A.L., Kiehl D.,
RA Probst M., Ordoas J.M., Aslanidis C., Lackner K.J.,
RA Bloomfield Rubins H., Collins D., Robins S.J., Wilson P.W.F.,
RA Schmitz G.;
RT "Common variants in the gene encoding ATP-binding cassette transporter
RT 1 in men with low HDL cholesterol levels and coronary heart disease.";
RL Atherosclerosis 154:607-611(2001).
RN [115]
RP VARIANT TD LEU-1506.
RX MEDLINE=21369429; PubMed=11476961;
RA Lapicka-Bodzioch K., Bodzioch M., Kruehl M., Kiehl D., Probst M.,
RA Kleb B., Andrikovics H., Boettcher A., Hubacek J., Aslanidis C.,
RA Suttorp N., Schmitz G.;
RT "Homogeneous assay based on 52 primer sets to scan for mutations of
RT the ABCA1 gene and its application in genetic analysis of a new
RT patient with familial high-density lipoprotein deficiency syndrome.";
RL Biochim. Biophys. Acta 1537:42-48(2001).
RN [116]
RP VARIANTS TD ASN-1289 AND TRP-2081, AND VARIANT LYS-219.
RX MEDLINE=21369433; PubMed=11476965;
RA Huang W., Moriyama K., Koga T., Hue H., Ageta M., Kawabata S.,
RA Mawariri K., Yamura T., Eto T., Kawamura M., Yamamoto T., Sasaki J.;
RT "Novel mutations in ABCA1 gene in Japanese patients with Tangier
RT disease and familial high density lipoprotein deficiency with
RT coronary heart disease.";
RL Biochim. Biophys. Acta 1537:71-78(2001).
RN [117]
RP VARIANTS LYS-219; ALA-399; MET-771; PRO-774; ASN-776; ILE-825;
RP MET-883; ASP-1172; LYS-1587 AND CYS-1731.
RX MEDLINE=21138379; PubMed=11238261;
RA Clee S.M., Zwinderman A.H., Engert J.C., Zwarts K.Y.,
RA Molhuizen H.O.F., Roomp K., Jukema J.W., van Willand M., van Dam M.,
RA Hudson T.J., Brooks-Wilson A., Genest J. Jr., Kastelein J.J.P.,
RA Hayden M.R.;
RT "Common genetic variation in ABCA1 is associated with altered
RT lipoprotein levels and a modified risk for coronary artery disease.";
RL Circulation 103:1198-1205(2001).
RN [118]
RP VARIANT TD THR-255, AND VARIANT ATHEROSCLEROSIS ASP-1611.
RX MEDLINE=21645894; PubMed=11785058;
RA Nishida Y., Hirano K., Tsukamoto K., Nagano M., Ikegami C., Roomp K.,
RA Ishihara M., Sakane N., Zhang Z., Tsuji K., Matsuyama A., Ohama T.,
RA Matsura F., Ishigami M., Sakai N., Hiraoaka H., Hattori H.,
RA Wellington C., Yoshida Y., Mitsuji S., Hayden M.R., Egashira T.,
RA Yamashita S., Matsuzawa Y.;
RT "Expression and functional analyses of novel mutations of ATP-binding
RT cassette transporter-1 in Japanese patients with high-density
RT lipoprotein deficiency.";
RL Biochem. Biophys. Res. Commun. 290:713-721(2002).
RN [119]
RP FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION
RP TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL
RP TRANSPORT.
CC - TISSUE SPECIFICITY: WIDELY EXPRESSED, BUT MOST ABUNDANT IN
CC MACROPHAGES.
CC - DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
CC ATP BINDING CASSETTE (ABC) DOMAIN.
CC - DISEASE: DEFECTS IN ABCA1 ARE A CAUSE OF HIGH DENSITY LIPOPROTEIN
CC DEFICIENCY TYPE I (HDLI), ALSO KNOWN AS TANGIER DISEASE (TD). TD
CC IS A RECESSIVE DISORDER CHARACTERIZED BY ABSENCE OF HIGH DENSITY
CC LIPOPROTEIN (HDL) CHOLESTEROL FROM PLASMA, HEPATOSPLENOMEGALY,
CC PERIPHERAL NEUROPATHY, AND FREQUENTLY PREMATURE CORONARY ARTERY
CC DISEASE (CAD).
CC - DISEASE: Defects in ABCA1 are a cause of high density lipoprotein

Query Match 99.8%; Score 11770; DB 1; Length 2261;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2255; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACWQRLRLMLKNTFRRRQTCOLLLEVAMPFLIFLLISVRLSYPRYEQHECHFPNKA 60
DB 1 MACWQRLRLMLKNTFRRRQTCOLLLEVAMPFLIFLLISVRLSYPRYEQHECHFPNKA 60
QY 61 MSAGLPLPWVQGLICNANPCFRPPPGABGVGNFNKSIYARLFSDARRLLLSQKDT 120
DB 61 MSAGLPLPWVQGLICNANPCFRPPPGABGVGNFNKSIYARLFSDARRLLLSQKDT 120
QY 121 SMKDMKRVYRTLOQIKKSSNNLKLODELVDNTEFSGELFVNLSLPKSTYDKMLRADVILH 180
DB 121 SMKDMKRVYRTLOQIKKSSNNLKLODELVDNTEFSGELFVNLSLPKSTYDKMLRADVILH 180
QY 181 KVFLOGYQLHLTSLGNSKSEEMIQDQEVSELCGLPEKELAAERYLRSNMHLKPL 240
DB 181 KVFLOGYQLHLTSLGNSKSEEMIQDQEVSELCGLPEKELAAERYLRSNMHLKPL 240
QY 241 RLINSTSPPSKELAEATYTLHSLGTLAQELFSMRSNMDROEYVFLTNVSSSSSTOI 300
DB 241 RLINSTSPPSKELAEATYTLHSLGTLAQELFSMRSNMDROEYVFLTNVSSSSSTOI 300
QY 301 YQAVSRIVCGHPGGGLTKSLNWEEDNNYKALFGNGTEEDAEFTYDSTPYCNDILMK 360
DB 301 YQAVSRIVCGHPGGGLTKSLNWEEDNNYKALFGNGTEEDAEFTYDSTPYCNDILMK 360
QY 361 NLESSPLSLIIMKALKPLVLGKILYTPDPATROVAEYVNTFOELAVFHDEGMWEL 420
DB 361 NLESSPLSLIIMKALKPLVLGKILYTPDPATROVAEYVNTFOELAVFHDEGMWEL 420
QY 421 PKIWTMENSOEMDLVRLMLDSRDNDHEWQOQIDGMTAODIYVAFLAHPEDVOSSNGS 480
DB 421 PKIWTMENSOEMDLVRLMLDSRDNDHEWQOQIDGMTAODIYVAFLAHPEDVOSSNGS 480
QY 481 VYWRARAFETNOAIRTISRMECVNLKLEPATEVWMLINKSMELDDRKKMAGIVFG 540
DB 481 VYWRARAFETNOAIRTISRMECVNLKLEPATEVWMLINKSMELDDRKKMAGIVFG 540
QY 541 ITPGSELPHVHYKIRMDIDNVERTNKIKDGYMDPGPRADPEDMRYVWGAFYLDQV 600
DB 541 ITPGSELPHVHYKIRMDIDNVERTNKIKDGYMDPGPRADPEDMRYVWGAFYLDQV 600
QY 601 EQAIIIVLTGETEKKTVYQOMPFCYVDIDILRVMSRSMPLFMTLAMIYSAVYIKGIV 660
DB 601 EQAIIIVLTGETEKKTVYQOMPFCYVDIDILRVMSRSMPLFMTLAMIYSAVYIKGIV 660
QY 661 YEKEARLKEFMRIMGIDNSTIMFSWFISSLIPLVASAGLLVYTLKGNLPTSDPSVAV 720
DB 661 YEKEARLKEFMRIMGIDNSTIMFSWFISSLIPLVASAGLLVYTLKGNLPTSDPSVAV 720
QY 721 FLISFVAVVITLQCLISTLFSRANLAAAGGIYFTLYLPYVLCVAMODYVFTLKIFAS 780
DB 721 FLISFVAVVITLQCLISTLFSRANLAAAGGIYFTLYLPYVLCVAMODYVFTLKIFAS 780
QY 781 LLSVPAFPGCEYFALPEBOGIGVQWMDNLPESEVEDGFNLTTSSISMLPDTFLYGVMT 840
DB 781 LLSVPAFPGCEYFALPEBOGIGVQWMDNLPESEVEDGFNLTTSSISMLPDTFLYGVMT 840
QY 841 YTAIVAPGQYIPRPWYFQCTKSYMGESDEKSHPGSNOKRSELCMEDEPHHLKIGVS 900
DB 841 YTAIVAPGQYIPRPWYFQCTKSYMGESDEKSHPGSNOKRSELCMEDEPHHLKIGVS 900
QY 901 IQNLVYVYRDMKVAAVDGALNLFEGOITSFLGNAGAKTTMSILTGFPPTSGTAYIL 960
DB 901 IQNLVYVYRDMKVAAVDGALNLFEGOITSFLGNAGAKTTMSILTGFPPTSGTAYIL 960
QY 961 GKDIRSEMSTIRONLGVCPQHNVLFDMLTYEETIMFYARLKGISSEKHYAKEMQALDVG 1020
DB 961 GKDIRSEMSTIRONLGVCPQHNVLFDMLTYEETIMFYARLKGISSEKHYAKEMQALDVG 1020

QY 1021 LPSSKLSKTSQLSGQMKRLSVLAFVGSKVYILDEPTAGVDPYSRRIWELLKTYRQ 1080
DB 1021 LPSSKLSKTSQLSGQMKRLSVLAFVGSKVYILDEPTAGVDPYSRRIWELLKTYRQ 1080
QY 1081 GRTIILSTHMHDEADVIGDRITAIISHGKLCVGSGLFKNLQGLGYTLTYKKDYESSLS 1140
DB 1081 GRTIILSTHMHDEADVIGDRITAIISHGKLCVGSGLFKNLQGLGYTLTYKKDYESSLS 1140
QY 1141 SCRNSSSTVYTLKKEDSVSSSDAGLSGDSHESDTLITDVSAINLIRKHSEARLYEDI 1200
DB 1141 SCRNSSSTVYTLKKEDSVSSSDAGLSGDSHESDTLITDVSAINLIRKHSEARLYEDI 1200
QY 1201 GHELTLYVLYEAKEGAVELFHEIDRLSDGLISSYGISETTLEIFLKYAESGVDAE 1260
DB 1201 GHELTLYVLYEAKEGAVELFHEIDRLSDGLISSYGISETTLEIFLKYAESGVDAE 1260
QY 1261 TSQGLTPARRNRRAFGDKQSLRPETEDDAADPNDSDIDPESRETDLISGMDGKSYQV 1320
DB 1261 TSQGLTPARRNRRAFGDKQSLRPETEDDAADPNDSDIDPESRETDLISGMDGKSYQV 1320
QY 1321 GMLTLOQFVALLMKRLLIARRSRKGFPAQVILPAVFVCLALVSLIVPPGKYPSELO 1380
DB 1321 GMLTLOQFVALLMKRLLIARRSRKGFPAQVILPAVFVCLALVSLIVPPGKYPSELO 1380
QY 1381 PMMYNEQYTFVSNDAPEDTGTLELINALTKDPGFGTRKMEGNP1PDPFCQAGEEWTAP 1440
DB 1381 PMMYNEQYTFVSNDAPEDTGTLELINALTKDPGFGTRKMEGNP1PDPFCQAGEEWTAP 1440
QY 1441 VPQITMDLPQNGMTQNPSPACOCSSDKIKKMLPVCPPGAGLPPPOKONTADIIIDL 1500
DB 1441 VPQITMDLPQNGMTQNPSPACOCSSDKIKKMLPVCPPGAGLPPPOKONTADIIIDL 1500
QY 1501 TGRNISTDLVTVYQYIATKSLKNKIWNEFRYGGSLGVSQTQALPQSOEYNDATIKOMK 1560
DB 1501 TGRNISTDLVTVYQYIATKSLKNKIWNEFRYGGSLGVSQTQALPQSOEYNDATIKOMK 1560
QY 1561 HUKLAKDSADREFLSLGRFMTGLDTRNNVYKWFENKMGMAISSFLYVNNALIRANLOK 1620
DB 1561 HUKLAKDSADREFLSLGRFMTGLDTRNNVYKWFENKMGMAISSFLYVNNALIRANLOK 1620
QY 1621 GENPSHYGITAENHPLNLTKOOLSEVALMTTSVDVLSICVIFAMSEVPASVFFLQER 1680
DB 1621 GENPSHYGITAENHPLNLTKOOLSEVALMTTSVDVLSICVIFAMSEVPASVFFLQER 1680
QY 1681 VSKAKHLOFISGVKRYIYWLNSFWMDKCNVYVPATLVIIIFICQOXSYSYSTMLPYAL 1740
DB 1681 VSKAKHLOFISGVKRYIYWLNSFWMDKCNVYVPATLVIIIFICQOXSYSYSTMLPYAL 1740
QY 1741 LLLLYGMSITPLMYPASVFPKIPSTAYVYVLTSMVNFJGINGSVATFVLELFTDKMLNNIN 1800
DB 1741 LLLLYGMSITPLMYPASVFPKIPSTAYVYVLTSMVNFJGINGSVATFVLELFTDKMLNNIN 1800
QY 1801 DILKSVFLIFPHCLGRLIDMVKQAMADALERRGENREYVPSLWDLVGNLFPAMAVEG 1860
DB 1801 DILKSVFLIFPHCLGRLIDMVKQAMADALERRGENREYVPSLWDLVGNLFPAMAVEG 1860
QY 1861 VYFELLITVLIQYREFIRRPVNAKSLPUNDEDEYRRRROKRIIDGGGNDLLEIKELTKI 1920
DB 1861 VYFELLITVLIQYREFIRRPVNAKSLPUNDEDEYRRRROKRIIDGGGNDLLEIKELTKI 1920
QY 1921 YRRKKRPAYDRICVGIIPGEGCGILGVNAGKSSFFKMLTDDTVTRDAPLNNKSTLSN 1980
DB 1921 YRRKKRPAYDRICVGIIPGEGCGILGVNAGKSSFFKMLTDDTVTRDAPLNNKSTLSN 1980
QY 1981 IHEVQNMNGYCPQDATALTELLTGREHVEFPALLRGVPEKEVKGVEMAIRKLGLVKGGEK 2040
DB 1981 IHEVQNMNGYCPQDATALTELLTGREHVEFPALLRGVPEKEVKGVEMAIRKLGLVKGGEK 2040
QY 2041 YAGNTSGGKRRKRLSTAMALLIGPPVYFLDEPTGMDPARFRLNNCALSYVKBGRSVYLT 2100
DB 2041 YAGNTSGGKRRKRLSTAMALLIGPPVYFLDEPTGMDPARFRLNNCALSYVKBGRSVYLT 2100
QY 2101 SHSMECEALCTRMAIMVNGRFRCLGSVOHLKNRFGDGYTIVRIVAGSNPDLKPVODFFG 2160

```

Db 2101 SHSMEECALCTRMALVINGRFRIGSYOHUKNRFSGYITVVAISGNDPLKFPVQDFG 2160
QY 2161 LAFPGSYLKEKRRMLQYOLPSSLSLARIPSTLSQSKRRHIEDYVSOTTLDOVYVF 2220
Db 2161 LAFPGSYLKEKRRMLQYOLPSSLSLARIPSTLSQSKRRHIEDYVSOTTLDOVYVF 2220
QY 2221 AKDOSDDHKLDSLHKNQTVVDAVLTSLQDEKVESYV 2261
Db 2221 AKDOSDDHKLDSLHKNQTVVDAVLTSLQDEKVESYV 2261

RESULT 2
ABCL_MOUSE STANDARD; PRT: 2261 AA.
ID ABCL_MOUSE
AC PA1233;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette transporter 1) (ATP-binding cassette 1) (ABC-1).
GN ABCA1 OR ABC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DRA/2; TISSUE=Macrophage;
RX MEDLINE=94375008; PubMed=8088782;
RA Luciani M.F., Denizot F., Savary S., Mattei M.-G., Chimini G.;
RT "Cloning of two novel ABC transporters mapping on human chromosome 9."
RL Genomics 21:150-159(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Qiu Y., Cavelier L., Chiu S., Rubin E., Cheng J.-F.;
RT "Human and mouse ABCA1 comparative sequencing and transgenesis studies identify potential regulatory sequences."
RL submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CAMP-DEPENDENT AND SUTFOXYLUREA-SENSITIVE ANION TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL TRANSPORT (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST LEVELS ARE FOUND IN PREGNANT UTERUS AND UTERUS.
CC -1- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES, EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN ATP BINDING CASSETTE (ABC) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage for and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X75926; CAA53530.1; ALT_INIT.
DR EMBL: AF287263; AAC39073.1; ALT_INIT.
DR MGD: MGI:96607; Abca1.
DR InterPro: IPR003593; AAA.
DR InterPro: IPR003439; ABC_transport.
DR InterPro: IPR001687; ATP_GTP_A.
DR InterPro: IPR003838; DUF214.
DR InterPro: IPR000897; SRP54.
DR Pfam: PF00005; ABC_tran; 2.
DR Pfam: PF02687; DUF214; 1.
DR Pfam: PF00448; SRP54; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Glycoprotein; Transmembrane; Transport.

```

```

FT TRANSMEM 26 42 POTENTIAL.
FT TRANSMEM 640 656 POTENTIAL.
FT TRANSMEM 690 706 POTENTIAL.
FT TRANSMEM 717 733 POTENTIAL.
FT TRANSMEM 749 765 POTENTIAL.
FT TRANSMEM 771 787 POTENTIAL.
FT TRANSMEM 1041 1057 POTENTIAL.
FT TRANSMEM 1351 1367 POTENTIAL.
FT TRANSMEM 1661 1677 POTENTIAL.
FT TRANSMEM 1708 1724 POTENTIAL.
FT TRANSMEM 1737 1753 POTENTIAL.
FT TRANSMEM 1775 1791 POTENTIAL.
FT TRANSMEM 1854 1870 POTENTIAL.
FT NP_BIND 933 940 ATP (POTENTIAL).
FT NP_BIND 1946 1953 ATP (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 349 349 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 478 478 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 489 489 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 521 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 820 820 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1144 1144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1294 1294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1453 1453 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1499 1499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1504 1504 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1637 1637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2044 2044 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2238 2238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1567 1568 MISSING (IN REF. 2).
FT CONFLICT 2024 2024 MISSING (IN REF. 2).
SQ SEQUENCE 2261 AA; 254011 MW; FA62B21FD1D09F9 CRC64;

Query Match 95.4%; Score 11256; DB 1; Length 2261;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 2149; Conservative 55; Mismatches 57; Indels 0; Gaps 0;

```


- RA Nathans J., Leppert M., Dean M., Lupski J.R.;
 RT "A photoreceptor cell-specific ATP-binding transporter gene (ABCR) is
 RT mutated in recessive Stargardt macular dystrophy.";
 RL Nat. Genet. 15:236-246(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97345663; PubMed=9202155;
 RA Azarian S.M., Travis G.H.;
 RT "The photoreceptor rim protein is an ABC transporter encoded by the
 RT gene for recessive Stargardt's disease (ABCR).";
 RL FEBS Lett. 409:247-252(1997).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS STGD TRP-18 AND CYS-212.
 RX MEDLINE=98163759; PubMed=9503029;
 RA Gerber S., Rozet J.-M., van de Pol T.J.R., Hoyng C.B., Munnich A.,
 RA Blankenagel A., Kaplan J., Cremers F.P.M.;
 RT "Complete exon-intron structure of the retina-specific ATP binding
 RT transporter gene (ABCR) allows the identification of novel mutations
 RT underlying Stargardt disease.";
 RL Genomics 48:139-142(1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS STGD.
 RX MEDLINE=98141123; PubMed=9490294;
 RA Nasonkin I., Illing M., Koehler M.R., Schmid M., Molday R.S.,
 RA Weber B.H.F.;
 RT "Mapping of the rod photoreceptor ABC transporter (ABCR) to 1p21-p22.1
 RT and identification of novel mutations in Stargardt's disease.";
 RL Hum. Genet. 102:21-26(1998).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=99175213; PubMed=10075733;
 RA Sun H., Molday R.S., Nathans J.;
 RT "Retinal stimulates ATP hydrolysis by purified and reconstituted ABCR,
 RT the photoreceptor-specific ATP-binding cassette transporter
 RT responsible for Stargardt disease.";
 RL J. Biol. Chem. 274:8265-8281(1999).
 RN [6]
 RP DISEASE.
 RX MEDLINE=98133912; PubMed=9466990;
 RA Cremers F.P.M., van de Pol D.J.R., van Driel M.A., den Hollander A.I.,
 RA van Haren F.J., Knoers N.V.A.M., Tijmes N., Bergen A.A.B.,
 RA Rohrschneider K., Blankenagel A., Pinckers A.J.L.G., Deutman A.F.,
 RA Hoyng C.B.;
 RT "Autosomal recessive retinitis pigmentosa and cone-rod dystrophy
 RT caused by splice site mutations in the Stargardt's disease gene
 RT ABCR.";
 RL Hum. Mol. Genet. 7:355-362(1998).
 RN [7]
 RP VARIANTS ARMD2, AND VARIANTS
 RX MEDLINE=97442530; PubMed=9295268;
 RA Allikmets R., Shroyer N.F., Singh N., Seddon J.M., Lewis R.A.,
 RA Bernstein P.S., Pelffer A., Zabriskie N.A., Li Y., Hutchinson A.,
 RA Dean M., Lupski J.R., Leppert M.;
 RT "Mutation of the Stargardt disease gene (ABCR) in age-related macular
 RT degeneration.";
 RL Science 277:1805-1807(1997).
 RN [8]
 RP VARIANTS STGD W-18; C-212; H-636; M-1019; V-1038; C-1108; W-1640;
 RP S-1977 AND H-2107, AND VARIANTS FFM P-11; P-541; V-1038; E-1091;
 RP C-1508; F-1970 AND R-1971.
 RX MEDLINE=98454319; PubMed=9781034;
 RA Rozet J.-M., Gerber S., Souled E., Perrault I., Chatellin S., Ghazi I.,
 RA Leowski C., Dullier J.-L., Munnich A., Kaplan J.;
 RT "Spectrum of ABCR gene mutations in autosomal recessive macular
 RT dystrophies.";
 RL Eur. J. Hum. Genet. 6:291-295(1998).
 RN [9]
 RP VARIANTS STGD.
 RX MEDLINE=99138655; PubMed=9973280;
 RA Lewis R.A., Shroyer N.F., Singh N., Allikmets R., Hutchinson A.,
 RA Li Y., Lupski J.R., Leppert M., Dean M.;
 RT "Genotype/phenotype analysis of a photoreceptor-specific ATP-binding
 RT cassette transporter gene, ABCR, in Stargardt disease.";
 RN [10]
 RP VARIANTS STGD, AND VARIANTS.
 RX MEDLINE=99192348; PubMed=10090887;
 RA Maugeri A., van Driel M.A., van de Pol D.J.R., Klevering B.J.,
 RA van Haren F.J., Tijmes N., Bergen A.A.B., Rohrschneider K.,
 RA Blankenagel A., Pinckers A.J.L.G., Dahl N., Brunner H.G.,
 RA Deutman A.F., Hoyng C.B., Cremers F.P.M.;
 RT "The 2588G->C mutation in the ABCR gene is a mild frequent founder
 RT mutation in the western European population and allows the
 RT classification of ABCR mutations in patients with Stargardt disease.";
 RL Am. J. Hum. Genet. 64:1024-1035(1999).
 RN [11]
 RP VARIANT STGD TYR-54, AND VARIANT ALA-863.
 RX MEDLINE=20077755; PubMed=10612508;
 RA Zhang K., Geribaldi D.C., Kniazeva M., Albini T., Chiang M.F.,
 RA Kerrigan M., Sunness J.S., Han M., Allikmets R.;
 RT "A novel mutation in the ABCR gene in four patients with autosomal
 RT recessive Stargardt disease.";
 RL Am. J. Ophthalmol. 128:720-724(1999).
 RN [12]
 RP VARIANTS STGD V-60; R-206; N-300; P-541; A-849; P-974; V-1038; C-1108;
 RP L-1408; R-1488; D-1652; P-1729; E-1961; W-2038; W-2077; H-2107; R-2128
 RP AND Y-2150.
 RX MEDLINE=99221420; PubMed=10206579;
 RA Fishman G.A., Stone E.M., Grover S., Derlacki D.J., Haines H.L.,
 RA Hocky R.R.;
 RT "Variation of clinical expression in patients with Stargardt dystrophy
 RT and sequence variations in the ABCR gene.";
 RL Arch. Ophthalmol. 117:504-510(1999).
 RN [13]
 RP VARIANTS GLU-1961 AND ASN-2177.
 RX MEDLINE=20349288; PubMed=10880298;
 RA Allikmets R., Tamur J., Hutchinson A., Lewis R.A., Shroyer N.F.,
 RA Dalakisvili K., Lupski J.R., Steiner K., Paulkroff D., Holz F.G.,
 RA Weber B.H.F., Dean M., Atkinson A., Gail M.H., Bernstein P.S.,
 RA Singh N., Pelffer A., Zabriskie N.A., Leppert M., Seddon J.M.,
 RA Zhang K., Sunness J.S., Udar N.S., Velchits S., Silva-Garcia R.,
 RA Small K.W., Simonelli F., Testa F., D'urso M., Brancato R.,
 RA Rinaldi E., Ingvaest S., Taube A., Wadellius C., Souled E., Ducrocq D.,
 RA Kaplan J., Assink J.M., ten Brink J.B., de Jong P.T.V.M.,
 RA Bergen A.A.B., Maugeri A., van Driel M.A., Hoyng C.B., Cremers F.P.M.,
 RA Paloma E., Coco R., Balcells S., Gonzalez-Duarte R., Kernani S.,
 RA Stanga P., Bhattacharya S.S., Bird A.C.;
 RT "Further evidence for an association of ABCR alleles with age-related
 RT macular degeneration.";
 RL Am. J. Hum. Genet. 67:487-491(2000).
 RN [14]
 RP VARIANTS STGD E-60; T-60; E-65; L-68; R-72; C-212; S-230; S-247;
 RP V-328; K-471; P-541; O-572; R-607; K-635; C-653; Y-764; R-765; A-901;
 RP I-959; K-1036; V-1038; P-1063; D-1087; C-1097; C-1108; L-1380; K-1399;
 RP P-1430; V-1440; H-1443; L-1486; Y-1488; M-1537; P-1689; L-1705;
 RP T-1733; R-1748; P-1763; K-1885; H-1898; E-1961; S-1975; S-1977; G-2077
 RP W-2077 AND V-2241, AND VARIANTS O-152; H-212; R-423; I-552; R-914;
 RP O-943; T-1562; I-1868; M-1921; L-1948; F-1970; A-2059; N-2177 AND
 RP V-2216.
 RX MEDLINE=20442027; PubMed=10958763;
 RA Rivera A., White K., Stoeck H., Steiner K., Hemmrich N., Grimm T.,
 RA Jurkies B., Lorenz B., Scholl H.P.N., Apfelstedt-Sylla E.,
 RA Weber B.H.F.;
 RT "A comprehensive survey of sequence variation in the ABCA4 (ABCR) gene
 RT in Stargardt disease and age-related macular degeneration.";
 RL Am. J. Hum. Genet. 67:800-813(2000).
 RN [15]
 RP VARIANTS CORD3 GLU-65; CYS-212; PRO-541; ALA-863; GLY-863 DEL;
 RP VAL-1038; LYS-1122; TYR-1480 AND ASP-1598.
 RX MEDLINE=20442040; PubMed=10958761;
 RA Maugeri A., Klevering B.J., Rohrschneider K., Blankenagel A.,
 RA Brunner H.G., Deutman A.F., Hoyng C.B., Cremers F.P.M.;
 RT "Mutations in the ABCA4 (ABCR) gene are the major cause of autosomal
 RT recessive cone-rod dystrophy.";
 RL Am. J. Hum. Genet. 67:960-966(2000).
 RN [16]

RP VARIANTS STGD ASP-340; GLN-572; ALA-863; SER-965; VAL-1038; ALA-1780
RP AND HIS-1898, AND VARIANT GLN-943.
RX MEDLINE-20208356; PubMed-10746567;
RA Shroyer N.F., Lewis R.A., Lipski J.R.;
RT "Complex inheritance of ABCR mutations in Stargardt disease: linkage
RT disequilibrium, complex alleles, and pseudodominance";
RL Hum. Genet. 106:244-248(2000).
RN [17]
RP VARIANTS STGD.
RX MEDLINE-20098082; PubMed-10634594;
RA Papathanou M., Oaka L., Bessant D., Lois N., Bird A.C., Payne A.,
RA Bhattacharya S.S.;
RT "An analysis of ABCR mutations in British patients with recessive
RT retinal dystrophies";
RL Invest. Ophthalmol. Vis. Sci. 41:16-19(2000).
RN [18]
RP VARIANTS STGD C-212; D-767; I-897; V-1038; K-1087; K-1399; Q-1640 AND
RP E-1961, AND VARIANT HIS-212.
RX MEDLINE-20174852; PubMed-10711710;
RA Simonelli F., Testa F., de Crecchio G., Rinaldi E., Hutchinson A.,
RA Atkinson A., Dean M., D'Urso M., Allikmets R.;
RT "New ABCR mutations and clinical phenotype in Italian patients with
RT Stargardt disease";
RL Invest. Ophthalmol. Vis. Sci. 41:892-897(2000).
RN [19]
RP CHARACTERIZATION OF VARIANTS, AND MUTAGENESIS OF GLY-966; LYS-969;
RP GLY-1975 AND LYS-1978.
RX MEDLINE-20472331; PubMed-11017087;
RA Sun H., Smallwood P.M., Nathans J.;
RT "Biochemical defects in ABCR protein variants associated with human
RT retinopathies";
RL Nat. Genet. 26:242-246(2000).
RN [20]
RP VARIANT STGD ASN-972, AND VARIANTS GLN-943; ILE-1868 AND LEU-1948.
RX MEDLINE-21478761; PubMed-11594933;
RA Eksandh L., Ekstrom U., Abrahamson M., Bauer B., Andreasson S.;
Query Match 49.8%; Score 5870.5; DB 1; Length 2273;
Best Local Similarity 50.0%; Pred. NO. 0;
Matches 1165; Conservative 356; Mismatches 635; Indels 171; Gaps 27;
QY 6 QLRLLKNTLFFRRQTCQLLEVAWPLFLFLISVRLSYRPEYQEHCFPNKAMPSAG 65
DB 6 QIQLLLKNTLRRKQIRFVELWPLSLFVLWLRNANPLSHHECFPNKAMPSAG 65
QY 66 TLPAVQICIANNPCTRTPTGEPVGVGNFKSIVARLFSPDARLLLYSQKDTSKMD 125
DB 66 MLPWLGIFCVNPNPCFOSPTPGESPISVSNYSILARYRDFQELIMANAPESQHLGRI 125
QY 126 RKVARTLOOI-----KSSSNLKIOPFLVNETFSGFLYHNSLPRKSTV----DKM 172
DB 126 WTEHLISQFMMDTLRTHPERLAGRGIRIROLKDEETLTLFLKINIGLSVYLLINSQ 185
QY 173 LRADVILAKVFLQGYQLHLTSL--CNGSKSEMIQLGDOEVE-----LCGLPKREKLAAE 226
DB 186 VRPQPAHGV---PDALAKDIACEALLERFLIFSQGRGAKTVRAVACLSQGTQMWIE 241
QY 227 RVLFSNMDILKPIILRTLANSPPFSKELAEKATKTLHSLGLTLAGOELFSKMSW---SDM 281
DB 242 DTLVANDVFEK-----LFRVLPFLIDS---RSQGLNLSRWGGLISLSDMS 281
QY 282 -----ROEVMFLTNV-----NSSSSSTOYQAVSRVYCHPGGGGLIKLSLWYE 326
DB 282 PRIOEFHRSMDLLWTRPLMONGPEFTTKLMGTLISDLGCPREGGSRVLSFMYWE 341
QY 327 DNNKALFGNGTEDEAETFYDNSTPYPCNDLMKNLESSPLSRITAKMLPFLVGLKILYT 386
DB 342 DNNKALFGIDSTRRKIDRTYSDRTTSCNALIOSLESNPLTKIAMAARAPFLMGLKILYT 401
QY 387 PDPAITROVAEYVKTFOELAVHDELGAMVELSPKTIWTEWNSOEMDLVAMLDSFND 446
DB 402 PDSPAARILKANSTFELEHVRKLVKAMEVGPQIWFYEFNDNSTQNMIRDLTGNPTVK 461

QY 447 HFEQOJLGDLDWTAODIYAFLLAKHPEDVOSSNGSVYTRREARNETNOAIRISREMECVN 506
DB 462 DFLNROLGEEGITAELAILNFIKGPRESQADMANFMDWDFINITDRRLVNOLEBCLV 521
QY 507 LKLEELAEVWALINKSMELDERKFMAGIYFTGTGTSIELPHVKKIRKIDNIVERT 566
DB 522 LKFESEYNEPQTLQALSLSEENFMWAGVFPDMYPTMSLPRVKKIRKIDNIDVEKT 581
QY 567 NKIKDGYWDPGRPADPEFEDRYWCGFAYLQDVBOAILITVLTGTEKTKGYVMQMPYC 626
DB 582 NKIKDGYWDSGRPADPEFEDRYWCGFAYLQDVBOAITRSQVQAEAVPQIYLOMPYC 641
QY 627 YVDDITFLRWMSMPLFMTLAMIYSAVITIKIYVEKARKETMRINGLONSLWESMF 686
DB 642 FYDDSEFMIINCFPLEWLAIVYSMVKSVILEKELRKETLKNOCVSNVATWCTWF 701
QY 687 ISLPLVASAGLVVITLKNLIPYSDPSVYFVLSFAVVTILQCELISTFSRANIA 746
DB 702 LDFSISMSIFLLTFLFHWGRIHNSDPFLFLFLAFSTATIMLCFLSTFFSKASLA 761
QY 747 AACGIIYTYLPLVYLCVADYVGFILKIPASLSPYAFGCEYFALPEQSIGVOW 806
DB 762 AACSGVITYTYLPLPHILCFAMQDRMTAEKRAVSLSPVAFGCEYLYVREEOGLQOW 821
QY 807 DNLFESEVEDGPNLTTSISMMLPDTFLGVMTWYTEAVFPGOYGPWPYPTKSYWF 866
DB 822 SNTGNSPTGDEFSFLSNOMMLDAVYGLAWIYDVPFDYGTPLPWFYLLDESTWL 881
QY 867 G-----EESDESHPSGNSQKRSEICMEEPHTLKLGYSTONLVKY 907
DB 882 GCGCSTREBRALKEPTELETEDEHP-----EGIHDSFFREHGPWGVCAVKNLYKI 937
QY 908 YRDGMKVAVDGLALNTYEQOISFLHNGAGKTTMSITLGTFPPTSGATYLKGDINSE 967
DB 938 FEBCGPRAVDRINITEFENQITAFGLHNGAGKTTLSITGLTPSGVILGAGDIETS 997
QY 968 MSTIRONLGVCPQHNVLFMFLVTEEHVYARLKGSEKRYAKEMOMALDVGDLSSKLK 1027
DB 998 LNAVRSLSGMCPOHNLFLHLLIYAEHMLFYAQLKGSOEADLEHAMEDETLGL--HKRN 1056
QY 1028 SKTSOLSGMQRKLVALAFVGSQKVVILDEPAGVPSRRGIVELLKTYROGRTIIS 1087
DB 1057 EEAQDLSGQMRKLSVAIAFVGVDAKVILDEPISGVDPYSRRSRIWDLTKYRSGRTIIS 1116
QY 1088 THHMDADVGLGRILAIISHGKLCVSSSLFLKNQLTGYTLTLVYKDVSSSSSQRNSS 1147
DB 1117 THHMDADLIGDRIALIAOGRLYCSGTPLELKNCFGTGLYTLVLR--MKNIOSQRKGSBG 1175
QY 1148 TVSYLKKEDSVQSSSDAGISDHSDDTLTIVYSAISNLIRKHVSEARLVEDIGHETLV 1207
DB 1176 TCSCSSKGRS---TTPRAVVDLTPBOYLDGVNELMDVYLHVPRAKIVECIGDELIFL 1232
QY 1208 LPEAKAEGAFVELFHEIDRLSDIGISSYGISSETTLEBIFLKVAEESGVDAETSDGTL 1267
DB 1233 LPMKNKRRHAYASLFRLEETLADLGLSFGISDTPLEBIFLKVEDSDSGCLFPAAG-- 1289
QY 1268 ARNRRAFPDQKSCLPFEDDAADPNDSI-----DEPSRETLISGM 1311
DB 1290 AQQKRENVNRIHCLGP--BEKAGQTPQDSNVCSPGAPAAHPGQPPPEPCGPOINTGT 1348
QY 1312 DGKGSYQVAGMKLTQOOFALLMKRLLIARRSKKGFPAOIVLPAVFCATLVFSLLVPEF 1371
DB 1349 -----QVLQHVQALLVKKRQHITRSKDELAQIVLPATVFLALMLSVIYIPF 1397
QY 1372 GKYPSELOPMWYNEQYTVSVNDAPEDTGTLELLNALTKDPGRTGCMGNPIPTPCOA 1431
DB 1398 GEYPALTLHPWYQOQYTFEFSMDPESEQFTYLDVLLKMPFGNRCLEGMWLPYPC-G 1456
QY 1432 GEEEMTAYVQIIMLPONGMNTMNPSPACQSSDKKMLPVCPPGAGLPPPPQKQ 1491
DB 1457 NSTPMKTPSPVSPNITQLQKOKMTQVNPSPSCSTREKTLVLPPECPGAGGLPPPPQKQ 1516
QY 1492 NTADILLQDLGRNISIDYLVKTYVQIIAKSLKKNIWNERRGGSFSGVNTQALPPSQEV 1551

```

DB 1517 KSEIILQDITDKNISDELKTI PALIRSSLSKSEWMDORTGIGISG-----GKLVPVPT 1572
QY 1552 NDAIKOMKHLKLAKDSADRELNIGR-----EMTGIDYIPNNVKV 1592
DB 1573 GEAUV-----GFLSDLRIMNVSOGPIREASKELDPDLKHELETDNKV 1617
QY 1593 WNNKGMWHAISSFLVNNAINNIRANIOKGENSHGITAFAHNPMLTKOOLSEVALMTS 1652
DB 1618 WNNKGMWHAISFLVNNAINNIRANIOKGENSHGITAFAHNPMLTKOOLSEVALMTS 1677
QY 1653 VNLVISCIVAFMSEFVPAFVFLIOERYSKAKHOETISGVVPVYLSNFMDCNYYV 1712
DB 1678 VDAVVAICIFMSFVPAFVFLIOERYSKAKHOETISGVVPVYLSNFMDCNYYV 1737
QY 1713 PATLVIIIFCFQOKSVYSSTNIPVALALLLYGMSITPLMYPASFEVKIPSTAVVLTJS 1772
DB 1738 SAGLVVGIIFGOKKAYTSPENILPALVALLLYGMAVILPMYVPAFELFDPSTAVVLTJS 1797
QY 1773 VNLFGINSVATFVLELFTDNK-LNNINDILKSVFLFPHPCLOGLIDMKYKQAMDA 1831
DB 1798 ANLEFGINSATFLELFENNRTILRRNAVILKLILVFPHECLGRGLIDALSOAVTDV 1857
QY 1832 LREFGENRFVSPSLMDLVGRNLFAVAEGVFLITVLIOYREFTRPRPVNAKSLPLNDE 1891
DB 1858 YARFGEHSANFPHDLICKNLFAVVEGVYFELTLVQRFHLSOMIAETKPELVDE 1917
QY 1892 DEDVRRERORILLDGGQNDILEIKELIKYRRKKRPAYDRICVGTIPGECFGLGNCAG 1951
DB 1918 DDDVAEERORITTGKNDILFELHETIKYIPGTSPADVRLCVCVGPCEGLGNCAG 1977
QY 1952 KSTFPMLTGDTTTRGDAFLKNSILSNIEVHONMGYCPDFDITELTGREHVEFPA 2011
DB 1978 KTTTKRMLTGDTTTRVSGDAVAGSKILNINISVHONMGYCPDFDITELTGREHVEFPA 2037
QY 2012 LIRGVEKEVKGVMALIRKIGLVKYYKRYAGNYSGNKRKRLSTAMALIGPPVFLDEP 2071
DB 2038 RIRGVAEIEIEKVANNMSIKSLGLVYADCLAGTYSGNKRKRLSTALIGCPVLILDEP 2097
QY 2072 TTGMOPKARFLMNCALSVYKGRSVVLTSMSMECEALCTRMALMVNGRRCGLSVHL 2131
DB 2098 TTGMOPQARRMLMNVISLIRGRVAVVLTSMSMECEALCTRMALMVNGRRCGLSVHL 2157
QY 2133 KRFSDGYTIVIRIAGSN---PDKAPVQDFGLAPGCVLKEKRNMLQYOLPESLSSL 2187
DB 2158 KSKFGGYIVTKIKSPMDLLPOLNVPQFGNFPSCVQREKRYNNLQOVSS--SSL 2215
QY 2188 ARIEISLSQSKRHLIEDYVSQTTLDQVFNFAKQSDDDLKDLSTH 2236
DB 2216 ARIEISLSQSKRHLIEDYVSQTTLDQVFNFAKQSDDDLKDLSTH 2261

```

RESULT 4

```

ABC2_HUMAN STANDARD: PRT: 2436 AA.
AC Q9BC27.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ATP-binding cassette, sub-family A, member 2 (ATP-binding cassette
DE transporter 2) (ATP-binding cassette 2).
GN ABCA2 OR ABC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed-11178988;
RA Kaminski M.E., Plehler A., Pullmann K., Porsch-Ozcurumez M., Duong C.,
RA Bated G.M., Buchler C., Schmitz G.;
RT "Complete coding sequence, promoter region, and genomic structure of
RT the human ABCA2 gene and evidence for sterol-dependent regulation in

```

```

RT macrophages."
RL Biochem. Biophys. Res. Commun. 281:249-258(2001).
CC -1- FUNCTION: PROBABLE TRANSPORTER, ITS NATURAL SUBSTRATE HAS NOT BEEN
CC FOUND YET. MAY HAVE A ROLE IN MACROPHAGE LIPID METABOLISM AND
CC NEURAL DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.
CC
CC THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION
CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -
CC THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
CC MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
CC ENTITIES REQUIRES A LICENSE AGREEMENT (SEE http://www.isb-sdb.ch/announce/
CC OR SEND AN EMAIL TO license@isb-sdb.ch).
CC
DR EMBL: AF327705; AAK14335.1; JOINED.
DR EMBL: AF327658; AAK14335.1; JOINED.
DR EMBL: AF327659; AAK14335.1; JOINED.
DR EMBL: AF327660; AAK14335.1; JOINED.
DR EMBL: AF327661; AAK14335.1; JOINED.
DR EMBL: AF327662; AAK14335.1; JOINED.
DR EMBL: AF327663; AAK14335.1; JOINED.
DR EMBL: AF327664; AAK14335.1; JOINED.
DR EMBL: AF327665; AAK14335.1; JOINED.
DR EMBL: AF327666; AAK14335.1; JOINED.
DR EMBL: AF327667; AAK14335.1; JOINED.
DR EMBL: AF327668; AAK14335.1; JOINED.
DR EMBL: AF327669; AAK14335.1; JOINED.
DR EMBL: AF327670; AAK14335.1; JOINED.
DR EMBL: AF327671; AAK14335.1; JOINED.
DR EMBL: AF327672; AAK14335.1; JOINED.
DR EMBL: AF327673; AAK14335.1; JOINED.
DR EMBL: AF327674; AAK14335.1; JOINED.
DR EMBL: AF327675; AAK14335.1; JOINED.
DR EMBL: AF327676; AAK14335.1; JOINED.
DR EMBL: AF327677; AAK14335.1; JOINED.
DR EMBL: AF327678; AAK14335.1; JOINED.
DR EMBL: AF327679; AAK14335.1; JOINED.
DR EMBL: AF327680; AAK14335.1; JOINED.
DR EMBL: AF327681; AAK14335.1; JOINED.
DR EMBL: AF327682; AAK14335.1; JOINED.
DR EMBL: AF327683; AAK14335.1; JOINED.
DR EMBL: AF327684; AAK14335.1; JOINED.
DR EMBL: AF327685; AAK14335.1; JOINED.
DR EMBL: AF327686; AAK14335.1; JOINED.
DR EMBL: AF327687; AAK14335.1; JOINED.
DR EMBL: AF327688; AAK14335.1; JOINED.
DR EMBL: AF327689; AAK14335.1; JOINED.
DR EMBL: AF327690; AAK14335.1; JOINED.
DR EMBL: AF327691; AAK14335.1; JOINED.
DR EMBL: AF327692; AAK14335.1; JOINED.
DR EMBL: AF327693; AAK14335.1; JOINED.
DR EMBL: AF327694; AAK14335.1; JOINED.
DR EMBL: AF327695; AAK14335.1; JOINED.
DR EMBL: AF327696; AAK14335.1; JOINED.
DR EMBL: AF327697; AAK14335.1; JOINED.
DR EMBL: AF327698; AAK14335.1; JOINED.
DR EMBL: AF327699; AAK14335.1; JOINED.
DR EMBL: AF327700; AAK14335.1; JOINED.
DR EMBL: AF327701; AAK14335.1; JOINED.
DR EMBL: AF327702; AAK14335.1; JOINED.
DR EMBL: AF327703; AAK14335.1; JOINED.
DR EMBL: AF327704; AAK14335.1; JOINED.
DR MIM: 600047; -
DR InterPro: IPR003593; AAA.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR001687; ATP_GTP_A.
DR Pfam: PF00005; ABC_tran; 2.
DR SMART: SM00382; AAA; 2.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport; Transmembrane; Repeat; Glycoprotein.
FT TRANSMEM 21 40 POTENTIAL.

```


FT TRANSMEM 706 728 POTENTIAL.
FT TRANSMEM 749 771 POTENTIAL.
FT TRANSMEM 786 808 POTENTIAL.
FT TRANSMEM 813 835 POTENTIAL.
FT TRANSMEM 850 872 POTENTIAL.
FT TRANSMEM 892 914 POTENTIAL.
FT TRANSMEM 1793 1815 POTENTIAL.
FT TRANSMEM 1846 1865 POTENTIAL.
FT TRANSMEM 1875 1897 POTENTIAL.
FT TRANSMEM 1904 1926 POTENTIAL.
FT TRANSMEM 1988 2010 POTENTIAL.
FT NP_BIND 1025 1032 APP (POTENTIAL).
FT NP_BIND 2088 2095 APP (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 369 369 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 477 477 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 485 485 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 531 531 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 545 545 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1409 1409 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1497 1497 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1550 1550 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1558 1558 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1613 1613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1678 1678 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1776 1776 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2055 2055 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 2436 AA; 269971 MW; 9E6688D615DE06D CRC64;

Query Match 35.9%; Score 4230.5; DB 1; Length 2436;
Best Local Similarity 39.8%; Pred. No. 2.4e-259;
Matches 998; Conservative 347; Mismatches 730; Indels 435; Gaps 61;

QY 6 QLRLLMKNTFRROTQLLLEVPPLFTLLISVRLSPYEOHECFPKA-MPSA 64
DB 6 QLRLLMKNTFRROTQLLLEVPPLFTLLISVRLSPYEOHECFPKA-MPSA 64
QY 65 GTPWVGICNNANPCFRYPTEGEAGVGNFNKSTIVARLFSFSDARLL-LYSQKD 120
DB 65 GTPWVGICNNANPCFRYPTEGEAGVGNFNKSTIVARLFSFSDARLL-LYSQKD 120
QY 66 GILPVMOSLCPDQORDFEGL-----QYANSTVOLLERLDRIYVEGULFPDAP 115
DB 66 GILPVMOSLCPDQORDFEGL-----QYANSTVOLLERLDRIYVEGULFPDAP 115
QY 121 SMKDMKVLTLTIQIKKSSNKLQDLFYDNETFSG-----FLYHNLSTP 165
DB 121 SMKDMKVLTLTIQIKKSSNKLQDLFYDNETFSG-----FLYHNLSTP 165
QY 116 SLSELEALR--QHLEALSGPGTSGHLDRTSVSSFLSDVARNPQELMRFLTONLSL 173
DB 116 SLSELEALR--QHLEALSGPGTSGHLDRTSVSSFLSDVARNPQELMRFLTONLSL 173
QY 166 KSTYDKMLRDV---LLHKVPLQIOLHLS-LCNGS-----KSEEMT--- 204
DB 166 KSTYDKMLRDV---LLHKVPLQIOLHLS-LCNGS-----KSEEMT--- 204
QY 174 NSTQALILARVDPPEYHLLFGPSSALDSQGLHKQEPWRSUGNPLRMEELLAPA 233
DB 174 NSTQALILARVDPPEYHLLFGPSSALDSQGLHKQEPWRSUGNPLRMEELLAPA 233
QY 205 ---Q---GDOEYSELGIPKKEKLAEE-----RVLRSMID 235
DB 205 ---Q---GDOEYSELGIPKKEKLAEE-----RVLRSMID 235
QY 234 LLEDLCTPGSGELGRILTYBPESOKGALQYRDVAVSGQAARARRESGLSAELRQUDV 293
DB 234 LLEDLCTPGSGELGRILTYBPESOKGALQYRDVAVSGQAARARRESGLSAELRQUDV 293
QY 236 LKPLRTLNSTSPFPKELAEE--TKTLHSLGLTQDELPSMRSWSDMRQEVFLTNVS 293
DB 236 LKPLRTLNSTSPFPKELAEE--TKTLHSLGLTQDELPSMRSWSDMRQEVFLTNVS 293
QY 294 AK-VSQDLGIDAPNGSSSQAPPRRLQALLGDLD-----AKVLQDQDVLS 341
DB 294 AK-VSQDLGIDAPNGSSSQAPPRRLQALLGDLD-----AKVLQDQDVLS 341
QY 294 SSSSTQIYQAVSRIVCGHPBGGLIKISLWMEYDNNKALFGNGTEDEDAETFDNSTP 353
DB 294 SSSSTQIYQAVSRIVCGHPBGGLIKISLWMEYDNNKALFGNGTEDEDAETFDNSTP 353
QY 342 ALALLLPQAGCTGRTGPPRPAAGAGGAN-----GTGAGAVMGPMATAEBCAPSAALATP 396
DB 342 ALALLLPQAGCTGRTGPPRPAAGAGGAN-----GTGAGAVMGPMATAEBCAPSAALATP 396

QY 354 YCNILMKNLSSPLSRILMKALPLLVG----- 381
DB 354 YCNILMKNLSSPLSRILMKALPLLVG----- 381
QY 397 ---DLQOCGSAFY--LMAGLQPLTCNNRTIERPALRGNMSSLGFTSGEONLGLV 451
DB 397 ---DLQOCGSAFY--LMAGLQPLTCNNRTIERPALRGNMSSLGFTSGEONLGLV 451
QY 382 ---KILYPTDPATROYMAEVNKTQELAVPHDEGMEELSPKIMTEMSEMD 434
DB 382 ---KILYPTDPATROYMAEVNKTQELAVPHDEGMEELSPKIMTEMSEMD 434
QY 452 HLMSTNPKILVAPAGEVDVRLKANETFAFVGNVTHAQVWLISAIRSLFEOGRLOQ 511
DB 452 HLMSTNPKILVAPAGEVDVRLKANETFAFVGNVTHAQVWLISAIRSLFEOGRLOQ 511
QY 435 LVRLMLDSRDNHFMEOQDLGIDMTAODIVAFIAKHPEDVOSSNGSVYTMTEANETN-- 492
DB 435 LVRLMLDSRDNHFMEOQDLGIDMTAODIVAFIAKHPEDVOSSNGSVYTMTEANETN-- 492
QY 512 HLRLV-----QOYVAELRLHE---ALNLSDELPRALRQDFFS 547
DB 512 HLRLV-----QOYVAELRLHE---ALNLSDELPRALRQDFFS 547
QY 493 ---QALRTIS-----REMECVNLKLEBIALEWILNKSME--LLDRKKFWAG 535
DB 493 ---QALRTIS-----REMECVNLKLEBIALEWILNKSME--LLDRKKFWAG 535
QY 548 LPSGALLQOQDITDMAACGMIOFMSKSVDFKGFPEBSIVVTLNQAQODVTFAS 607
DB 548 LPSGALLQOQDITDMAACGMIOFMSKSVDFKGFPEBSIVVTLNQAQODVTFAS 607
QY 536 IYFTGTPGSEILPHVKKYKIRMDIDNERTNKIKDGYWDPGRADPEDMRYWGCFAY 595
DB 536 IYFTGTPGSEILPHVKKYKIRMDIDNERTNKIKDGYWDPGRADPEDMRYWGCFAY 595
QY 608 VIFQTRKDGSS-LPHVHYKIKRONSSFTEKTNETLRAVWRPGPNVG--GRFYFLYGFVW 662
DB 608 VIFQTRKDGSS-LPHVHYKIKRONSSFTEKTNETLRAVWRPGPNVG--GRFYFLYGFVW 662
QY 596 LODVVEQATIRVLGTE--KKGVYVQOMPRQCYVDIFLRMSMSMPLMTLMTYSAY 654
DB 596 LODVVEQATIRVLGTE--KKGVYVQOMPRQCYVDIFLRMSMSMPLMTLMTYSAY 654
QY 663 IODMMERATIDTFVGHVDERPESTYOMFPYCYTRDDFLVIEHMMPLCMVISMVTSYAM 722
DB 663 IODMMERATIDTFVGHVDERPESTYOMFPYCYTRDDFLVIEHMMPLCMVISMVTSYAM 722
QY 655 IKGIYVEKEARLKEKTRIMGIDNSILMFSEISSILPLVSAGILVYLKLGMLPYSD 714
DB 655 IKGIYVEKEARLKEKTRIMGIDNSILMFSEISSILPLVSAGILVYLKLGMLPYSD 714
QY 723 TIQIHVAEENHLKEMVTMGILNANVHWVMTTFQVQLSISVATLTAIILKYGVLMHSH 782
DB 723 TIQIHVAEENHLKEMVTMGILNANVHWVMTTFQVQLSISVATLTAIILKYGVLMHSH 782
QY 715 PSVVEFVSFVAVNTILOCFLISTLFSRANLAACGGIITLYLPLVLC-----VAMQD 769
DB 715 PSVVEFVSFVAVNTILOCFLISTLFSRANLAACGGIITLYLPLVLC-----VAMQD 769
QY 783 VIIIMFLAVVAVATIMCFELSVLSYSAKALASACGGIIFYSVPMYVAIREVADK 842
DB 783 VIIIMFLAVVAVATIMCFELSVLSYSAKALASACGGIIFYSVPMYVAIREVADK 842
QY 770 YVGFILKIPASLISVAFGEYFALPEEOGIGVOMNLPSPPEEGFNLTSSML 829
DB 770 YVGFILKIPASLISVAFGEYFALPEEOGIGVOMNLPSPPEEGFNLTSSML 829
QY 843 ITAFK-KCLASLMSTTAGLSGKYALYEVAGVGIQMTTFQSOPBEGDPNILLAVTILM 901
DB 843 ITAFK-KCLASLMSTTAGLSGKYALYEVAGVGIQMTTFQSOPBEGDPNILLAVTILM 901
QY 830 FDTFLYGVMTYVTEAVFPQYVGPFRMYFPCTKSYWGE--ESDEKSHPSNOKRMS-- 884
DB 830 FDTFLYGVMTYVTEAVFPQYVGPFRMYFPCTKSYWGE--ESDEKSHPSNOKRMS-- 884
QY 902 VDAVYGLITWITVIAVHPQMYGLPRPMYFPLQKSWLGSGRLEAWEMPMARFRLISM 961
DB 902 VDAVYGLITWITVIAVHPQMYGLPRPMYFPLQKSWLGSGRLEAWEMPMARFRLISM 961
QY 885 ---ETC-----MEEPHLKLGVSIONLVKYYRQGMKAVDGLALNFEQIT 929
DB 885 ---ETC-----MEEPHLKLGVSIONLVKYYRQGMKAVDGLALNFEQIT 929
QY 962 EBDQACAMSRPFEETRGMEEPETHPLVYVCDKLTXYKDKDKLALKLKLSINTYENOV 1021
DB 962 EBDQACAMSRPFEETRGMEEPETHPLVYVCDKLTXYKDKDKLALKLKLSINTYENOV 1021
QY 930 SFLGNHAGKTTMTSLNGSLPPTSGTAYILGKDIRSEMTIRONLGVCPQHNVLFDLT 989
DB 930 SFLGNHAGKTTMTSLNGSLPPTSGTAYILGKDIRSEMTIRONLGVCPQHNVLFDLT 989
QY 1022 SFLGNHAGKTTMTSLNGSLPPTSGTAYILGKDIRSEMTIRONLGVCPQHNVLFDLT 1081
DB 1022 SFLGNHAGKTTMTSLNGSLPPTSGTAYILGKDIRSEMTIRONLGVCPQHNVLFDLT 1081
QY 990 VEEHIMFYARLKGLEKHNKAMEMALDVLPSKSLKSKTSQSGMQRKLSVALAFV 1049
DB 990 VEEHIMFYARLKGLEKHNKAMEMALDVLPSKSLKSKTSQSGMQRKLSVALAFV 1049
QY 1082 VEEHIMFYARLKGLEKHNKAMEMALDVLPSKSLKSKTSQSGMQRKLSVALAFV 1140
DB 1082 VEEHIMFYARLKGLEKHNKAMEMALDVLPSKSLKSKTSQSGMQRKLSVALAFV 1140
QY 1050 GSKVVLIDEPYAGVDPYSRGIMELLKRYGRGTITLSTHMDVADYLDGRIALISBKL 1109
DB 1050 GSKVVLIDEPYAGVDPYSRGIMELLKRYGRGTITLSTHMDVADYLDGRIALISBKL 1109
QY 1141 GSRALILDEPTAGVDPYARRAILMDILKYPRTILLSTHMDVADYLDGRIALISBKL 1200
DB 1141 GSRALILDEPTAGVDPYARRAILMDILKYPRTILLSTHMDVADYLDGRIALISBKL 1200
QY 1110 CCYGSLELAKNQLGTYVTLTKKDYESSLSCRRSSSVYSLKKEDEVSSSSDAGGS 1169
DB 1110 CCYGSLELAKNQLGTYVTLTKKDYESSLSCRRSSSVYSLKKEDEVSSSSDAGGS 1169
QY 1201 KCCGSPFLKGYGGDYRTLLVKRPAEG-----GPOEPGLAS 1238
DB 1201 KCCGSPFLKGYGGDYRTLLVKRPAEG-----GPOEPGLAS 1238
QY 1170 DHESDFLTLIDS--ATSNLRKHVSERARVEDIGHELYVLPYEAKEGAFELRHEID 1227
DB 1170 DHESDFLTLIDS--ATSNLRKHVSERARVEDIGHELYVLPYEAKEGAFELRHEID 1227
QY 1239 SPFGARPLSSCGSELOYSQIRKHHVASCLVSDTSELSTILPSEAKKAGAFRLQHIER 1298
DB 1239 SPFGARPLSSCGSELOYSQIRKHHVASCLVSDTSELSTILPSEAKKAGAFRLQHIER 1298
QY 1228 RSLDGISSYGETTLLEIFLVAEE-----SGVDA-ETSDGFLP----- 1267
DB 1228 RSLDGISSYGETTLLEIFLVAEE-----SGVDA-ETSDGFLP----- 1267
QY 1299 SDALHLSFGLMDTTLLEVLFLKVEEODSLSENSADYKESRKDVLPGAEGPASGEHAG 1358
DB 1299 SDALHLSFGLMDTTLLEVLFLKVEEODSLSENSADYKESRKDVLPGAEGPASGEHAG 1358
QY 1268 -----ARRNRA--FGDQSCIRPPTEDDADPNDSIDPEBSR 1303
DB 1268 -----ARRNRA--FGDQSCIRPPTEDDADPNDSIDPEBSR 1303
QY 1359 NLARCELTQOSASIQSASSVSGARBEGATYDGYDRPLP--DNPQDP--NVSIDEV 1415
DB 1359 NLARCELTQOSASIQSASSVSGARBEGATYDGYDRPLP--DNPQDP--NVSIDEV 1415
QY 1304 ETDILSGMDKGSYGVKWKLTQOQFVALMLKRLILARRSRKGFPAQIVLPAVFICIALV 1363
DB 1304 ETDILSGMDKGSYGVKWKLTQOQFVALMLKRLILARRSRKGFPAQIVLPAVFICIALV 1363


```

DB 1750 AIIIRANLPKSKGNPAAYGIVTNRHNPKNKTSASLS-IDYLLQGTDDVIAIFIIIVAMSFEVA 1808
QY 1671 SEFVPELIOEVSRAKHLIOFISGVKPIYVMNLSVWMCNVVPAVLVIIIFIOFOOKSVV 1730
DB 1809 SEFVPELAEESTAKHLIOFISGVNPGVILANVIMLNLVPAICCVIILFEVDLPAT 1868
QY 1731 SSTNPLVALLLLLYSGITPLMPYASFVKRIPSTAVYVLTYSNLEIGINGSVATFVLEL 1790
DB 1869 SPINFAVLSTFLLYGWTIPPIYPAFMEVPESSAVFELIVINLEIGITATVATFVLLOL 1928
QY 1791 FT-DNKLNINIDLKSELLEFPHCGRGILDMVKQAMADALERGE-NRFPSPLSMPL 1848
DB 1929 FEHDKLVANVSTLSCFLEFPNINLGHLEMAVMEYINLEYAKIGQFMKMSPEEMDI 1988
QY 1849 VGRNLFMAVEGVFELITLIGREFIRPVPYNAKLSPLNDEDEDVRRERORILDDGGO 1908
DB 1989 VTRGLVAMTEGVFELITLMQYNFLRQPLRPSVTKPEVD-DVDVASRQGVLRGDAD 2047
QY 1909 NDLEIKELTKIYRK---KKPAVDRCVGIPEGECEGLGVNAGAKSSFFKMLTGDITY 1965
DB 2048 NDVKKIENLTKYVKSRIKIGILAVDRCLGVRGECEGLGVNAGAKSTFFKMLTGDDEST 2107
QY 1966 TRCGAPFNKSIISNIEHVQNMGCYCPQDAITELLTGREHVEFPALLRGVEKGVKG 2025
DB 2108 TGEFAFNGHSVYLKDLQVOOSIGYCPQFALDELTAHRLDLYTRLRKIPKDAQVY 2167
QY 2026 EMALIRKILGVKYGKYGAGVNTSGNKRRLSTAMALLIGSPVYVLEDEPTGMDPKARPLMN 2085
DB 2168 KWALEKLEIKRYADKPAGTYSGNGKRRLSTALIALIGYPAIFIDEPTGMDPKARPLMN 2227
QY 2086 CALSVVEGVSVLTSHSMECEALCTRMAIVNGRPRCGSVQHLKNRGDDYTIIVRI 2145
DB 2228 LIIDLITGSSVLTSHSMECEALCTRLIIVNGRLCLGSIQHLKNRGDDGYMTIVR 2286
QY 2146 AGSNPDLKPYODFEGFGLPSSVLEKERNMLQYOLPSSLSLARIPSSLSQSKRLHIED 2205
DB 2287 TKSQGNKDVYRFRNRPPEAMLEKERNHGVQYOLKSEHSLAQVFESKMGVGVGLIED 2346
QY 2206 YVSQTTLDQVFNFAQDSDD 2227
DB 2347 YVSQTTLDQVFNFAKQSDN 2368

RESULT 6
ABC3_HUMAN STANDARD; PRT; 1704 AA.
ID ABC3_HUMAN
AC Q99758; Q92473;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ATP-binding cassette, sub-family A, member 3 (ATP-binding cassette transporter 3) (ATP-binding cassette 3) (ABC-C transporter).
GN ABC3 OR ABC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid carcinoma;
RX MEDLINE=9632608; Pubmed=8706931;
RA Klugbauer N., Hofmann F.;
RT "Primary structure of a novel ABC transporter with a chromosomal
localization on the band encoding the multidrug resistance-associated
protein.";
RL FEBS Lett. 391:61-65(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97179225; Pubmed=9027511;
RA Connors T.D., van Raay T.J., Petry L.R., Klinger K.W., Landes G.M.,
RA Burn T.C.;
RT "The cloning of a human ABC gene (ABC3) mapping to chromosome

```

```

RT 16p13.3.
RL Genomics 39:231-234(1997).
CC -1- FUNCTION: MAY BE A TRANSPORTER, ITS NATURAL SUBSTRATE HAS NOT BEEN
CC FOUND YET (BY SIMILARITY). MAY ACT AS AN EFFLUX PUMP FOR
CC CHEMOTHERAPEUTICS DRUGS.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, FOLLOWED BY BRAIN,
CC PANCREAS, SKELETAL MUSCLE AND HEART. WEAKLY EXPRESSED IN PLACENTA,
CC KIDNEY AND LIVER. ALSO EXPRESSED IN MEDULLARY THYROID CARCINOMA.
CC -1- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
CC ATP BINDING CASSETTE (ABC) DOMAIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/or\_send\_an\_email\_to\_license@sib-sib.ch).
CC
CC EMBL; U78735; AAC50967.1;
CC EMBL; X97187; CAA65825.1;
CC MIM; 601615;
CC
CC InterPro: IPR003593; AAA.
CC InterPro: IPR003439; ABC_transportr.
CC InterPro: IPR001687; ATP_GTP_A.
CC PIRAT; PF000005; ABC_Ctran; 2.
CC SMART; SM00382; AAA; 1.
CC PROSITE; PS00211; ABC_TRANSPORTER; 1.
CC KW ATP-binding; Transport; Transmembrane.
CC FT TRANSMEM 22 42 POTENTIAL.
CC FT TRANSMEM 249 269 POTENTIAL.
CC FT TRANSMEM 307 327 POTENTIAL.
CC FT TRANSMEM 344 364 POTENTIAL.
CC FT TRANSMEM 373 393 POTENTIAL.
CC FT TRANSMEM 405 425 POTENTIAL.
CC FT TRANSMEM 447 467 POTENTIAL.
CC FT TRANSMEM 925 945 POTENTIAL.
CC FT TRANSMEM 1100 1120 POTENTIAL.
CC FT TRANSMEM 1144 1164 POTENTIAL.
CC FT TRANSMEM 1183 1203 POTENTIAL.
CC FT TRANSMEM 1213 1233 POTENTIAL.
CC FT TRANSMEM 1245 1265 POTENTIAL.
CC FT TRANSMEM 1306 1326 POTENTIAL.
CC FT NP_BIND 566 573 ATP (POTENTIAL).
CC FT NP_BIND 1416 1423 P -> S (IN REF. 2).
CC FT CONFLICT 36 36 L -> P (IN REF. 2).
CC FT CONFLICT 196 196
CC SO SEQUENCE 1704 AA; 191387 MW; AF0098DAF7A04F5F CRC64;

Query Match 22.4%; Score 2642.5; DB 1; Length 1704;
Best Local Similarity 35.7%; Pred. No. 6.3e-159;
Matches 639; Conservative 300; Mismatches 523; Indels 327; Gaps 48;

QY 534 AGIVFTGIRGSGIE-LPHVKKYKIRMDIDYVERTN-----KIKDGYW----- 574
DB 131 AAVFENHPNHSKEPLPLAVKYLHFR---SYTRRNVTMTQSGFPLKTEGHTSLRPL 187
QY 575 --DPGRADPFBD--MRYVGGFAVLDVYBOAIIIVLTGTE---KKGVIYQMOPY 624
DB 188 FPNPGRRELTPDGGPGVIRGFLAVQAVDAIRMEYHADATRQLRQLTVTKRPY 247
QY 625 PCYVDIEFLRWRSRKLPLMTLAMIYSVAVITIKGIYEEKERLKTMTIMGDSIILF 684
DB 248 PPIADPFLVAIOYOYLPLILLSTFYTALTARAAVQEKRLKYMKGSLSWLHWSA 307
QY 685 WFTSSLIPLVSAAGLVVILKLG-----NLDPSPSVVFLVFAVVTILOCFLISTL 739
DB 308 WFLFPLFLIIAASFMTLLFCYKAVPNAVLSRSPDSLVAFLAFLCFAISTISFSFMT 367

```


CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; 229117; CAA82384.2; -
 DR EMBL; 229117; CAA82383.2; -
 DR PIR; S40724; S40724.
 DR PIR; S40725; S40725.
 DR Wormpep; C48B4.4A; CE24856.
 DR Wormpep; C48B4.4B; CE24857.
 DR Interpro; IPR003593; AAA.
 DR Interpro; IPR003439; ABC_transport.
 DR Pfam; PF00005; ABC_tran; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
 DR Hypothetical protein; ATP-binding; Transport; Alternative splicing.
 NP_BIND 567 574 ATP (POTENTIAL).
 NP_BIND 1398 1405 ATP (POTENTIAL).
 FT VARSPIC 979 980 MISSING (IN ISOPRM C48B4.4A).
 FT SEQUENCE 1691 AA; 189770 MW; AA89734EC8F669E6 CRC64;

Query Match 13.0%; Score 1537; DB 1; Length 1691;
 Best Local Similarity 24.9%; Pred. No. 7, 8e-89;
 Matches 482; Conservative 345; Mismatches 679; Indels 428; Gaps 58;

QY 458 WTADIV-----AFLAKHPEDVOSSNGSV-----TWREAFENETN-----492
 D 24 WTELELLIPCLLGLPLVLYVKNADHTSPENIDNFQVGTVDVPLESNEFIKPIYKRW 83
 QY 493 -----QAIRTI-----SRMECVNKL-----EPATEWMLINKS 523
 D 84 CLRSADVVGITSKDAAKKRVDDIMKKFAERPOSAKLKLVSKNSSSEQLT--VLKND 140
 QY 524 MELDE-----RKFWAGIVFTGTPGSEIELPHVKKIRMDIDVERTNKIKDGYWDCP 578
 D 141 LPMNEFCAINSYAAGVFEVDVYTNKL-----NYRILGKTFEETWHLTEISYNYPG 196
 QY 579 RADPFEDM-----KYWGGFAYLDVYQALIRVLGTGEKKTGYVMQMPYCYVD-----629
 D 197 SSGYRSRIPSSPPWTSATLFFQHAIESFLSSVOSGAPDLITLRGLPBRKYTSVA 256
 QY 630 ---DLEFLRMKSHMPLMTLMTAMISAVIIGIYKEKARLKEMRIKGLDNLSTFMSMT 687
 D 257 FIDF-----PFMAFVTFIVHITRELAENHA-VKPYILAGLSTFMTFAHV 307
 QY 688 SSLIPLLVAGLVLVILKGLNLPYSDSVFVFLSVFAVVTLLQGLISTFLSRANLAA 747
 D 308 MAFKPFVI--FLCSITPLTFVMEFVSPALIVLVLVGLGAVIFGAFVASFNNNSAI 365
 QY 748 ACGGIIIFTLXPLVLCVANODVYGLTKIFASL--LSPV-----AFGCGCEFFAL 796
 D 366 K-----ALLVAGMAMGISYKLRPELDQISSCELYGLNLINGAFALAVASID 412
 QY 797 FEEGIGVQMDNLF-ESPVEDGFNLTTSIMMLFTFELGVMTVYEA-VFGQYQIPR 854
 D 413 YMRERELNLTNNNDSSLH--FSLQMALVMMIVDILMMSIGALVYDHI RTSADSLRT 469
 QY 855 PWIFPCIKSWFGESSEKSHPG--SNQRMSEICMEEPETH-----895
 D 470 LFDE-----APEDENDQDTVTAQNTIRNEQMPNMASTSLNPNMADSDILEGSTE 522
 QY 896 -----KLGVSIONLVKVRDGMKAVAVDGLALNFEGQITSLFLNGNAGKTTMSILNG 948
 D 523 DGAADTARADIIYANLKVITSTGERAVDGLSLAARGQCSILLGHGAKSTTFSSIAG 582
 QY 949 LFPPTSGTAVILKDIENSESTIRONLGVCPQHNVLFMDLVEBEHIMFARLKLSEKHV 1008
 D 583 IIRTNRIITICGVADYENEPGETRHHIGMCPQYNPLIDQITVSEHKLIVGLKGAENKE 642
 QY 1009 KAEKEMALDVGLPSSKIKSKTSQLSGGMOKRLSVLALFVGGKVVILDEPTAGVDPSR 1068

D 643 KQMKRLSDVKU--DEKENEKAVNISGMMKRLCYCMALIGSEVVLDEPTAGDPCAR 701
 QY 1069 RGIWELLKYRQRTIITLSTHMEADVDLGRDIAITSHKLCVSSPLTKNOLGTGYL 1128
 D 702 QDVQKVERKANRTIILTHYWEDEFRIGDWFILMSHOKLVAAGNQLKAKKFTGYLL 761
 QY 1129 TLVKKDVESLSSCRNSSSTVYLKREDSVSSSDAGLSHESDTLTIDVSAISNLR 1188
 D 762 TVV-----LDHNGDKRKMAV--ILTDVCT 783
 QY 1189 KHYSEARIVEDIGHETLVLYPEAKEGAFVLEPHID-----DR 1228
 D 784 HYKKEERGMHQOETITLPEARKKE--FVPLQALVLEIQDRNRSNVEDMPTLKSQ 841
 QY 1229 LSDGISYGISETLEELFLVKAESGYDAETSDGTLPARRNRARFGQSCLRPTED 1288
 D 842 LATLEMRSPGLSLNLTLEQFITGDK-----VKAIASRQNSRSHNSRASPSLKP 894
 QY 1289 DAADPRDSIDPESRETDLISGMDKGSYQVKGWKLTOQOFVALLMKRLILAKSRGKF 1348
 D 895 AGYDQSSSTKSDSYOK--LMDSOARGP-EKSGVAKMAQFISIRKKFLYSRRMAOLF 951
 QY 1349 AOLVPAVFCIALVPSLIVPEGKYPSELQPMWYNEQYTPVSDADPDGTLELMAAL 1408
 D 952 TOVLIP--IILIGVSLF-----TLKSNNTD-----977
 QY 1409 TDDPGFGTRCMESNPIDPTPCQAGEEWTPAPVOTINDLPONGMWTQONSPACQCSSD 1468
 D 978 -----FSVRSLS-----TP--SGIE-----PSKVYRFENG--1001
 QY 1469 KIKKMLVPCPPAGGLPPQQRKQNTADILQDITGRNISLYLVKTYVQILAKSLAKTIWN 1528
 D 1002 -----IPEANPEKILRKSGGEVLYNKNPLPNTLSL-----IG 1039
 QY 1529 EFRYGGFSLGVSNTQALPSPQSEVNDALIKOMKHLKIAKSSADRLNISGRMTGLDTRN 1588
 D 1040 E-----MPRA-----ITGHTMNS--D 1053
 QY 1589 NKVWENNGMHAISSEFLVNNAILRANLQKGNPSHYGITAENHPINLTKQOLEVAL 1648
 D 1054 NLEALFNMYRYHVLPTLISMIRARLTGVDAEISSGVFLSKTSNSNLLPSQL-----1108
 QY 1649 KTSVDVLVSLGVIFAMSVYPASFVVELLOEVSAAKHLQFISGVKPYIYMLSNVWMC 1708
 D 1109 ---IDVLAPMLILFAVNTSTFWFLFEERTQFAHQQFLTGSPITFEYSASLITYGI 1164
 QY 1709 NYVPATVILIIIFCFOOKSYVSTNLPVALLLILYGMSTPLPMYPASFVKIPSTAYV 1768
 D 1165 LVSLICLIFLPMFLAF-----HMYDHLAIVILFVLFYFSSVPFIYAVSFLFQSSKANV 1220
 QY 1769 VLSYNLFGINGSATVYVLELTQNKLNINDILKSFL-----IPHFCLRGGLDMV 1823
 D 1221 LLIWQVYISGAALLAVELFW-----IFNIDEMKSLIVNIFMFLPVSFAFGSAII--1272
 QY 1824 KQAMADALERGENRFPSP-----LSMDLVGRNLFAMAVEGFVFLIVLVLOYRFR--1877
 D 1273 -----TINYG--MLPSEELMNMHDCGNAMLMGTBFVGCSPALVLLQFXYFRFL 1322
 QY 1878 -----PRVNAKLSPLNDE--DEIVRERORILIDGGQNDILEIKELTKYRRKKRPA 1928
 D 1323 SOVMTVRRSSHNNOVPMAGDLPRVCSEYSEERBRVHRVNSQSAIVIKDLFTF--GRETA 1380
 QY 1929 VDRICVGPFGCFGLLVNAGAKSTTKMLTGGTYYRGAFPLANKSILSNHIEVQNM 1968
 D 1381 VNEICLAVQKCFGLLVNAGAKSTTKMLTGGTYYRGAFPLANKSILSNHIEVQNM 1968
 QY 1989 GYCPQFADITTELTREHVEFFALLRGVPEKEVGVGEMALRKGLVYKGYAGYNTSG 2048
 D 1436 GYCPFDALMDLTRELELTLAQNHGRENKA--KALLIECYGMATAHADKLVYRFSGG 1493
 QY 2049 NKRKLSTMALIGPVPVLEDEPTTGMDPKARRLMCAISVKEGKS--VVLTSHSMEC 2107
 D 1436 GYCPFDALMDLTRELELTLAQNHGRENKA--KALLIECYGMATAHADKLVYRFSGG 1493

```

Db 1494 OKRKISVGVALLAPTOQMTILDEPTAGIDPKAREVWELLMLCREHSNLSMLTSHSDEC 1553
Qy 2108 EALCLTRMALINWGRFCISGVOLHKNRGDCYTIYVRIRAGSNPDLPKPYDFFGLAPGSV 2167
Db 1554 EALCSIRIVANLNGSLIAIGSSOELKSLYGNNTMTLSLEYEPQORDMVVO-TVOTRLPMSV 1612
Qy 2168 LKEKHNNM---LOYOLPSSLSTL-ARFISLSQSKKRRLHIEYVSQOTLDQVFNFA-- 2221
Db 1613 LTTTSTNKTNLKMDPKPEKDCWSAKFEMVQALAKDLGVKDFILAQSSLEETFLRLAGL 1672
Qy 2222 -KDQSDDDLKDLDS 2234
Db 1673 DEDQDLFTSHTEIS 1686

RESULT 8
DRRA_STRPE STANDARD; PRT; 330 AA.
AC P32010:
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Daunorubicin resistance ATP-binding protein drra.
GN DRRA.
OS Streptomyces peucetius.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1950;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29050;
RX MEDLINE-92020891; PubMed=1924314;
RA Guilfoile P.G., Hutchinson C.R.;
RT "A bacterial analog of the mdr gene of mammalian tumor cells is
RT present in Streptomyces peucetius, the producer of daunorubicin and
RT doxorubicin."
RL Proc. Natl. Acad. Sci. U.S.A. 88:8553-8557(1991).
CC -1- FUNCTION: DRRA AND DRB MAY ACT JOINTLY TO CONFER DAUNORUBICIN AND
CC DOXORUBICIN RESISTANCE BY AN EXPORT MECHANISM.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: M73758; AAA74717.1; -
DR PIR: S27707; S27707.
DR InterPro: IPR003593; AAA.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR001687; ATP_GTP_A.
DR Pfam: PF00005; ABC_tran. 1.
DR SMART: SM00382; AAA: 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport; Antibiotic resistance.
FT NP_BIND 41 48 ATP (BY SIMILARITY).
SQ SEQUENCE 330 AA; 35700 MW; 582D66C90D54E6B9 CRC64;

Query Match 3.5%; Score 411; DB 1; Length 330;
Best Local Similarity 28.4%; Pred. No. 1.2e-18;
Matches 112; Conservative 69; Mismatches 122; Indels 92; Gaps 10;

```

```

Qy 1008 VKAEMQMALDVGLPSK---LKSKTSQLSGGMORKISVALAFVGSKVYILDEPTAGVD 1064
Db 116 ARERAEALIDEGGLDADRDLKT---YSGMRRRLDIASIVYTPDLLFLDEPTGLD 171
Qy 1065 PYSRGRIWELL-LKYRGRTIILSTHMDADVYIGDRITAIISHGKLCVSSFLKNQIG 1123
Db 172 PRSRNQWMDIYRALVDAGTIVLTQYLDADQADNIAVIDHGRVIAEGTTEGLKSSIG 231
Qy 1124 TGYVLTFLVKDVESSLSCRRSSSTVSYLKKEDSVQS-----SPDAGLCSHESDTLT 1177
Db 232 -----SNVLRRLRHDAQSRAEERLISAEIGVTIHRDSDPTA 268
Qy 1178 ID-----VSAISNLIRKHVSEARLVEDIGHIELTYVLPYEAKRGAVVELFHEIDR 1228
Db 269 LSARIDPPRGMRALAEISRTH----- 290
Qy 1229 LSDGISGSGSETTLEIFLKVAEESGVAETSQ 1263
Db 291 ---LEVRSFISIGSSIDEVFLALTGHPADDRSTBE 322

RESULT 9
MOD1_RHISN STANDARD; PRT; 343 AA.
ID MOD1_RHISN
AC P5476:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Modulation ATP-binding protein I.
GN NOD1 OR Y4HF.
OS Rhizobium sp. (strain NGR234).
OC plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes."
RL Nature 387:394-401(1997).
CC -1- FUNCTION: FORMS, WITH NODJ, A MEMBRANE TRANSPORT COMPLEX INVOLVED
CC IN THE NODULATION PROCESS. IT PROBABLY EXPORT A MODIFIED BETA-1,4-
CC LINKED N-ACETYLGLUCOSAMINE OLIGOSACCHARIDE.
CC -1- SUBCELLULAR LOCATION: Membrane-associated.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: AE000076; AAB91694.1; -
DR InterPro: IPR003593; AAA.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR001687; ATP_GTP_A.
DR Pfam: PF00005; ABC_tran. 1.
DR SMART: SM00382; AAA: 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW NODulation; Membrane; ATP-binding; Transport; Plasmid.
FT NP_BIND 77 84 ATP (POTENTIAL).
SQ SEQUENCE 343 AA; 37917 MW; F49A7ECS6E099A33 CRC64;

Query Match 3.2%; Score 382.5; DB 1; Length 343;
Best Local Similarity 35.1%; Pred. No. 8.1e-17;
Matches 91; Conservative 46; Mismatches 101; Indels 21; Gaps 6;

```

QY 872 EKSPGNS- - - - - OKRMEICMEEPHLEKLGVSIONLVVYRDGMKVAVDGLALNFEG 926
 Db 24 OKCHGNSADNSLSRSKSDVAIE- - - - - LTNVSKSYGD- - - - - KVVVDOLSFITTS 70
 QY 927 QITFELHNGAGKTTMSITLGLFPPTSGATYILGKDIRSEMSTIRONLGVCPQHNVLFD 966
 Db 71 ECFELGPNAGKSTVSRVLVGLAPDPEGITVIGEPVAPARLARSRIGVVPQFTLDR 130
 QY 987 MLVVEEHIMFYARLKGISEKHVKAEMQALDVGLPSSKLSKYSOLSGCMQRKLSVALA 1046
 Db 131 EFTARENLVYGRYFGLHTRELEAIPPL- LDFARLESKADVPYAQLSGCMQRRLTAC 189
 QY 1047 FVGGSKVILDEPTAGDPSRRTGIELLIK-YRGGRTILSHHDEADVLGDRATIS 1105
 Db 190 LINDPOLLIIDEPTGDDPHARHLIWERLSLALGKTIILTHFMEADRLCDRLCIVIE 249
 QY 1106 HGKLCVG-SSTFLKNOLG 1123
 Db 250 HGRKIVEGRPHALIDEIG 268

RESULT 10
 MODL_RHIS3
 ID MODL_RHIS3 STANDARD: PRT: 304 AA.
 AC P72335:
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Modulation ATP-binding protein I.
 GN MODI.
 OS Rhizobium sp. (strain N33).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=103798;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96303537; PubMed=8755627;
 RA Cloutier J., Laberge S., Prevost D., Antoun H.;
 RT "Sequence and mutational analysis of the common nodBCL1 region of
 RT Rhizobium sp. (Oxytropis arctobia) strain N33, a nitrogen-fixing
 RT microsymbiont of both arctic and temperate legumes.";
 RL Mol. Plant Microbe Interact. 9:523-531(1996).
 CC -1- FUNCTION: FORMS, WITH NODJ, A MEMBRANE TRANSPORT COMPLEX INVOLVED
 CC IN THE MODULATION PROCESS. IT PROBABLY EXPORT A MODIFIED BETA-1,4-
 CC LINKED N-ACETYLGLUCOSAMINE OLIGOSACCHARIDE.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: U53327; AAB16898.1; -
 DR InterPro: IPR003593; AAA.
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR001687; ATP_GTP_A.
 DR Pfam: PF00005; ABC_tran; 1.
 DR SMART: SM00382; AAA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW Modulation; Membrane; ATP-binding; Transport; Complete proteome.
 FT NP_BIND 38 45 ATP (POTENTIAL).
 SO SEQUENCE 304 AA; 33698 MW; 7C6A3B0364CCE14 CRC64;

Query Match 3.1%; Score 366; DB 1; Length 304;
 Best Local Similarity 35.0%; Pred. No. 7.3e-16;
 Matches 77; Conservative 54; Mismatches 85; Indels 4; Gaps 3;

OY 896 KLGVSIONLVKVVYRDGMKVAVDGLALNFEGQITSLGHNAGKTTMSITLGLFPPTSG 955

Db 3 KVAIDLAVKKSFGD- - - - - KLIVNGLSFTVASSGCEFLGPNAGKSTIARMLIGMTVPDAG 60
 QY 956 TAVILGKDIRSEMSTIRONLGVCPQHNVLFDMLVVEEHIMFYARLKGISEKHVKAEMQ 1015
 Db 61 KTTVIGEPVAGSRRLARSISGVVPQDNDQEFYRENLVYGRYFGLHTRELEAIPPL- 119
 QY 1016 ALDVGLPSSKLSKYSOLSGCMQRKLSVALAFVGGSKVILDEPTAGDPSRRTGIELLIK- 1074
 Db 120 LDFARLESKADVPYAQLSGCMQRRLTACALINDPOLLIIDEPTGDDPHARHLIWERL 179
 QY 1075 LKRYGRTILSHHDEADVLGDRATISHSKLCVGS 1114
 Db 180 RFLARGKTIILTHFMEADRLCDRLCIVLEHGRKLAEGS 219
 RESULT 11
 YADG_ECOLI
 ID YADG_ECOLI STANDARD: PRT: 308 AA.
 AC P36879;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical ABC transporter ATP-binding protein yadG.
 GN YADG OR B0127.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / W3110;
 RX MEDLINE=94261430; PubMed=8202364;
 RA Fujita N., Mori H., Yura T., Ishihama A.;
 RT "Systematic sequencing of the Escherichia coli genome: analysis of
 RT the 2.4-4.1 min (110,917-193,643 bp) region.";
 RL Nucleic Acids Res. 22:1637-1639(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. STRONG, TO
 CC RHIZOBIACEA NODI.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: D26562; CAB20301.1; -
 DR EMBL: AE000122; AAC73238.1; -
 DR PIR: S45204; S45204.
 DR Ecogene: EG12320; yadG.
 DR InterPro: IPR003593; AAA.
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR001687; ATP_GTP_A.
 DR Pfam: PF00005; ABC_tran; 1.
 DR SMART: SM00382; AAA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW Hypothetical protein; ATP-binding; Transport; Complete proteome.
 FT NP_BIND 38 45 ATP (POTENTIAL).
 SO SEQUENCE 308 AA; 34647 MW; 9EFA3C2BFBFF3F47 CRC64;


```

Query Match: 2.9%; Score 339.5; DB 1, Length 1280;
Best Local Similarity 18.7%; Pred. 4,1e-13;
Matches 272; Conservative 201; Mismatches 470; Indels 509; Gaps 56

QY 776 KIPASLSPVAFGECEYFALFEEOGIGVQWQDNLFESPVEEDGKNTLTSISMLEPDTFL- 834
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 256 EVLAIAITVTAIFGQKKELERYNK-----NLEEA--KRGIGKKAITANISGAFFL 305
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
QY 835 -----YGMWY-LEAFPGGYGPR---PWYFPCKKSWPEES----- 870
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 306 IYASYALAFYGTTLVLSGEYSIGQTLVYFVSVLIGASVQASPSIEAFANGAAYET 365
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
QY 871 ----DEKSHPGSNQKRMSEICEEBPTHLKLGVSIQNLVKKYRGMKVAV--DGLALNFE 925
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 366 FKIIDNKPISIDSYSK-----SGHKPDNIKGLFERNVHFYSRKKEVKKILKGLNLKVG 419
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
QY 926 GQITSPFGHNAGAKCTTMSILTGLEPPRPSTGATYILGKIDRS-EKSTIRQNLGVCPOHNVL 964
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 420 GQYVALVGNSSGCKSTTYQLMKRLDTPREGWVSDGQDITRTINRFLREIIGVASEPVL 479
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
QY 985 FDMLTVEEHIMWFARLKGISEKHVAEEMQALD--VQLP---SSKLSKTSQLSGQMOR 1039
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 480 F-ATTIAENT-RYGRENVTMDEIKAAVEANAYDPIKMLPKHPTLVGEGAGQSLSSGQK 537
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
QY 1040 KLSVALAFVGGSNVYLLDEPTAGVDPRYSRGIWELLKTYRGRIITLITSHND---EADY 1096
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

```

Dd	538	R1ARARALVRNPKILLIDEDNTSALDISESEVNOVALDARKKRTGTIVIAHRLSTYRNDV	597
OY	1097	LG--DRLAIISHGKLCVGSSEFLKNOGTGYLLTVKRDV---ESSLSSCRNSSSTVSY	1151
Dd	598	IAGEDDGYIVKEG-----NHDELMTKEK---GIYFKLVMTQTAGNEVELENADESKS---	646
OY	1152	LKEDSVSOSSDAGLCSDESOTLTIIVDSAISNLIRKHYSEARLVEDIGHELTVLPEY	1211
Dd	647	--EIDALEMSSNDR-----SSLIRK-----	665
OY	1212	AAKGAFVLEFHEIDRLSDLGISGYISFTLLEFLVAEESGVADATSDGTLPARRN	1274
Dd	666	-----	668
OY	1272	RRAGDKOSCLRPTEDDADPNDSIDIDESPREDTLLSGMDKGSYOYGMKLTQOOEVA	1331
Dd	669	RRVRSQAOQRKUSTKEAL--DESIPP-----VSFMIRKMLNTE	707
OY	1332	LLMKRLIARSRKGFPAQVLAFAVFCALVSLVLPFGATPSLELOPMYNEQYTFV	1391
Dd	708	--WPFYV-----GVPICALINGLOPAPAFIIPSKII-----	736
OY	1392	SNADPEDGTLELINALTKRPGFTRGMEBNP1PDIPOAGEEMWTAPVQTIIMDLPN	1451
Dd	737	-----GVFTR-----	741
OY	1452	GNMTQNPSPACQSSDKIKKMLPVCPCPAGG1PPOQRONTADILODITGRNISDYLVK	1511
Dd	742	-----IDDETRKQNSNLSL-----FLAL	762
OY	1512	TYVOIIAKSLKNIWNEFRYSGFSLGVSNTQALPPSOEVNDAIKOMKHLKLANDSS-A	1570
Dd	763	GLISFT-----FLOGFTREGKA-----GEILTKRLRYMVRMSLQDVSWF	804
OY	1571	DRFLNSIGREFGTGDTNNNKWPNPNKGMHAISFLVANNALANLQKGNPSHYGT	1630
Dd	805	DDPKNTGALTR1-ANDAAOV---KG-AISRLAVITONT-ANLGTG1-----I	849
OY	1631	AFNPNLNTKQOJSEVALMTSDVIVSICVIRAMSFVPASFVFLDIOEVSAKHLOFI	1690
Dd	850	SFIQMOIT-----LLILAIVPIIALGVEMK-----MISGALDKKELE-	891
OY	1691	SGVAPVITWLSNFWDMCNCVNPATV111IFICQOK---SYVSSNLPVALL--LLY	1745
Dd	892	GAGK1ATEAIENTF-----RTVSLHQEKPFMYAOSLOVYRNSLKAHIF	938
OY	1746	G--WST1P1MTPASFEVKIKISTAYVVLTSVNLFTGINGSVAIFVLELFDNKLANNIDIL	1803
Dd	939	GITSEFQAMMYF5YACCFRFGAYLA-----HKLMSFEDVL	975
OY	1804	KSVFLFPFHCGLGLIDWKNOAMADALERGENRFV-----SPLSMDVGRNLFAMAV	1858
Dd	976	----LVSAVVPGMAMGVOSSEAPDYAKAKISAHAHIMIEKTPILDSYSTREG1MP1TL	1031
OY	1859	EGVVEFLITVLOIRFFIRP-RVNAKLSPLNDEDEVRERORILIDGGONDILEIKEL	1917
Dd	1032	EGNVTFGBV---FNYPTRBDIPVLOGLS-----LEVKK-	1062
OY	1918	TK1TRRRKRAVDRIKICVIRPGEFCGLGVNAGKSGSTKMLTGDTTYTGRDAP1ANKSI	1977
Dd	1063	-----GOTLALVSSGGCKSTVQVLLERFYDLAGVLLDGRKEI	1101
OY	1978	LS-NIHEHONMGYCPQ---PD-----A1RELLTGRHVEFFALLNGV	2016
Dd	1102	KRLVOMLRALHGLVSOEPL1PFCST1AEN1ANGDSRVV5OGEIYRAAKEANITAFISL	1161
OY	2017	PEKEVGVGEMAI1KGLGVYKERYAGANTSGGNKRKLSTAMALIGGPVVE1DEBPTGMD	2076
Dd	1162	PNKYSTKVDGKQD-----LSGGKQK1A1ARALVRBQPHILLDEATSLD	1207
OY	2077	PKARF1MNCALSVYKGRSVL1TSHSMECEALCTRNA1MNGRFLGVSQHLKRNFG	2136
Dd	1208	TESKEVVOE-ALBKAREGRIC1V1ARLST1ON-AD1IVFONGVVKHGH1OOLADQK	1265

OY 2137 DGYTIVRIAGS 2148
 Db 1266 IYFSMVSVOAGT 1277

RESULT 15

NCBI_TaxID=382;
 OC Rhizobiaceae; Rhizobium
 OX NCBI_TaxID=382;
 RN 11)
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396509; PubMed-11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
 Guria M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
 Kallman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RA "Nucleotide sequence and predicted functions of the entire
 RT Sinorhizobium meliloti pSyma megaplasmid.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 RN [2]
 RP SEQUENCE OF 143-355 FROM N.A.
 RC STRAIN=1021;
 RA Barnett M.J., Long S.R.;
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: FORMS, WITH NODD, A MEMBRANE TRANSPORT COMPLEX INVOLVED
 CC IN THE NODULATION PROCESS. IT PROBABLY EXPORT A MODIFIED BETA-1,4-
 CC LINKED N-ACETYLGLUCOSAMINE OLIGOSACCHARIDE.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

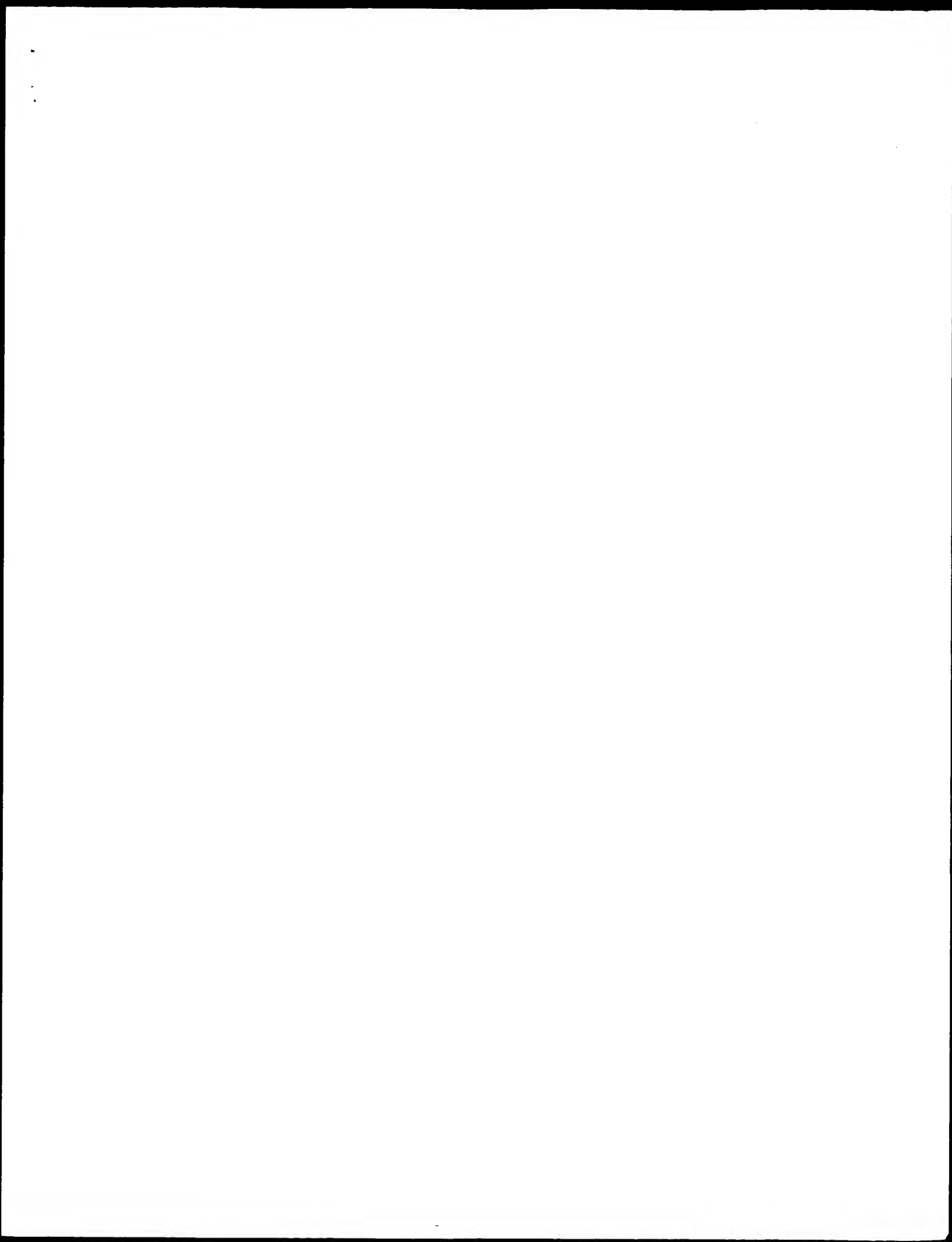
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AE007237; AAK65130.1;
 CC EMBL: AF043118; AAB97762.1;
 CC InterPro: IPR003593; AAA.
 CC InterPro: IPR003439; ABC_transportr.
 CC InterPro: IPR001687; ATP_GTP_A.
 CC Pfam: PF00005; ABC_tran.1.
 CC PROSITE: PS00211; ABC_TRANSPORTER.1.
 CC Modulation: Membrane; ATP-binding; Transport; Plasmid;
 CC Complete proteome.
 CC NP_BIND 89 96 ATP (POTENTIAL).
 CC FT SEQUENCE 355 AA; 39268 MM; 4DC8696D98C335DC CRC64;

Query Match 2.8%; Score 331.5; DB 1; Length 355;
 Best Local Similarity 33.9%; Pred. No. 1.5e-13;
 Matches 74; Conservative 52; Mismatches 85; Indels 7; Gaps 4;

OY 891 EPTHLKLGSIONLVKVVYDGMKVAVDGIALNLFYEGQITSPFGHNGAGKTTMTSILITGIF 950
 Db 52 KPT---VAIDVASVTKSYD--KPYINGISTVVAAGCEFGILGPNAGAKSTITIRAILGMT 106

OY 951 PPTSGTAVIIGKDIRSEMTIRONLGYCPQHNVLFPMLIYEEHIMFYARKLGISEKHVKA 1010
 Db 107 TPGTGELTVLGVPPSRARLARIRIGVPOEDMLDEFTVRENLLVGRFRKSTREIEA 166
 OY 1011 EMEQMALDVGLPSSKLSKTSQSGMORLSVALAFVGGSKVVIDEPTAGVDPYSRRG 1070
 Db 167 VIPSL-LEFARLENKADARVSDLSGGMKRRITLARLINDPOLIIDEPTTGIDPRARL 225
 OY 1071 IWEILLK-VYQGRITILSTHMDADVDLGRNIAIISHG 1107
 Db 226 IWERLSILARGKTIILTHIMEAEERLCDCVLEAG 263

Search completed: September 15, 2002, 13:02:25
 Job time: 394 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2002, 12:58:01 ; Search time 71.36 Seconds
(without alignments)
5481.243 Million cell updates/sec

Title: US-09-595-526B-2

Perfect score: 11797
Sequence: 1 MACWPQLRLMLKMLTFRRR.....VDVAVLTFPLDEKKESTV 2261

Scoring table:
BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 562222 segs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea:***
2: SP bacteria:***
3: SP fungi:***
4: SP human:***
5: SP_invertebrate:***
6: SP_mammal:***
7: SP_mhc:***
8: SP_organelle:***
9: SP_phage:***
10: SP_plant:***
11: SP_rodent:***
12: SP_virus:***
13: SP_vertebrate:***
14: SP_unclassified:***
15: SP_virus:***
16: SP_bacteriap:***
17: SP_archaeap:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	11786	99.9	2261	4	Q96S56	Q96S56 homo sapien
2	11774	99.8	2261	4	Q96T85	Q96T85 homo sapien
3	5888	49.9	2310	11	Q35600	Q35600 mus musculu
4	5864.5	49.7	2281	6	Q02698	Q02698 bos taurus
5	5775.5	49.0	2146	4	Q9BZC4	Q9BZC4 homo sapien
6	5763.5	48.9	2146	4	Q9NR73	Q9NR73 homo sapien
7	5732	48.6	2159	11	Q91V24	Q91V24 mus musculu
8	5376	45.6	2008	4	Q96S58	Q96S58 homo sapien
9	4249.5	36.0	2434	11	Q9ESR9	Q9ESR9 ratus norv
10	4240.5	35.9	2436	4	Q9HC28	Q9HC28 homo sapien
11	3345.5	28.4	1529	4	Q9HPU0	Q9HPU0 homo sapien
12	3229.5	27.4	2277	4	Q96UT3	Q96UT3 homo sapien
13	2485.5	21.1	1713	5	Q9VRG4	Q9VRG4 drosophila
14	2060	17.5	1802	5	Q9FXV8	Q9FXV8 caenorhabdi
15	2041.5	17.3	1660	5	Q9VUJ9	Q9VUJ9 drosophila
16	2012.5	17.1	867	4	Q96HC2	Q96HC2 homo sapien

17	2012	17.1	1843	5	Q9GOS2	Q9GOS2 leishmania
18	1984	16.8	1816	10	Q9SDB1	Q9SDB1 arabidopsis
19	1863.5	15.8	1447	5	Q01790	Q01790 caenorhabdi
20	1794.5	15.2	1750	5	Q9BKL1	Q9BKL1 trypanosoma
21	1538.5	13.0	1704	5	Q76287	Q76287 caenorhabdi
22	1534.5	13.0	1463	5	Q9VVK6	Q9VVK6 drosophila
23	1534.5	13.0	1981	5	Q9VVK7	Q9VVK7 drosophila
24	1342	11.4	1581	4	Q94911	Q94911 homo sapien
25	1271.5	10.8	1544	5	Q9NKF0	Q9NKF0 drosophila
26	1257	10.7	1363	4	Q9H7T8	Q9H7T8 homo sapien
27	1219.5	10.3	1382	5	Q9V912	Q9V912 drosophila
28	1158.5	9.8	1564	5	Q9XM49	Q9XM49 caenorhabdi
29	1152	9.8	1500	5	Q9VRE4	Q9VRE4 drosophila
30	1028	8.7	1502	6	Q95JZ4	Q95JZ4 macaca fasc
31	1013.5	8.6	1373	4	Q9NSL2	Q9NSL2 homo sapien
32	1010.5	8.6	1431	5	Q9XUD4	Q9XUD4 caenorhabdi
33	929.5	7.9	581	6	Q95JL1	Q95JL1 macaca fasc
34	846	7.2	269	4	Q9NTR0	Q9NTR0 homo sapien
35	826	7.0	953	10	Q9FKF2	Q9FKF2 arabidopsis
36	819.5	6.9	856	4	Q96MD8	Q96MD8 homo sapien
37	805	6.8	950	10	Q9FLT5	Q9FLT5 arabidopsis
38	800	6.8	1197	5	Q9VRG3	Q9VRG3 drosophila
39	788.5	6.7	1011	10	Q9STU0	Q9STU0 arabidopsis
40	748	6.3	1384	12	Q9EMR9	Q9EMR9 ansacta moo
41	693	5.9	900	10	Q9STT5	Q9STT5 arabidopsis
42	691.5	5.9	917	10	Q9FLT8	Q9FLT8 arabidopsis
43	679	5.8	865	4	Q96MS4	Q96MS4 homo sapien
44	671	5.7	737	4	Q96PZ9	Q96PZ9 homo sapien
45	670.5	5.7	592	5	Q96OV4	Q96OV4 drosophila

ALIGNMENTS

RESULT 1
ID Q96S56 PRELIMINARY; PRT; 2261 AA.
AC Q96S56;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ABCA1.
GN ABCA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka A.R., Abe-Dohmae S., Arakawa R., Sadanami K., Kidera A.,
RA Kioka N., Anachi T., Yokoyama S., Ueda K.;
RT "A new topological model of functional human ABCA1-signal peptide
cleavage and glycosylation of a large extracellular domain.";
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB055982; BAB63210.1; -;
DR EMBL: 2261 AA; 254300 MW; 21A2CF8F3F518D6D C6C64;
SQ SEQUENCE

Query Match	99.9%	Score 11786;	DB 4;	Length 2261;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 2257;	Conservative 4;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MACWPQLRLMLKMLTFRRRQTCOLLELVAMPFLIFILISVRSSTYPRYQHECHFPNKA	60	
DB	1	MACWPQLRLMLKMLTFRRRQTCOLLELVAMPFLIFILISVRSSTYPRYQHECHFPNKA	60	
QY	61	MPSAGTLPMVOGIIICNANNPCFRYPPTGEPAGVGVGNFNKSIVARLFSDARLLLYSQDPT	120	
DB	61	MPSAGTLPMVOGIIICNANNPCFRYPPTGEPAGVGVGNFNKSIVARLFSDARLLLYSQDPT	120	
QY	121	SMKDMRKVLRLLQKIKSSSNMLKQDFLVNDETFSGLYHNLSLPKSTVDKMLRADVILH	180	
DB	121	SMKDMRKVLRLLQKIKSSSNMLKQDFLVNDETFSGLYHNLSLPKSTVDKMLRADVILH	180	

QY 181 KVLQGYQLHLTSLCNGSKSEEMLOLGDQVSELCGLPKREKLAAREVLSNMDDILKPL 240
Db 181 KVLQGYQLHLTSLCNGSKSEEMLOLGDQVSELCGLPREKLAAREVLSNMDDILKPL 240
QY 241 RTLNSTSPFSKELAEATKTLHLSLGLTAELEFSMSKSMROEVMFLTNVSSSSSTOI 300
Db 241 RTLNSTSPFSKELAEATKTLHLSLGLTAELEFSMSKSMROEVMFLTNVSSSSSTOI 300
QY 301 YQAVSRIVCGHPREGGKIKSLMWYEDNNYKALFGNGTDEDAEETFDNSTTTCYCDMLK 360
Db 301 YQAVSRIVCGHPREGGKIKSLMWYEDNNYKALFGNGTDEDAEETFDNSTTTCYCDMLK 360
QY 361 NLESSPLRIIKWALKPLVGLKLLYTPDPTRQVMAEVNKTFOELAVFHOLEGMEELS 420
Db 361 NLESSPLRIIKWALKPLVGLKLLYTPDPTRQVMAEVNKTFOELAVFHOLEGMEELS 420
QY 421 PKITWEMENQOEMDLVMLDSRDNHFEQOLDLMTAODIVAFALAKHPEOVSSNGS 480
Db 421 PKITWEMENQOEMDLVMLDSRDNHFEQOLDLMTAODIVAFALAKHPEOVSSNGS 480
QY 481 VYTWREAFNETNOAIRTISRMECVNLKLEPATEVWLINKSMEILLDERKFWAGIVFTG 540
Db 481 VYTWREAFNETNOAIRTISRMECVNLKLEPATEVWLINKSMEILLDERKFWAGIVFTG 540
QY 541 ITTGSTIELPHHVYKKTMDIDNERTNKIKDGYWDPGRADPEEDMKRYWGGFAYLODYV 600
Db 541 ITTGSTIELPHHVYKKTMDIDNERTNKIKDGYWDPGRADPEEDMKRYWGGFAYLODYV 600
QY 601 EOAIRIVLTGTEKKTGYVMOOMPYPYVDIDIFLWMSRSMPLFMTLAMYSAVIVIKGIV 660
Db 601 EOAIRIVLTGTEKKTGYVMOOMPYPYVDIDIFLWMSRSMPLFMTLAMYSAVIVIKGIV 660
QY 661 YEKEARLKEPMRIMGDNLHMFSTISLPLVSAGLLVILKGNLPPYSDPSVAV 720
Db 661 YEKEARLKEPMRIMGDNLHMFSTISLPLVSAGLLVILKGNLPPYSDPSVAV 720
QY 721 FLVSFAVNTILOCFILSTLFSRANLAAAGCIYFTLYLPYVLCVAMODYVGTTLKIFPS 780
Db 721 FLVSFAVNTILOCFILSTLFSRANLAAAGCIYFTLYLPYVLCVAMODYVGTTLKIFPS 780
QY 781 LLSVPAFGCEGFALFEEOGIGVOMDNLFESPVEEDGNLTSTISMLFDTFLYCVMT 840
Db 781 LLSVPAFGCEGFALFEEOGIGVOMDNLFESPVEEDGNLTSTISMLFDTFLYCVMT 840
QY 841 YIAVAPGOGYIPRPMYFCTKSYWFGESDEKSHPSGMOKRISLTCMEEPHHLKIVS 900
Db 841 YIAVAPGOGYIPRPMYFCTKSYWFGESDEKSHPSGMOKRISLTCMEEPHHLKIVS 900
QY 901 IQMLVAVYRDGMKVAVDGALANFEYEGOITSFLGNAGKTTTMSILTGLFPPTSGTAYIL 960
Db 901 IQMLVAVYRDGMKVAVDGALANFEYEGOITSFLGNAGKTTTMSILTGLFPPTSGTAYIL 960
QY 961 GKDIRSEMSTIRONLGVCPQHNLFLMDLVEEIHVYARLKGISEKHVAEMEOMALDVG 1020
Db 961 GKDIRSEMSTIRONLGVCPQHNLFLMDLVEEIHVYARLKGISEKHVAEMEOMALDVG 1020
QY 1021 LPSKSLKSKTSLSGMOKRLSVALAFAVGSKVYLDEPTAGVDPYSRSGIEMELLKTYRQ 1080
Db 1021 LPSKSLKSKTSLSGMOKRLSVALAFAVGSKVYLDEPTAGVDPYSRSGIEMELLKTYRQ 1080
QY 1081 GRTIITLSTHMDADVLAGRIALISHGKLCVSSSLFLKNOLGTGYLLLVKKDVSSLS 1140
Db 1081 GRTIITLSTHMDADVLAGRIALISHGKLCVSSSLFLKNOLGTGYLLLVKKDVSSLS 1140
QY 1141 SCNNSSSYLYLKKEDSVSSSDAGISGDHSDTLTIDVSAISNLRKHVSEARIVEDI 1200
Db 1141 SCNNSSSYLYLKKEDSVSSSDAGISGDHSDTLTIDVSAISNLRKHVSEARIVEDI 1200
QY 1201 GHELTYVVLPEAAKEGAFELFHEIDRLSDGISSTYGISETTLLEBFLKVAEESGVDAE 1260
Db 1201 GHELTYVVLPEAAKEGAFELFHEIDRLSDGISSTYGISETTLLEBFLKVAEESGVDAE 1260

QY 1261 TSDGTLPARNRRAFGDKOSCLRPFTEDDAADPNDSIDIDESPSETDLLSGMDGKSYOVK 1320
Db 1261 TSDGTLPARNRRAFGDKOSCLRPFTEDDAADPNDSIDIDESPSETDLLSGMDGKSYOVK 1320
QY 1321 GKKLTQOQFVALKRLRLIARRSRKGFPAQIYLVAVFYCALVSLVPPRGKIPSELO 1380
Db 1321 GKKLTQOQFVALKRLRLIARRSRKGFPAQIYLVAVFYCALVSLVPPRGKIPSELO 1380
QY 1381 PMWNEOQTFVNDAPEDGTLELLNALTKDPGFCRMEBNPIPDPPCOAGEEMWTAP 1440
Db 1381 PMWNEOQTFVNDAPEDGTLELLNALTKDPGFCRMEBNPIPDPPCOAGEEMWTAP 1440
QY 1441 VPQITMDLFQNGNWTQNPSPACQSSDKIKMLPVCPPGAGLEPPQKONTADILLODL 1500
Db 1441 VPQITMDLFQNGNWTQNPSPACQSSDKIKMLPVCPPGAGLEPPQKONTADILLODL 1500
QY 1501 TGRNISDYLVTYVOIITAKSLKNKIWNEFPGYGGSLGVSNTQALPPOEVNDAIKOMK 1560
Db 1501 TGRNISDYLVTYVOIITAKSLKNKIWNEFPGYGGSLGVSNTQALPPOEVNDAIKOMK 1560
QY 1561 HLKLAQSSADREFLNSLGRFMTGIDTRNNVWVFNKGMHAISSFLVANNAILRANLOK 1620
Db 1561 HLKLAQSSADREFLNSLGRFMTGIDTRNNVWVFNKGMHAISSFLVANNAILRANLOK 1620
QY 1621 GENPSHYGITAPNHPNLTKOOLSEVALMTTSVDYLVSYCYIFAMSFYSPASFVFLIOER 1680
Db 1621 GENPSHYGITAPNHPNLTKOOLSEVALMTTSVDYLVSYCYIFAMSFYSPASFVFLIOER 1680
QY 1681 VSKAKHLOFISGVKRVITWLSNFWDMKCNVYPAIVLIIIFICQOQSYVSTMLPJAL 1740
Db 1681 VSKAKHLOFISGVKRVITWLSNFWDMKCNVYPAIVLIIIFICQOQSYVSTMLPJAL 1740
QY 1741 LLLYGSITPLMPASVFEKIPSTAYVVLTVSVLFJGINSVATVELEFTDNKLNIN 1800
Db 1741 LLLYGSITPLMPASVFEKIPSTAYVVLTVSVLFJGINSVATVELEFTDNKLNIN 1800
QY 1801 DILKSVFLIFPHFCGRRLIDMVKNQAMADALBERGKREKVSPLSMIDLVCGRNLEPAMAVEG 1860
Db 1801 DILKSVFLIFPHFCGRRLIDMVKNQAMADALBERGKREKVSPLSMIDLVCGRNLEPAMAVEG 1860
QY 1861 VFFLITVLIQREFIRPRVNAKLSPLNDEDEVRREBORIILDGGOINDLEIKELTKI 1920
Db 1861 VFFLITVLIQREFIRPRVNAKLSPLNDEDEVRREBORIILDGGOINDLEIKELTKI 1920
QY 1921 YRRKRKPAVDRICVCIIPGCEGILGVNAGAKSSTFKMLGDTTVTGDAFLKNSITLSN 1980
Db 1921 YRRKRKPAVDRICVCIIPGCEGILGVNAGAKSSTFKMLGDTTVTGDAFLKNSITLSN 1980
QY 1981 IHEVQNNMGYCPQFDALITELLTGREHVEFFALLRGVPEKEKVGEMAIRKGLVKYGEK 2040
Db 1981 IHEVQNNMGYCPQFDALITELLTGREHVEFFALLRGVPEKEKVGEMAIRKGLVKYGEK 2040
QY 2041 YAGNYSGNKRRKLSLTAALIGGPPVYVLEDEPTTGMDBKARFLMNCALSVYKBEGRSVLT 2100
Db 2041 YAGNYSGNKRRKLSLTAALIGGPPVYVLEDEPTTGMDBKARFLMNCALSVYKBEGRSVLT 2100
QY 2101 SHSMEECALCTRMAIWMNGRFRCLGSVOHLKNAFSGGTYIYVIAIASNPDILKPVODFFG 2160
Db 2101 SHSMEECALCTRMAIWMNGRFRCLGSVOHLKNAFSGGTYIYVIAIASNPDILKPVODFFG 2160
QY 2161 LAFPGSVLYKEKHNMLQYOLPSSLSLARJFSILOSRRKRLIEDYVSQTTLDQYFVNF 2220
Db 2161 LAFPGSVLYKEKHNMLQYOLPSSLSLARJFSILOSRRKRLIEDYVSQTTLDQYFVNF 2220
QY 2221 AKDOSDDHLKDLSLHKNOTVVDVAVLTSPLODEKVESYV 2261
Db 2221 AKDOSDDHLKDLSLHKNOTVVDVAVLTSPLODEKVESYV 2261

RESULT 2
Q96T85
ID Q96T85 PRELIMINARY; PRT; 2261 AA.
AC Q96T85;

01-DEC-2001 (Tremblrel, 19, Created)
01-DEC-2001 (Tremblrel, 19, Last sequence update)
01-DEC-2001 (Tremblrel, 19, Last annotation update)
ATP-BINDING CASSETTE 1 SUB-FAMILY A MEMBER 1.
GN ABCA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21251004; PubMed=11352567;
RA Qiu Y., Cavelier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
RT "Human and Mouse ABCA1 Comparative Sequencing and Transgenesis Studies
Revealing Novel Regulatory Sequences.";
RL Genomics 73:66-76(2001).
DR EMBL: AF287262; AAK43526.1; -.
KW ATP-binding.
SQ SEQUENCE 2261 AA; 254238 MW; 248DF04C8FF041A5 CRC64;

Query Match 99.8%; Score 11774; DB 4; Length 2261;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2256; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MACWPQLRLMKNTFFRRROTCLLEFVAMPLEFLILISVRLSPYRPEOHECHPKMA 60
DB 1 MACWPQLRLMKNTFFRRROTCLLEFVAMPLEFLILISVRLSPYRPEOHECHPKMA 60
QY 61 MSAGTILPVVGGIICNANPCFRYPTRPGAPGVGNFNKSIYARLEFSARRLILYSOKDT 120
DB 61 MSAGTILPVVGGIICNANPCFRYPTRPGAPGVGNFNKSIYARLEFSARRLILYSOKDT 120
QY 121 SKMDKRVLRITLQOIKKSSSNLKLODFLVNDFTEGFLYHNLSPKSTYDKMLRADVILH 180
DB 121 SKMDKRVLRITLQOIKKSSSNLKLODFLVNDFTEGFLYHNLSPKSTYDKMLRADVILH 180
QY 181 KVFLOGYOLHTSLICNGSSEEMIOIGDOVESELGLPEKLAABERYLRSMDILKPTL 240
DB 181 KVFLOGYOLHTSLICNGSSEEMIOIGDOVESELGLPEKLAABERYLRSMDILKPTL 240
QY 241 RTLNSTSPPSKELAEATKTLHSLGTLAQELFSMKSMDKROEYVFLTNVSSSSSTOI 300
DB 241 RTLNSTSPPSKELAEATKTLHSLGTLAQELFSMKSMDKROEYVFLTNVSSSSSTOI 300
QY 301 YQAVSRIVCGHPEGGLKTKSLNWTEDNNYKALFGNGTEDEAETFYDNSTPYCNDLMK 360
DB 301 YQAVSRIVCGHPEGGLKTKSLNWTEDNNYKALFGNGTEDEAETFYDNSTPYCNDLMK 360
QY 361 NLESSPLSRITMKALKPLVGLKTLTPDTPATROVMAEVNKTFOELAVFHDLRGMEELS 420
DB 361 NLESSPLSRITMKALKPLVGLKTLTPDTPATROVMAEVNKTFOELAVFHDLRGMEELS 420
QY 421 PKTWTMENSOEMDLVRLMLDSRDNDHFWEQOLDGIDMTAODIYVFLAKHPEDVSSNGS 480
DB 421 PKTWTMENSOEMDLVRLMLDSRDNDHFWEQOLDGIDMTAODIYVFLAKHPEDVSSNGS 480
QY 481 VYTWREAFNETNOALRTISRMECVNLKLEPIATEVWMLINKSMELDERKFMAGIVFTG 540
DB 481 VYTWREAFNETNOALRTISRMECVNLKLEPIATEVWMLINKSMELDERKFMAGIVFTG 540
QY 541 ITFGSIELPHHYVYKTRMDIDNVERTNKIKDGYWDGPRADPEDMDRYWVGAYLODYY 600
DB 541 ITFGSIELPHHYVYKTRMDIDNVERTNKIKDGYWDGPRADPEDMDRYWVGAYLODYY 600
QY 601 EQAIIIRVLGTEKKTGVYMOOMPYPYVDIDFLRVASRSMPLFMTLAWIVSAVVIKGIIV 660
DB 601 EQAIIIRVLGTEKKTGVYMOOMPYPYVDIDFLRVASRSMPLFMTLAWIVSAVVIKGIIV 660
QY 661 YEEEARLKEKTRIMGLDNLSTLWFSWFTSSILPLVYAGLLVYLKGNLPLSPDSVAVY 720
DB 661 YEEEARLKEKTRIMGLDNLSTLWFSWFTSSILPLVYAGLLVYLKGNLPLSPDSVAVY 720

QY 721 FLSEAVAVTIILOCFLLSTLFSRANLAAACGIIYFTLLPYVLCVAMODYVGTLLKIFAS 780
DB 721 FLSEAVAVTIILOCFLLSTLFSRANLAAACGIIYFTLLPYVLCVAMODYVGTLLKIFAS 780
QY 781 LLSPVAFGCEYFALFEEOGIGVOMDNLFPESPEDEGFMJTTISISMJLFDTELYGVMTW 840
DB 781 LLSPVAFGCEYFALFEEOGIGVOMDNLFPESPEDEGFMJTTISISMJLFDTELYGVMTW 840
QY 841 YIEAVFPGOYIGIPRPWYFPCTKSYWFEESDEKSHPSNOKRSEICMEEPHHLKGVAS 900
DB 841 YIEAVFPGOYIGIPRPWYFPCTKSYWFEESDEKSHPSNOKRSEICMEEPHHLKGVAS 900
QY 901 IONLVKYYRDMKAVVAGLALNFEEOITSEFLGNGAGKTTMSILUTGLPPTSGTAYIL 960
DB 901 IONLVKYYRDMKAVVAGLALNFEEOITSEFLGNGAGKTTMSILUTGLPPTSGTAYIL 960
QY 961 GKDIRSEKSTIRONLGVCPHNVLFDMJVEEHIMFYARLKLSEKHVAKEMEQMALDVG 1020
DB 961 GKDIRSEKSTIRONLGVCPHNVLFDMJVEEHIMFYARLKLSEKHVAKEMEQMALDVG 1020
QY 1021 LPSSKLSKTSQLSGGMORKLSVALAFVGGSKVYILDEPTAGVDPYRRGIMWELLKYRO 1080
DB 1021 LPSSKLSKTSQLSGGMORKLSVALAFVGGSKVYILDEPTAGVDPYRRGIMWELLKYRO 1080
QY 1081 GRTIILSTHMDDEADVLGDRITAIISHGKLCVGSLEFLKNDLGTGYVLTLYKKDVESLS 1140
DB 1081 GRTIILSTHMDDEADVLGDRITAIISHGKLCVGSLEFLKNDLGTGYVLTLYKKDVESLS 1140
QY 1141 SCRNSSTVSYLKKEDSVSSSDAGJGSDHESOTLTIDVSAISNLIRKHSEARLYEDI 1200
DB 1141 SCRNSSTVSYLKKEDSVSSSDAGJGSDHESOTLTIDVSAISNLIRKHSEARLYEDI 1200
QY 1201 GHETLYVLYPAAREGAVELFHEIIDLSDGISVSGISSTTEELFELVLAESRGVDAE 1260
DB 1201 GHETLYVLYPAAREGAVELFHEIIDLSDGISVSGISSTTEELFELVLAESRGVDAE 1260
QY 1261 TSDGTLFARRNRRRAFGDKOSCLRPTEDDAADPNDSDIDPESRTDLLSGMDGKGSYQV 1320
DB 1261 TSDGTLFARRNRRRAFGDKOSCLRPTEDDAADPNDSDIDPESRTDLLSGMDGKGSYQV 1320
QY 1321 GSKLTOGOFVALLMKRLLIARRSKRFPFAQIYLAVEYCTALVSLIYPPRGKPSLEIQ 1380
DB 1321 GSKLTOGOFVALLMKRLLIARRSKRFPFAQIYLAVEYCTALVSLIYPPRGKPSLEIQ 1380
QY 1381 PMWMEYOYTFVSNDAPEDTGTELLNALTDPGFGTRCMESNPIDPPOCAGEEEMTTAR 1440
DB 1381 PMWMEYOYTFVSNDAPEDTGTELLNALTDPGFGTRCMESNPIDPPOCAGEEEMTTAR 1440
QY 1441 VPOTIMDLFONGNMWMPSPACOCSSDKIKMLPYCPGAGGLPPORKONTADILIDL 1500
DB 1441 VPOTIMDLFONGNMWMPSPACOCSSDKIKMLPYCPGAGGLPPORKONTADILIDL 1500
QY 1501 TGRNISDYLVKTYVOI IAKSLKNKIWNEFRYGGFSLGVSQTQALPISOEVNDAIKOMKK 1560
DB 1501 TGRNISDYLVKTYVOI IAKSLKNKIWNEFRYGGFSLGVSQTQALPISOEVNDAIKOMKK 1560
QY 1561 HIKLAKDSSADREPLNSLAREMTGLDTRNNKVMFNKMGHAISSFLYINNAIIRANLQK 1620
DB 1561 HIKLAKDSSADREPLNSLAREMTGLDTRNNKVMFNKMGHAISSFLYINNAIIRANLQK 1620
QY 1621 GENPSHYGITAFAHPLNLTQOOLSEVALMTTSVDVLSICVIFAMSFVPASVFFVLIOER 1680
DB 1621 GENPSHYGITAFAHPLNLTQOOLSEVALMTTSVDVLSICVIFAMSFVPASVFFVLIOER 1680
QY 1681 VSKAKHLOFISGVKVIYIWLNSFWDMCNYYPALVLIIFICQOQNSYVSTLPLVAL 1740
DB 1681 VSKAKHLOFISGVKVIYIWLNSFWDMCNYYPALVLIIFICQOQNSYVSTLPLVAL 1740
QY 1741 LLLLGWSTITPLMPYPASFPKIPSTAYVVLVSNVLFIGNSVATFVLELTTDKLNNIN 1800
DB 1741 LLLLGWSTITPLMPYPASFPKIPSTAYVVLVSNVLFIGNSVATFVLELTTDKLNNIN 1800
QY 1801 DILKSVFLIPHFCLGRLIDMKVKNQAMADALEREGENREVSPLSWDLVGRNLFAMAVEG 1860

Qy	1029	KTSDSGMGRKLSVALAPVGGSKYV I D E P P A G V D P Y S R K I W E L L A K Y R Q G P T I I L S T	1088
Db	1058	E A O D L S G M G R K L S V A L A F G D S K V V V D E P T S G V D P Y S R R S I W D L L K Y S G R T I I M S T	1117
Qy	1089	H H M E A V L D R I A I T S H G L C V S S L P L K N O L G Y L T V K - K D V S - - - - - S L S	1140
Db	1118	H H M E A D L D G R I A I T S O G R L Y S G P L P L K N C F G T G F L T I V R K M K N I Q S O R G C E Y C	1177
Qy	1141	S C R N S S T V S Y L K K E D S V S S S D A G L S D H S E D T L T I D V S A I S M I K R H V S E A R L Y E D I	1200
Db	1178	S C T S K G S T S C P R P V D E T I - - - - - E G Y V L D G V G L M D L V H N P E A K I V E C I	1225
Qy	1201	G H E L T Y V L P E A K E G A F V E L P H E I D D L S D G I S S Y G I S E T T L E I T L P K A E S G V D A E	1260
Db	1226	G O E I F I L P L P N K N E F O R A Y A S L F R E E L T L A D L G L S F I S D T P L E I F I L K Y T E D A G A S G M	1285
Qy	1261	T S D G T L P A R R R A F G D K O S C - - - - - L P P T E - - - - - D A A D P N D S D I D P E S H E D L	1308
Db	1286	F V G G - - - A O Q R E O A G L R H P C S A P T E K L K O Y A O A P T G S P G O V D P P K Q O P S E P E D - - -	1338
Qy	1309	S G M D G K S G Y O V K G W L Q O O F V A L L M K R L L I A R S K R G F A O I V P A F V C I A L V S L I V	1368
Db	1339	- - - - - P C V P E N T G A R L L I Q H V O A L L V K R R H N T I R S K D P V A O I V P A F V F V L A L M L S I V	1393
Qy	1369	P P F K S Y S L E Q P W M I N E O Y T E V S N D A P E D T G L L E L N A L T K D C G F T R C M G N E I D P T P	1428
Db	1394	P P F E F P A L T L H P M Y G H O Y T F F S M D E P N N E H L E V L A D V L N R P G F N R C L K E M L P E Y P	1453
Qy	1429	C Q A G E E M T T A P R V Q T I M D L F O G N M T M O N P S A O C S S D K I K K M L P V C P C G A G L P R P Q	1488
Db	1454	C - I N A T S K P T P S P N T I L H F O K O K T A A P S P S C S T R E L T M L P C P E D A G L P R P Q	1512
Qy	1489	R K O M T A D L I D L T R N I S D L V K T Y V O I L A K S L K N I W N E R Y G G S L G Y S N T O L P S	1548
Db	1513	R T G S T E V L O D L T R N I S D L V K T Y T P A L I R S S L A K S F W N E O R Y G G I S G - G K L P A T I S	1571
Qy	1549	Q E V N D A I K O M K K H L I A K D S S A D P L N S L G R - - - - - F M T G L D T R N N	1589
Db	1572	G E - - - - - A L V G F S L G L O M M N V S G C V T R E A S K E M L D F L K H E T D N	1613
Qy	1590	V K W F N N K G W H A I S S E L N V I N N A L I R A N I O K G N P S H G I T A F N P N L N T K O O L S E V A L M	1649
Db	1614	I K W E N N K G H A L V S F L N V A H M L I R A S L R P R O D P R E Y I T V I S O P L N T K E O L S D I V L	1673
Qy	1650	T T S V D V L S I C V I P A M S F V S A S F V F L I O P R V S K A H L O F I T G V R P V I T M L S N F W M D C N	1709
Db	1674	T T S D A V A A I C V I T A M S F V S A S F Y L I O E R Y T K A K H L O F I G S V S T Y T W L N F I M D I M N	1733
Qy	1710	V V P A T V I I L F I C F O O K S Y V S S T N L P V A L L L L Y G W S I T P L M P A S F V K I P S T A V V	1769
Db	1734	Y A V S G L V G I F G F O K A Y T S P N D P A L V S I L M L G M A V I P M Y P A S P L F E V P S T A Y V A	1793
Qy	1770	L T S V M L F I G I N G S A T V L E L F T D N K - L N I N D I L K S V L I P P H C L G G L I D M Y K N A M	1828
Db	1794	L S C A M L F E G I N S S A I T V L E L F E N N R I L L F E M L K L L I V P H C L G G L I D L A S A V	1853
Qy	1829	A D A L E R F E G N F R A P L S M D I V G R L F E M A E V G F L I T V L I O Y R F I P R P V A N K L S P L	1888
Db	1854	T D V A Q O B E E S A N P P O M D L I G K L V A M A L E G V Y V L L L L I O H N F L E L T R M I A E A R E P V	1913
Qy	1889	N D E D V A R E R O R I L D G G O N D I L E I K E L T Y I R R R K R D A V D R I C V G I P P G E C F G L G V N	1948
Db	1914	F D E D D V A E E R O V M S G N K T D I L K E L T K V Y S G S S P A V D R L C V G V P R C E C F G L G V N	1973
Qy	1949	G A G S K S T F K M L T G C T Y T R D A P L K N K S I L S N I H E V H O M W K G C P O F D A T E L L T R E H V E	2008
Db	1974	G A G K T T F K M L T G C T Y T S G D A V A G K S I T S I S D V H O N N G C P O P D A L D L L T R E H L Y	2033
Qy	2009	F F A L L R G P E K E V K V E M A I R K L G L V K Y E K A G Y S G N K R K L S T A M A L I G C P V V L	2068
Db	2034	L Y A R L R G V P S A E I K V A N W M G I O S L G L S V A D R L A G I Y S G N K R K L S T A L A L G C P P L L L	2093
Qy	2069	D E P T T G M P K A R P L M C A L S V Y K E G S V V L I T S H S E E C A L C T R M A I W N G R F P C L G S V	2128

Dd	2094	DEPTGMPQARRMIMNTIVSIRRGRAVVLTSHEMCEALCTPLAIVMGSTPGCLGTI	2153
Qy	2129	QLKLNRFSDGYTIVYRIGSN---PDLKPVDFFGLAPPSVYLKEKHNNMLQYOLPSSL	2184
Dd	2154	QLHKXKPFDDGYIVTMKKIKSPKODLLRPDIINPVDFQFGNPGSGVERHNSMLDQVPS--	2211
Qy	2185	SLSAIFESILSCSKKRHLIEDYSVSQTLLDOVFVNFAKDQSDDHKLKLSLH	2236
Dd	2212	SLSAIFOLLISHKDSLLIEEYSVTQLLDGVFNFAKQOTE--TYDLLPH	2260
 RESULT 4 C02698 PRELIMINARY; PRT: 2281 AA. C02698			
AC	002698:		
DT	01-JUL-1997 (TREMBLrel. 04, Created)		
DT	01-JUL-1997 (TREMBLrel. 04, last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)		
DE	ABC TRANSPORTER.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Bovinae; Bos.		
CC	NCBTaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=RETINAL ROD CELL;		
RX	MEDLINE=97248596; PubMed=9092582;		
RA	Tilling M., Molday L.L., Molday R.S.;		
RT	"The 220-kDa rim protein of retinal rod outer segments is a member of		
RL	J. Biol. Chem. 272:10303-10310(1997)."		
DR	EMBL: U90126; AAC48716.1; -		
DR	InterPro: IPR003593; AAA.		
DR	InterPro: IPR003439; ABC_transportr.		
DR	InterPro: IPR01687; ATP_GTP_A.		
DR	Pfam: PF00005; ABC_tran; 2.		
DR	SMART: SM00382; AAA: 1.		
SQ	ATP-binding.		
	SEQUENCE 2281 AA; 257228 MW; 71CD040C9BF7A079 CRC64;		
 Query Match 49.7%; Score 5864.5; DB 6; Length 2281; Best Local Similarity 50.1%; Pred. No. 0; Matches 1158; Conservative 373; Mismatches 642; Indels 139; Gaps 26;			
Qy	6 QLRLLMKULTRRROTCOLLELVAMPFLFILLISVRLSYPPYEOCHECHFPNKAMPSAG	65	
Dd	6 QIRLLMKMTLRKRKRIKFVELWLPISLFVLIWLNRVNPVLYSHCHFPNKAMPSAG	65	
Qy	66 TLIPWVGIIICNNPNPFERYPTPGEARGVGNFNKSIVARLFSDARLLILYSOKDTSMDM	125	
Dd	66 MLPWLDGICNVANNPCFOSPFTAGESEGIYSNNNSILAIVAYKDFOELLMDAESOHLCGY	125	
Qy	126 RRVLTITQOI-----KSSSNLIKLODFLVNETFSGLTYHNLSLPKSTVDKMLRAD	176	
Dd	126 WRELRTLSQLMNTLRMHPRIRAGRIGRIREVCLKDEMILTLFYKNIGLSDSVYLLVNSQ	185	
Qy	177 VILKHYFLDGY-QLHLTSL-CNGSKNSEMIQIGDOEVSE-----LCGLPKELAAAEKVL	229	
Dd	186 V-RPQFAGVVDMLMKDJACGEALLERPLIPPORAATQVRSGLCSISQGTLOWMEDTL	244	
Qy	230 RSNNMLDKIRILTUNSTSPFPSKLEAEAKTTLHSIGTLAQELFMSRW----SDMR---	282	
Dd	245 YANVDFK-----LFHVPRLLDS-----RSGGMNLRSMGRLLSDMSPI	284	
Qy	283 -----QEVMFLT---NVNSSSSSTQIYAQVASRIYCGHPREGGGLIKSLMYEDNN	329	
Dd	285 QEFIRHPVQDMLWTVPLOTGFPEFTQJLMGILISDLDCGYPEGGGSRVFSFNVEDNN	344	
Qy	330 YALVGGNTEDEDAEFFYNSTTPPCNDLMKLESSPLRIITWKALKPLLKYKIITYPT	389	

Db 345 YKAFGLIDSTRKDEIYSYDERTTFCNALIQSIESNPLTKIANRAKPLLMGKILETPDS 404
 QY 390 PATROVAEYNKTFEOLAEVFNHDEGMEELSPKIMTFEMKSEMDLYRMLDSDRNDHF 449
 Db 405 PATRILKANKNSFTFEELERKLVKWEVEGPOIWFYFDSTQSMKRLTLENPRYKAF 464
 QY 450 EOODIDGDMTAODIVAFKAPHEDVOSSNGSVYTWREAFNEINOAIRTSIREMECVNLK 509
 Db 465 NROIGEEGIAEAVLNFLYNGPREGQADVDNFMWDIFNITDRALRLANOYLECILLDK 524
 QY 510 LEPIATEVWILNKSMELDERKFMAGIVFTGIPGSIELPHHYKRYKMDIDVVERTNK 569
 Db 525 FESVDDEFOILQORLLSLEENRFWAGVFPDMPHTSSLPYHKKYKIRMDIDVEKTKNT 584
 QY 570 KDWGPRPADREPDMRYWGGFAYLQDVVEQOAIIRVLTGTEKTKGVYMOOPRYCYD 629
 Db 585 KDRWDSGPRPADREDEFRYIMGFAYLQDMVEHCITRSQAOEEVPGIYLOQMPRYCEYD 644
 QY 630 DIFLRVSRMPLFMTLAWIYSAVITIKGIVYEKARKTKMTLMGDNSTIMFWSISS 689
 Db 645 DSEFTILNRCPIFMVLAWIYSVMYKSTVLEKELRKETKLNQGSNRYIMCTWFIDS 704
 QY 690 LIPPLVAGLIVLLKGNLIPYSDPSVEFLSVFAVVTILOCFITSTFSRANLAAC 749
 Db 705 FSIKMSICILLTFIMHGRILHYSNPFILFLPLAFSIATIMOCFLISTFSSASLAAC 764
 QY 750 GGIYFLYLYPYLVAMODYVGFYKIFASLSPAVAFGCEYFALFEBOGIGVOMDL 809
 Db 765 SGVYFLYLYPHLICFMORITADMKMAVSLSPVAFGTEFLAXFEBOGIGLOMSNI 824
 QY 810 FESVEEDGNLTTSISMELFTFLYGVMIYIEAVPPOGYIIPRYFPCSTSYMF-- 867
 Db 825 GNSMEDEDEFSFLMSKMMMLDALIYLLAWYLDQVFPBGYGRPLRYFLQESTYMGCE 884
 QY 868 -----BESDEKSHPGSNQ-----KRMSEICMEEPHTLKGVSLOMLVYKVRDGMKY 914
 Db 885 GCSTRERERALEKTEPITEEMEDEDEYREGINDCEFERELPGIYVGVCKVNLIFEPYGR 944
 QY 915 AYDGLATNFYEGOTSTFLNGHNGAKTTMSILGFRPTSGTAYILGKDIRSMSTIRON 974
 Db 945 AYDRLNTTFESQITLALGNGAGKTTLSIMGLDPPISGVIYVGGKDEIYMLDRIOS 1004
 QY 975 LGVCPONHVLFDMLVEBHTWFAURLKGLSEKHNKAKEMEQMALDVLGPPSSKLSKTSOLS 1034
 Db 1005 LGMCPONILFHNHLYVAENHLYFAOLKGRSMDAQOLEMEMLDGTI-HHKRNEEARLDS 1063
 QY 1035 GGMQRKLSVALATAYGGKVVYIDEPYAGVDPYRSRGITWELLKRYOGRITTLSTHMDRA 1094
 Db 1064 GGVQRKLSVALATAYGGKVVYIDEPYAGVDPYRSRGITWELLKRYOGRITTLSTHMDRA 1123
 QY 1095 DVLGDRITAITSHGKLCVSSFLKNOLGTYVLTLYKKOVESLSSCRSSSTVSYLAK 1154
 Db 1124 DILGDRITAITSHGKLCVSSFLKNOLGTYVLTLYKKOVESLSSCRSSSTVSYLAK 1182
 QY 1155 EDVYSSSSDAGISDGHESDTLITDVSALSNIIRKHVSEARLEVEDIGHETLYLPEYAK 1214
 Db 1183 GFSYRCFACAEALTRBEQVLDG--DYNELTDVHNHVRKAKIVECIGQELIFLPRKNNK 1239
 QY 1215 EGAFVELFHNITDRSLDGLISSYGISETTLEETFLKVAEESGVDAETSDGTLEPARRNRA 1274
 Db 1240 QRAVAISLFRLEETLADGLISSFGISDTPLEIFLKVTEDELDGHLFAGTOOKREN-- 1296
 QY 1275 FGDKOSCLRF-----FTJEDADAPNDSDIDPRESRETDILSGMDGSGYOVKWKLMQO 1328
 Db 1297 INLRHPSGSEKAGOTPOSSSHRGEPAHNRGQPRPEREGHSKRN-----CARLIVOH 1352
 QY 1329 FVALMKRLLIARRSRKGFPAQITLPAVYCAIVLPSLIVPRGKYPSELQPMWYNEQY 1388
 Db 1353 VOALLVYRFQHTIRSHKDLAQIYVLAIFYALMLSLIIPRGEVPALEHNMWGGQY 1412
 QY 1389 TTVSNAPREDTGTELLNALTCKPFGTCRMEGNPITPDPCQAGEEMKTAPYPOTIIML 1448
 Db 1413 TTFESMDQPDSEWLSALADVLVYKPGFGRCLKEWMLPEEPC-GNSSPMKTPSPSPDVTH 1471

QY 1449 FONGMNTMONPSPACOSSDKIKKMLPYCPGAGGLPPPOKRONATDILDTGRTNSDY 1508
 Db 1472 LDOOKMTAQPSPCSCSTREKUTMLPBCPBAGGLPPPOKRTQRTETLDTGRTNSDY 1531
 QY 1509 LKTYVOITIAKSLANKIWNFEYRGFSLGVSNTOALPPPOEVDNATIKOMKHLKLAKDS 1568
 Db 1532 LKTYPALIRSLSKSKFWNEQRYGISVG-----GKLPAPPTGEALV----- 1575
 QY 1569 SADRPLNSLGR-----FMTGIDTNNYKVMFNNGKGMHAISSFLNVI 1609
 Db 1576 -----GFLSDGLOLWNSVGGPMTRKAKEMPAFLKOLETEDNTIKWFNNKGHALVSFLNVA 1632
 QY 1610 NNAILRANLOKGENPSHYGITAENHPLNTYQOULSEVALMTTSVDVLSICVIFAMSEVP 1669
 Db 1633 HNAILRASLHKRKNBEEGIVISQPLMLTRKOLSEITVLTTSVDAVAIVCIRFAMSEVP 1692
 QY 1670 ASFVFLTOERSKAKHLOFISGVKPYVYKLSNPFVMDCNVVPATVITIFIGPOOKSY 1729
 Db 1693 ASFVFLTOERSKAKHLOFISGVKPYVYKLSNPFVMDCNVVPATVITIFIGPOOKSY 1752
 QY 1730 VESTNLPVALLLLLYGNSITPLMYPASFEVEKIPSTAVVLTSVLFTGINGSVATVLE 1789
 Db 1753 TSEMDLPALVALLMYGNAVIPMYPAFIDIPSTAVVLSANLFTGINSATVPLE 1812
 QY 1790 LFTDNK-LNNINDIYKSVFLIPPHCLGRGLIDMYKNOAMADALERGENRFPVPSLMDL 1848
 Db 1813 LFEENRTLRIRIAMRKLIIFPHCLGRGLIDIALSOAVVDVYAQOEFAHSSNPFOWDL 1872
 QY 1849 VGRNLFAMAVEGVFELLTVLLOYRFFLRPRVYNAKLSPLNDEDEDVYRERORTIDGGGO 1908
 Db 1873 ICKNLAAVAEYVFLTLTIQYOFFFSKRTTEPAKERTIDEDDDVAEEORIISGONK 1932
 QY 1909 NDILEIKELTKYRRKRRPAVDRIKIPGECFGLLVGNAGKSSIFKMLTGTDTYVTRG 1968
 Db 1933 TDLIRNELTKYSGTSSPAVDRLCYGVAPGECFGLLVGNAGKSTTFKMLTGTDTYVTRG 1992
 QY 1969 DAFUNKSTLSIHVHONMGYCPQFQDAITELTGRHEVEFPALLRCYREKVEYKYGEMA 2028
 Db 1993 DATVAKSTLITNISDVHOSMGYCPQFQDAITDLTGRHELYYARIRGPAVEIERVTWMS 2052
 QY 2029 IKKLGIVYGEKYAGNYSNGKRRKLTAMALIGBPVFLDEPTTGMPKARRFLMNCAL 2088
 Db 2053 IOSTGLSYADRLATYSGKRRKSTALICORPVLDEPTTGMPKARRFLMNCAL 2112
 QY 2089 SYVKGGRSVYLTSHSMECEBALCTRMALVNGRRRCLGSVOHLKRRGDTIYVIRLAGS 2148
 Db 2113 GIIREERAVVLTSHSMECEBALCTRLATMVGAFQCLQTOHLKSKRGDGYVTMKIRSP 2172
 QY 2149 N-----PDLKPYODFFGLAFPGSVLYKEKHNMLLOYOLPSSLSLARIFSILSOSKKRLIE 2204
 Db 2173 KDDLPLDGLPVDQFPGQNFPOSVQREHRYNTLOVOVSS--SLKARIRFLVSHKDSLIE 2250
 QY 2205 DYSVQSTLDQVYVNFAPKQSDDDHLDLSLH 2236
 Db 2231 EYSVTQTLTDQVYVNFAPKQNE--TYDLRPH 2259
 RESULT 5
 Q9BZC4 PRELIMINARY; PRT; 2146 AA.
 AC Q9BZC4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
 DE ABC TRANSPORTER MEMBER 7.
 GN ABCA7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21328888; PubMed=11435699;
 RA Broccardo C., Osorio J., Luciani M.-F., Schriani L.M., Prades C.,
 RA Shulem S., Arnold I., Naudin L., Lafargue C., Koster M., Jordan B.,
 RA Matel M.G., Dean M., Denelle P., Chimini G.,
 RT "Comparative analysis of the promoter structure and genomic
 RT organization of the human and mouse ABCA7 gene encoding a novel ABCA
 RT transporter.";
 RT Cytogenet. Cell Genet. 92:264-270(2001).
 RL EMBL; AF328787; AK009591.1;
 DR InterPro: IPR003593; AAA.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR01687; ATP_GTP_A.
 DR InterPro: IPR01899; Gram_pos_anchor.
 DR Pfam: PF00005; ABC_tran. 2.
 DR SMART; SM00382; AAA. 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN.1.
 DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN.1.
 DR ATP-binding.
 KW SEQUENCE 2146 AA; 234306 MW; 239172805AD97E75 CRC64;

Query Match 49.0%; Score 5775.5; DB 4; Length 2146;
 Best Local Similarity 50.3%; Pred. No. 0;
 Matches 1148; Conservative 368; Mismatches 605; Indels 161; Gaps 26;

QY 1 MACWPOLRLILMKNTLFRROTCOLLEAVAMPFLIFLISVRLSPPEOHECHPNKA 60
 DB 1 MAFWTDLMLLKNMFKRROPVQLLEMLPLFLFLLVAVRHSPLHEHCHFPNKP 60
 QY 61 MSPAGTLPWVGIGICANNPCERYPTPGEPAGVGNFNKSIYARLFSRARLLYSOKDT 120
 DB 61 LPSAGTVPMLQGLICVNTTCFQPLTGPBEPRLSNFNDSRLRLADRYVIGASAIR 120
 QY 121 SKMDKRVYRTLOQIKSSSNLKLDFLVNDFSGFLYHNLSLKSTYDKMLRADYIIL 180
 DB 121 TLAGLKLTLATLRAARSTQO-----PQPTKQSLPEPML-- 154
 QY 181 KYVLAGQYVHLTSLGNSKSEMIQDQVSELCGLPKELAAARVLRSMNDIKPIL 240
 DB 155 -----DVAEL-----LTSLL 164
 QY 241 RLINSTSPPEKELAEATYTLHLSIGTLAQELFSMRSMDQEVNLTNNSSSSSTQI 300
 DB 165 RT--ESLGLALGQAOEPLSLLEAGDLAQELALRLSLVELR--ALLQRPKTSGLPEL 219
 QY 301 YQAVSTVCGHPBGGLTKLSIMWYEDNNYKALFGNGTEEDAEFTYDSTPYCYDMLK 360
 DB 220 --LSALCSVGRSPSTVGPSPSLMWYASDLMELVG--QEPBSALPDSLSLPACSELIG 272
 QY 361 NLESSPLSRIIMKALPLVLGKILTYTDPATROVAEYVKTFOELAVFHDESGMEELS 420
 DB 273 ALDSHLSTRLMRRLPLILGKILFAPDPTPKLMAQVNRFEELTLRDVREVWEMLG 332
 QY 421 PKTWTWENSQEMDLYRMLDSRDNDHFWEQDLDGDMTAQODIVAFLAHPELVOS---- 476
 DB 333 PRIFTMNDSSNVMLQRLLOMDEGR-RQPRGGRD-----HMEALRFLDP 379
 QY 477 -SNGSVYTRAEAFENETNOAIRTISRFMECVNLKLEPIATEVLIKSMELDERFWMG 535
 DB 380 GSGG--YSMDADADYGLVLTIGRTYECISLKLKLAAPSEALVSRALQLLAHEHFMVG 437
 QY 536 IYFTGTPGSLPEL-----HYKKIRMDIDNVERTNKIKDGYWDPQRPADPEDMR 587
 DB 438 VVFLGPEDSDDPTHEPTPDGLGPHVRIKIRMDIDVYTRTNKIRDRFWDGPRADPLTDR 497
 QY 588 YWNGGFYLODVEAOAIRLTGTEKKGYYMOOMPVCYVDIDFLRWMSRSLPMTLA 647
 DB 498 YWNGGFYLODVEAOAIRLTGTEKKGYYMOOMPVCYVDIDFLRWMSRSLPMTLA 557
 QY 648 WTSVAVIINGIYKARLEKRMIRINGLDSILMFSWFLSLIPLVNSAGLVLVIKLG 707
 DB 558 WTSVAVIINGIYKARLEKRMIRINGLDSILMFSWFLSLIPLVNSAGLVLVIKLG 617

QY 708 NLTPSPDSVVEFLVSEFAVNTILQCFILSTLFSRANLAAACGIIYFTLYLPVLCVAM 767
 DB 618 DILPYSHPGVFLFLAFAVATVQSFLSASFBRANLAAACGIAFSLIYLPVLCVAM 677
 QY 768 QDYVGFLLKIFASLLSPVAFGECEYFALFEEOGIVQWMDLFSPEVEDGFNLTISIM 827
 DB 678 RDRLPAGGRVAAISLSPVAFGCESLALLEEGEGAQMHNVGTRPT-ADVFSLAQVSL 736
 QY 828 MLFTFLYGVNTWILEAVFPQGYIPRPWYFPCIKSWYFEESESEKHPGSMOKRMEIC 887
 DB 737 LLLAALYGLATWYLEAACPQGYIPRPWYFPCIKSWYFEESESEKHPGSMOKRMEIC 795
 QY 888 MEPEPTHLKGLVSIONLYKVVYRDMKVAVDGLANFEGQITSPFGHNGAGKTTMSILT 947
 DB 796 VEEARPGISPGVSYSRSLKRRPGSPQALRGLSDLPFGHTATLGHNGAGKTTTSLIS 855
 QY 948 GLPPTSGTAVILKDIRSEKSTIRONLVCVQPNVLFDMLYVEHIMFYARLKLSEKH 1007
 DB 856 GLFPSSGSAFILLGHVSRSSMAIRPHLYVCPOYNVLFDMLYVEHIMFYARLKLSEKH 915
 QY 1008 VKAEMQALDVGLPSSKTKSKTSQLSGQMKRLSVLALFVGSKVYILDEPTAGVDPYS 1067
 DB 916 VGEEDRLQDVGVL-VSKQSVQTRHLISGQMKRLSVLALFVGSQVYILDEPTAGVDPAS 974
 QY 1068 RGLIMELLKRYQGRITLSTHNDVADVLGDRITAIISHGKLCVGSFLKQLQGTGY 1127
 DB 975 RGLIMELLKRYQGRITLSTHNDVADVLGDRITAIISHGKLCVGSFLKQLQGTGY 1034
 QY 1128 LTLVKKDVESSLSCRNSSSTVSTLKEDSVSSQSSDAGLSDESPDTLIDVAISNLI 1187
 DB 1035 LTLVKKDVESSLSCRNSSSTVSTLKEDSVSSQSSDAGLSDESPDTLIDVAISNLI 1082
 QY 1188 RKHYSEARLVEDIGHLELYVLYPEAKEGAVFELFHEIDDLSDIGISSYSETTELEI 1247
 DB 1083 QHWVPGARLVEELPHELVLVLYPYGAHDSGATLFPREDTLALRLGLYISDTLSLEI 1142
 QY 1248 FLKVAESGVDAEDTSDGLTPARRNRAFG-DKQSLRPFTEDDAADPNDSDIDESRETD 1306
 DB 1143 FLKVAESGVDAEDTSDGLTPARRNRAFG-DKQSLRPFTEDDAADPNDSDIDESRETD 1200
 QY 1307 LLSGMDKGSQYQVGNKLTQOQFVALLMKRLLIRRSKGFQATIVPAYVVCALVPSL 1366
 DB 1201 QSGSDAVG--RYQGWALTRQQLALLLKRLRLARRSRGLFAQIVPALVGLALVPSL 1258
 QY 1367 IYPPRGYPSLELOPMWNTNEQYTFVNSDAPEDTGLELNLATLDPGFGTCMGENDIPD 1426
 DB 1259 IYPPRGYPSLELOPMWNTNEQYTFVNSDAPEDTGLELNLATLDPGFGTCMGENDIPD 1308
 QY 1427 TPCQAGEEBWTAPVPTIMDFONGNTWONPSPACCCSSDKIKMLPVCPPAGGLPP 1486
 DB 1309 PVOQSSHRFSAPVPAVAVYLASGNWTPESPSPACCCSSDPGARRLPDCPPAAGGPP 1368
 QY 1487 PQKQNTADLIQDILGRNISDVLVYVQITAKSLKNKIWNNEFRYGGFSLGVSNTQALP 1546
 DB 1369 POAVTSGEYVONLGRNISDVLVYVQITAKSLKNKIWNNEFRYGGFSLGVSNTQALP 1427
 QY 1547 PSQAEVNDALIKQKKHILAKLAKSSADRFNLSLGRFMTGLDTRNNVKNWNNKGMAHISFL 1606
 DB 1428 SCQELGRSVEELMALISPLPGALDRVLTNTAMHSDIADDSLIKWNNGKSHMSMAFV 1487
 QY 1607 NVINNAIILRANLOKGENSHVGTAFNRPILNTKOQLEVALMTSYVULVLSICVIFAMS 1666
 DB 1488 NNASNAIILRANLPGRPARHASTITLNLPLNTKQOLEVALMTSYVULVLSICVIFAMS 1547
 QY 1667 FVPASFVFLIDERYSKAKHLOFISGVPRVLYLWLSNFWDMQCNVVPATLVYIIFICQO 1726
 DB 1548 FVPASFVFLIDERYSKAKHLOFISGVPRVLYLWLSNFWDMQCNVVPATLVYIIFICQO 1607
 QY 1727 KSYVSTNLPLVALLLYGMSITPLMTPASVFKIIPSTAYVVLTVNLFLGINGSVATF 1786
 DB 1608 RAYVAPANPLALLLLLYGMSITPLMTPASVFKIIPSTAYVVLTVNLFLGINGSVATF 1667
 QY 1787 VLELFTDNKLNINILKSVFLIFPHFCLGRGLDMVYVNOAMADALEPGENRFPVPSLW 1846


```

Db 1668 VLEFSPDKLOEVRILKOVFLIPHPOLGGLDMVNMADAFRLDGRQOSPLRW 1727
QY 1447 DLVGRNLFAMAVEGVFELLTVLQYRFFIRPRPVNAKLSPINDDEDVRRERORILDDG 1906
Db 1728 EVGKNLLAMVIOGRLPFLFTLLQHSRQLLPQPRVRSILPLGEDDDVARERERYOGA 1787
QY 1907 GONDILEKELTKYRRKRAVDRICVGPFGCEFGLLGVNGAKSSTKMLTGTDTV 1966
Db 1788 TGGVVLRLNLTQYKQPRMPADRLDGLPFGCEFGLLGVNGAKSSTKMTVMYGDITAS 1847
QY 1967 RGAFLNKLSTLSNIEHQNMGYCPQFADATTELLTGREHVEFPALRGYEPKGVKYE 2026
Db 1848 RGEAVLGHSHVAREPSAHLMSGCPQSDAFELLTGREHVELLARKRGVPEAOVAGTAG 1907
QY 2027 WAKRLGLVWYKGYAGNYSQGNKRKLSTAMALIGPPVVELDEPTTGMDPKARPLMNC 2086
Db 1908 SGLARLGLSWYADRPACTYSGNKRKLATATLALGVDAVVELDEPTTGMDPSARFLMNS 1967
QY 2087 ALSVYKGRSVYLLSHMECEALCTMAIMVNGRFGCLSGVQHLKRGEDGYTIYVRIA 2146
Db 1968 LLAVVREGRSVYLLSHMECEALCSRLALMVNGRFGCLSGVQHLKRGFAAGHTLRLVP 2027
QY 2147 GSNPDLKPVDFGLAPGSLVKEKHNMLQYOL-PSLSLARIFSTLSQSKRLHTED 2205
Db 2028 AARS--QPAALFAVEFPFSGSLREAHGRLRFOLPGRCALARKVCELAHVGAHEHVED 2085
QY 2206 YVSQOTLLDOYFVNFADQSDDDLKDLISLHKQTV-VDAV-----LTSEFLQDEKVK 2257
Db 2086 FVSQOTLLEVEFLYFSKQGDKE---DTEBQKAGVGVDAFGLQHPKRVSGFLDEPSTA 2142
QY 2258 ES 2259
Db 2143 FT 2144

RESULT 6
Q9NR73 PRELIMINARY; PRT: 2146 AA.
ID Q9NR73
AC Q9NR73:
DT 01-OCT-2000 (TREMBLrel, 15, Created)
DT 01-OCT-2000 (TREMBLrel, 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel, 19, Last annotation update)
DE MACROPHAGE ABC TRANSPORTER.
GN ABCA7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RP MEDLINE=2034305; PubMed=10873640;
RA Kaminski W.E., Orso E., Diederich W., Klucken J., Drobnik W.,
RA Schmitz G.;
RT "Identification of a Novel Human Sterol-Sensitive ATP-Binding Cassette
RT Transporter (ABCA7).";
RL Biochem. Biophys. Res. Commun. 273:532-538(2000).
DR EMBL: AF250238; AAF85794.1; .
DR InterPro: IPR003439; AAA.
DR InterPro: IPR003439; ABC_transport.
DR InterPro: IPR001687; ATP_GTP_A.
DR Pfam: PF00005; ABC_tran; 2.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
KW ATP-binding.
SQ
SEQUENCE 2146 AA: 234469 MW: 679916EB2D75FFOD CRC64;

```

Query Match 48.9%; Score 5763.5; DB 4; Length 2146;
 Best local similarity 50.2%; Pred. No. 0;
 Matches 1146; Conservative 368; Mismatches 607; Indels 161; Gaps 26;

```

QY 1 MACQWPLRLMLKNLTFRRRQTCOLLLEVAWDLFTLLISVRLSYPRYEQHECHFPNKA 60
Db 1 MAFWTQPLMLMLKNFYRRROPVOLLLEMLPFLFTLLVAVRHSHPLLEHHECHFPNKP 60
QY 61 MSAGLTPVVOGILCANNCPRFPTPGAPGVGNFNKSIYARLFSDARRLLYSQDIT 120
Db 61 LPSAGTVPWLOGLICVNNTCPPQLTPGEPGRILNPNDSILVSRLLADARVYLGASAH 120
QY 121 SMKDMKRVLTQOLIKKSSNNKLQDFVDNTEFSGFVYHNLSKSTVDKMLRADVITIA 180
Db 121 TLAGLGLATILAAARSTQ-----PQPTKQSTLEPRLM-- 154
QY 181 KYFLQGYLHTLSLNGSKSSEMIQLDGQVSELGLPEKELAAAEVRLSRNMILKPI 240
Db 155 -----DVAEL-----LTSIL 164
QY 241 RLINSTPPSKELAEATITLHSLGTLAQELFSRMSMDMQEVMFLTNVSSSSSTQI 300
Db 165 RL--ESGLALQAOAPLHSLLEAEDLAQELALRSLEVEL--ALLQRPRTSGPLEL 219
QY 301 YQAVSRIVCGHPEGGLKIKSLNWEEDNNYKALFPGNGTEDEADTFYDNTTPYCNDLM 360
Db 220 ---LSBALCSVGRPSSTVPSLNMWEASDLMELV---QPEESALPPSSLSLSPACSELIG 272
QY 361 NLESSPLSRIITKALKPLVGLKILYTPPTPATROYAAEVNKTPOELAVFHOLEGMEELS 420
Db 273 ALDSHPLSLMLRRRLKPLTGKILFLAPDTPFTRKLAOVNRTFEBITLLRVRREVEMIG 332
QY 421 PKIWTFMESQMDLVYMLDSDRDNDHFEOQLDGLMTADIVAFLLKHPEYDVS---- 476
Db 333 PRIFTFPMDSNVYAMQRLLOMDECR--RQPPGRD-----HMBALSTFDP 379
QY 477 -SNGSVYTWREAFNETNOAIRTISRMECVNKLDEPLATEVWLINKSMELDERKFWAG 535
Db 380 GSGG--YSWODAHADVGLHVLGTGRVTECLSLDKLEAPSEALVSRALQLLAEHREWAG 437
QY 536 IYFTGTGTSILEPH-----HKYKTRMDIDNVERTNKIKQYMPGRADPEEMR 587
Db 438 VVFLGPESSDPTEHPPTDGLGPHVRIKTRMDIDVTPTNKRIRQEMVGPAAAPLVDLR 497
QY 588 YWGGFAVYLDQVDEQAIIRVLGTGTEKTYGVYMQQMPYCYVDIFLRYMSRSMPLFMTLA 647
Db 498 YWGGFVYIYQDLVERAAVRAVTSAMPFRAGIVLQCMHYPCYVDVFLKRLSSLPFLTLA 557
QY 648 WLYSVAVYIKGLIVYKKAELKTRIMKGLDNSIIMFSNFISSLPLVYSAQLVYILKLG 707
Db 558 WLYSVTLVYKAVVREKTRRLRDMRAGLSRAVIMLGMFLSLGPFILSALVLVYLKLG 617
QY 708 NLLPYSDPSVYVFLSVFAVYVITLQCFILSTLFSRANLAACGGITVTLVPLVLCVAV 767
Db 618 DILPISHQGVYFLAAARAVATVOSFLLSAFSRANLAACGGIATFSLVPLVLCVAV 677
QY 768 QDYVFTLKIFASLLSPVAFGCEYFALFBEQIGVQWMDLFPSPVEEDGFNLTTSISM 827
Db 678 RDLRLPAGGVAAASLLSPVAFGCGESLALDLBEGGAGAHVWGRPT-ADVFSLAQVSG 736
QY 828 MLFDPLFLGVMYTYLEAVFPQOYIGIPRWYTPCTKSYTFGSESDSKSPGNOKRMSEIC 887
Db 737 LILDALYGLATWYLEAVCPQOYIGIPRWYTPCTKSYTFGSESDSKSPGNOKRMSEIC 887
QY 888 MEEPTHTLKIGVSONLVKVVYRDGKAVAVDGLALNFEQGTITLGHNGAGKTTMSILT 947
Db 796 VDEAPRGISPGVSVSLKRRPGSQPRLRLSDLFQGHITLALGNGAGKTTTSLIS 855
QY 948 GLPPTSGTAVYILGKDIRSEKSTIRQNLGYCPQHNVLFDMLTVBEHIMFYARLKLSEKH 1007
Db 856 GLPPTSGSAPFLLGHVYSSMAAIRPHLYGCPQYNNVLFDMLTVDHEHWYFGRLLKLSAAV 915
QY 1008 VKAEEMQALDVGLPSSKSLKSKTSQLSGGMQRKLSVALAPVGSKVYITLDEPTAGVDPYS 1067
Db 916 VGPEQDRLLQDVGVL-VSKQSVQTRHLSGGMQRKLSVALAPVGSQVYITLDEPTAGVDPAS 974

```


Qy	1068	RQGIWELLKRYGORTIILSTHNDADVYLDGRITAIISHGKLCCVGSILFKMNOJSTGYV	1127
Db	975	RCGIWELLKRYGRRGLILSTHHLDEALIEDRAVVAAGGLCCCGSPFLRHRHLGSGYV	1034
Qy	1128	LTVKVKVVESSLSHCNSSSTVSYLKKEDSVSSQSDAGLSHDESDTLIDVSAISNLI	1187
Db	1035	LTVKARLPLTTN-----EKADTMEGSVDRQCKKNGSGVHGTPOLLAY	1082
Qy	1188	RKHYSARLVEDIGHLETVYVPEAKKGCAYVLFHEIDRLSDLGISSTGISETLLEE	1247
Db	1083	QHWVPGARLVEELPHELVLYLPYTAHOGSPATFLRELDTLAELRLTGIGIDTSLIEE	1142
Qy	1248	FLKVAEESGVDETSGTLPARRNRRAFG--DKOSCLRFEDTDADPNDSIDIPESHEED	1306
Db	1143	FLKVEECADDTMEGSCGQHLCTGIAGLDVTLRLKMPQETALE--NEBPAGSAPED	1200
Qy	1307	LLSGMDKSGSYVKKKLTQOQFVALLMKRLLIARSKGFFAOIVLPAYVCLAYFSL	1366
Db	1201	QGSQBPDAVG--RVQWALTLRQDLALLKRLFLARSHRGFLFAQIVLPALFVGLATFSL	1258
Qy	1367	IYVPGFYPLFLELOPMVNEQYTFVSNDAPEDTGTELLNLATQDPFGTRCMGEGNP	1426
Db	1259	IYVPGHYPLRLSLPTMGAQVYSFSEDAQBPQGARLLEALDEAG-----LEE	1308
Qy	1427	TPCOAGEEMTTARPQOTIMDLFONGNWTMQNPSPACCCSSDKTKKMLPVCPCGAGLP	1486
Db	1309	PPVHSHSRFSAPENVAEAKVYLASGNMTPEESPACCCSQPGARLRLPDCPAAAGPBP	1368
Qy	1487	PQRQNTADLIDDTGENTSDYLVKYYVYIILKSLKNITWNEPQYGFSGVSNTOALP	1546
Db	1369	POAVTSGEYVQNTGRNLSDPLKTYPRLYVQGLKTKYKWNREYRGYFSLG--GRDGLP	1427
Qy	1547	PSQENVDAIKOMKKHLKAKSDADRETLNSIGRFMTGLDTRNNKXWVNNKGWHAISSFL	1606
Db	1428	SGOELGSGVEELMALLSPLRPGALDILNLTMAHSHDADDSILKIMENNKGHSHVAFV	1487
Qy	1607	NVINATLIRNLKQENPSSHXYGTAFNRHPLNLTJKOLESVALMTSYOVULSICIVFAMS	1666
Db	1488	NRASNATLIRKALPPGRARHAHSTTLNHLNLTKEQLEBALMASSVDVULSICIVFAMS	1547
Qy	1667	FVPAFVFLFIOERVSKAKILOPISGVKPVYVWLSNFWDMCMNVVPAIVIIIFIGPOQ	1726
Db	1548	FVPAFSLTVLIEEVRTRAKHILQMLGSLPTLYWLGNFMDMCMNVLPACIYVLLFLEFQO	1607
Qy	1727	KSYVSTNLPYLAALLLXONSSTPLMYPASVFXKIPRAYVYVLSVLFJGINGSATF	1786
Db	1608	RAYVAPALPRLLELLLYWSTPLMYPASFEFSVPSTAYVYVLCIMLFJGINGSWATF	1667
Qy	1787	VLELFTDMKLNINIDILSKSYFLFPPHFCRGRLIDWYKNAQAMADALEFFGGENREVP	1846
Db	1668	VLELFSQDKLOEYVRILKYQFLFPPHFCRGRLIDWYKNAQAMADAFERLGRPOFOSPLRW	1727
Qy	1847	DLYGRNLFMAAVEGVFFLTVLIQYRFLRPRPVNAKISPLNDEDEYVRERORILDGG	1906
Db	1728	EYVGNKLLAMVIOGRLPLETTLLOHQSLOLDPVRSYPLRLEEDEYVAREEREVVOGA	1787
Qy	1907	GONDLITKELEYTKYRRKRPAYDRICVGPPECGILGVNGACKSSFTKMLTGDYTVT	1966
Db	1788	TQGDVLYARNLTLYKRYQGRKRPAYDRICLTGIPRECCGILGVNGACKTSTFMAYGSDTLAS	1847
Qy	1967	RGDAFLNKNSILSNIHEVHONMGYCPQDPAITELLTGREHVEFALLNGVPREKEYKGYE	2026
Db	1848	RKEAVLAGHVSARBPASAHNSIKGSCPOSDAIEFELLTGREHLELLARLNGVPEADQAYTAG	1907
Qy	2027	WAIKRLGYKKGEKYAANSYGGKMKRLSTAPMALIGSPVYVLEDEPTTMDKARREPLMC	2086
Db	1908	SGLARLGLSWPADRPAGTYSGGKMKRLATLALVGPDAVYVLEDEPTTMDGSAARREPLNS	1967
Qy	2087	ALSYVEERSVYVLSHSMERECALCTSMALWNGRRCGYSVOHILKNRFGQYTVIVARIA	2146
Db	1968	LTAAYVRERSVYVLSHSMERECALCSRITAMVNGFRCLGSPQHLKGRPAAGHTLLEVP	2027
Qy	2147	GSNPDLKVDQFPGCLAPPGSVLKEKHNMLOYL--PSSLSLARIFSLISQSKRHLIED	2205

DB	2028	AARS--QPAALFVAALFEFGSELREHGRRLRFLQPLPGRCALALAVFGELAVGAHEVED	2085
QY	2206	YVSQTLIDQYFVNFPAKQSDDDHLKDLSLKNOIV-VDVAV-----LTSFLDDEKXV	2257
DB	2086	FVSQTLMEEFVFLVFSKDGKDE---DTEOKEAGVGDVPAFLQHPKRVSOFLDDPSTA	2142
QY	2258	ES 2259	
DB	2143	ET 2144	
RESULT	7		
Q91V24			
ID	Q91V24	PRELIMINARY;	PRT: 2159 AA.
AC	Q91V24:		
DT	01-DEC-2001	(TREMBLrel. 19, Created)	
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE	ATP-BINDING CASSETTE TRANSPORTER SUB-FAMILY A MEMBER 7.		
GN	ABC47.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
RY	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=OL129, AND DBA/2;		
RX	MEDLINE=21328888; PubMed=11435699;		
RA	Broccardo C., Osorio J., Luciani M.-F., Schriml L.M., Prades C.,		
RA	Shulien S., Arnold I., Naudin L., Lafargue C., Rosler M., Jordan B.,		
RA	Mattei M.G., Dean M., Benfle P., Chhim G.;		
RT	Comparative analysis of the promoter structure and genomic		
RT	organization of the human and mouse ABCA7 gene encoding a novel ABCA		
RT	transporter.";		
RL	Cytogenet. Cell Genet. 92:264-270(2001).		
DR	EMBL: AF287142; AAK56863.1; -		
DR	EMBL: AF287141; AAK56862.1; -		
KW	ATP-binding.		
SEQUENCE	2159 AA; 236882 MW; CD2B3FE0DB8B22B CRC64;		
Query Match	48.6%; Score 5732; DB 11; Length 2159;		
Best Local Similarity	50.6%; Pred. No. 0;		
Matches 1144; Conservative 362; Mismatches 581; Indels 176; Gaps 31.			
QY	1	MACPQRLILKMLNLFRRRCQQLLEVAAPLFTILISVLSVPEYEOHCCHPNKA	60
DB	1	MALGTQMLMLKMNNTYRRORPQLQLLELWLPLELFTILVAANHSPLEHNECHPNKP	60
QY	61	MP5AGTLPPWOGITICANNPCFRYPPTGAPGVGNFNKSIYARLPSDARRLLYSOKPT	120
DB	61	LPSAGIVPMLQGLVCWVNNSCFQHPPTGKPGVLSNFKDLSIRLLADTRTVL---	116
QY	121	SMKDRKVLRTLOQIKSSNLKQDFLDVNEFFSGFLYHNLSLPSTYDKMLRAVILH	180
DB	117	SLDDMLDALGKLLPV-----	131
QY	181	KVFLQGYQLHFTSLGNSSEMIQLDQVESELGCLPKEKLAABEVL-RSNMIDLKPI	239
DB	132	-----LRAVGGARQE-----SDQPTSG--GSYTKLL--EKILORASLD--PY	169
QY	240	LRTLNSTPFPKSELAEATKTLHLSIGTLAQELFSKRSWSDMKROEYVLTNNVSSSSSTQ	299
DB	170	L-----GQADDSMKRFSDAIRDLAQELLTLPISLMEIR---ALLRRPGSAGSLE	215
QY	300	IYAVSRIVC---GHDEGGGLKTKSLNMYEDNNYKALFGNGTEEDAEFFYONSPTPCN	356
DB	216	L--VSEALCSTGSPSSGGL---SLNMYEANOINEMPG---PEVAAPALPONSLSPPAS	265
QY	357	DLAKNLESSPFLSRIIMKALKPILVGLKLTTPDPATROVAEYVNTFOELAVFHEGMM	416
DB	266	EFVGTLDHPVSVSLMRRLKPLILGLILFAPDPNTFTRKILMAQVONQFEELALLRDLHELM	325

QY 417 EELSPKWTWENSOEDMLVRLDSDNDHFWEQQLDGLDWTADIVAFIAHNPEDVOS 476
 Db 326 GVLSPQIFNFMNDSTNVAMQLRLDVGTCQ--RQCTPRAQKKLEIKDPL-----DP 376
 QY 477 SNGSVNWRFAFNNTNQAIFITISKFMCVLKNLEPIATWILINKSMELDERKKTWAGI 536
 Db 377 SRGG-YSMRRAHADMGRLAGILCOOMECVSLDKLEAVPSEBALVSRALLETGERRMAGI 435
 QY 537 VFTG-----ITPGSIE-----LPHVKKYKIRMDINVERTNKIDGYMDPGRADPFEDMR 588
 Db 436 VFLSPHRLDPSLSPALSPGHLREFKIRMDIDVTRKTKIRKFNDFPGSADPMDLRI 495
 QY 589 VMGSAFLDQVNBQAITRVLGTGKTYVMQMPYPCYVDILFLVMSRSMPLMTLAW 648
 Db 496 VMGSAFLDQVNBQAITRVLGTGKTYVMQMPYPCYVDILFLVMSRSMPLMTLAW 555
 QY 649 IYSAVAVIKIGIYEKEARLKEIWRIMGLDMSILMFWSITSLPLIVSAGLIVILKLN 708
 Db 556 IYSAVAVIKIGIYEKEARLKEIWRIMGLDMSILMFWSITSLPLIVSAGLIVILKLN 615
 QY 709 LLEPDSVVEFLSVFAVVTILQCELIITLFSRANLAAAGGIYFTLYLPVLCVAMQ 768
 Db 616 ILPSHVPVIFLFLAFAVATVAOSFLLSAFSRANLAAAGGLAVPALYLPVLCVAMR 675
 QY 769 DYGFITLIKIFASLIPPAFGCEYFALPEBOGIGYQMDLFPSPVEDGFINLTISMK 828
 Db 676 ERLHLGGLASLIPPAFGCEYFALPEBOGIGYQMDLFPSPVEDGFINLTISMK 734
 QY 829 LDFITLYGVTWYIEAVFPQOYGIIPRWYFCTKSYWFGESDEKHPGNSOKRMSEICM 888
 Db 735 LIDAVIYGLWALYEAFCPOYGIIPRWYFCTKSYWFGESDEKHPGNSOKRMSEICM 793
 QY 889 EEPETHLKGVSITONLVKYVRDGMKAAVVGIALNFEQGITSLFGLNGAGKTTMSILFG 948
 Db 794 EEPETHLKGVSITONLVKYVRDGMKAAVVGIALNFEQGITSLFGLNGAGKTTMSILFG 853
 QY 949 LFPPTGTAVILKIDIRSEMSTIRONIGVCPQHNVLFDMLTVEEHTMFARLKISEKIV 1008
 Db 854 LFPPTGTAVILKIDIRSEMSTIRONIGVCPQHNVLFDMLTVEEHTMFARLKISEKIV 913
 QY 1009 KALMEDMALDVGILPSSKLSKTSQLSGQMKLSVALAFVGSQVYLIDEPAGVDPYSR 1068
 Db 914 GPERELIRHVGIL-TLKRDTQTRHLSGQMKRSVAIAFVGSQVYLIDEPAGVDPYSR 972
 QY 1069 RGIMELLKYRGRTITLSTHMDADVLCGRDAITISHGKLCQVSGSLPKKNOLGTYL 1128
 Db 973 RGIMELLKYRGRTITLSTHMDADVLCGRDAITISHGKLCQVSGSLPKKNOLGTYL 1032
 QY 1129 TLVKVYESSLSGCRNSSSTVYLKEDSVSQSSDAGLGSDESDT----- 1175
 Db 1033 TLVKVYESSLSGCRNSSSTVYLKEDSVSQSSDAGLGSDESDT----- 1081
 QY 1176 -----LTIYSAISNLIRKHVSEARLVEDIGHEITVYLPEAKKEGAFVLFHEIDR 1228
 Db 1082 PARGANPIPTARILIEVQYHPCQQLVEDLPHELLVLPYAGALDGSFAVFEQLDQ 1141
 QY 1229 LSDLGISYGISETLLEILFLKVAESGVDAETSDGTLPARNRRAFGKQSL-RPTE 1287
 Db 1142 LELIGLIGYISDTNLEIFLKVVEDAHREGDSDRQHLR-----TCTQPTPG 1191
 QY 1288 DDAADPNDDIDIPESREDDLSGMDCKGSYQKGMKLTQOQVALLMKRLIARSKGF 1347
 Db 1192 PERSVLENEMLAQ-----GL-APNAAYQVQMTLTCQQRALLHRRFLIARSRGL 1242
 QY 1348 FAQIVLPAFVCIATVLSLIPPFKYSLELOPMYVNEQYVFNDADEPTGTLELNA 1407
 Db 1243 FAQIVLPAFVCIATVLSLIPPFKYSLELOPMYVNEQYVFNDADEPTGTLELNA 1302
 QY 1408 LKRDGFCGRCEGNIPDTPQOAGEEKTAP-VQGITMDLQNGNNTMQNPSFACCS 1466
 Db 1303 LKRDGFCGRCEGNIPDTPQOAGEEKTAP-VQGITMDLQNGNNTMQNPSFACCS 1362

QY 1467 SDKIKMLPVCPPGAGLPPQKONFADILLODITGRNISDYLVKTYOIIAKSLKNIW 1526
 Db 1363 QGARRILPDPCAGAGGPPPPAVAGLEQVONLGRNVSDPILKTYSLVRGLKTKWK 1422
 QY 1527 VNEPFRGFSLSGVSTQALPSPQEVNDALIKONKHKLAKDSSADRLNSLGRPTGLDT 1586
 Db 1423 VNEPFRGFSLSGVSTQALPSPQEVNDALIKONKHKLAKDSSADRLNSLGRPTGLDT 1481
 QY 1587 RNNVWVFNKKNHMAISSPLANTVNNAILRANLOKENSNGHITAFNPLWLTQOQSEV 1646
 Db 1482 RNNVWVFNKKNHMAISSPLANTVNNAILRANLOKENSNGHITAFNPLWLTQOQSEV 1541
 QY 1647 ALMTTSVDLVSIYIFMSPVASFVVELIOERYSAKHLOPISGVKPYVIMLSNFWMD 1706
 Db 1542 ALMTTSVDLVSIYIFMSPVASFVVELIOERYSAKHLOPISGVKPYVIMLSNFWMD 1601
 QY 1707 MCNYYVPATVYIIFTCQOQSYSTVLPVALLLLYGSITPPLKYPASVFKIDSTA 1766
 Db 1602 MCNYYVPATVYIIFTCQOQSYSTVLPVALLLLYGSITPPLKYPASVFKIDSTA 1661
 QY 1767 YVLTSMVLTGINGSVATFVLETFDNLKNNINDILKSVFLPPHPCGLGLDMYKNQ 1826
 Db 1662 YVLTSMVLTGINGSVATFVLETFDNLKNNINDILKSVFLPPHPCGLGLDMYKNQ 1721
 QY 1827 AMADALBERGENREVSPLSMIDVGRNLFAMAVEGVFELITVLIOYRFTIRPREVNAKS 1886
 Db 1722 AMADALBERGENREVSPLSMIDVGRNLFAMAVEGVFELITVLIOYRFTIRPREVNAKS 1781
 QY 1887 PLNDEDEVRERROKILDGONDIETELKELTKYRRKRPAVARICVDPGCGELIG 1946
 Db 1782 PLNDEDEVRERROKILDGONDIETELKELTKYRRKRPAVARICVDPGCGELIG 1841
 QY 1947 VNGACKSTFPMKLTGDTVTTRGDAFLKNKSLISNIEHVONMGYQOPDAITELLTGREH 2006
 Db 1842 VNGACKSTFPMKLTGDTVTTRGDAFLKNKSLISNIEHVONMGYQOPDAITELLTGREH 1901
 QY 2007 VEFPALRGPEKEVGKGAIRKILGYKGEYAGYSGGNRKISTMALIGGPPV 2066
 Db 1902 VEFPALRGPEKEVGKGAIRKILGYKGEYAGYSGGNRKISTMALIGGPPV 1961
 QY 2067 FLDEPTTGMDBKARFLMNCALSVKKGSRVYLTHSHMECEALCTPMALMVNGRFLC 2126
 Db 1962 FLDEPTTGMDBKARFLMNCALSVKKGSRVYLTHSHMECEALCTPMALMVNGRFLC 2021
 QY 2127 SVOHLKNEFGDGTIVRIAGSNPDLKPVODFSLAPPSYLAKKHNMLOYL-PSLS 2185
 Db 2022 SVOHLKNEFGDGTIVRIAGSNPDLKPVODFSLAPPSYLAKKHNMLOYL-PSLS 2079
 QY 2186 SLARIFSLISQSKRRLHIEDYSQOTLIDQVFNFAKDQSDDD 2228
 Db 2080 SLARIFSLISQSKRRLHIEDYSQOTLIDQVFNFAKDQSDDD 2122

RESULT 8
 ID Q96S58 PRELIMINARY; PRT; 2008 AA.
 AC Q96S58;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ABCA-SSN.
 GN ABCA/ABCA-SSN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21255283; PubMed=11355874;
 RA Tanaka A., Ikeda Y., Abe-Dohmae S., Arai K., Sadanami K.,
 RA Kidera A., Nakagawa S., Nagase T., Aoki R., Kioka N., Amachi T.,
 RA Yokoyama S., Ueda K.,
 RT "Human ABCA1 Contains a Large Amino-Terminal Extracellular Domain


```

QY 2259 S 2259
Db 2006 T 2006

RESULT 9
Q9ESR9 PRELIMINARY; PRT; 2434 AA.
ID Q9ESR9
AC Q9ESR9;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ABC2.
GN ABC2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=2042713; PubMed=10970803;
RA Zhao L., Zhou C., Tanaka A., Nakata M., Hirabayashi T., Amachi T.,
RA Shioda S., Ueda K., Inagaki N.;
RT "Cloning, characterization and tissue distribution of the rat ATP-
RT binding cassette (ABC) transporter Abc2/Abca2."
RL Biochem. J. 350:865-872(2000).
DR EMBL; AB037937; BAB16596.1; -.
DR InterPro; IPR003593; AAA.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 2.
DR SMART; SM00382; AAA; 2.
DR ATP-binding.
KW SEQUENCE
SQ 2434 AA; 270925 MW; CD424A9C4F63513F CRC64;

Query Match 36.0%; Score 4249.5; DB 11; Length 2434;
Best Local Similarity 39.1%; Pred. No. 9.4e-272;
Matches 992; Conservative 346; Mismatches 713; Indels 483; Gaps 60;

QY 6 QLRLLKNTLFRRTQQLLEVAWPLFLLISVRLSYPRYEHCRRPKAMPAG 65
Db 6 QLRLLKNTLFRRTQQLLEVAWPLFLLISVRLSYPRYEHCRRPKAMPAG 65
QY 125 MRKVLRTLOQ-----IKSSSNLKLDQDFVNDNETSGFLYHNLSLPKST 168
Db 125 MRKVLRTLOQ-----IKSSSNLKLDQDFVNDNETSGFLYHNLSLPKST 168
QY 116 LGSLELHQRLEALSSGPGWESHARPAVSSPLDSVARDKRELMLRMQNLSTPNST 175
Db 116 LGSLELHQRLEALSSGPGWESHARPAVSSPLDSVARDKRELMLRMQNLSTPNST 175
QY 169 VDKMLRDV----- 177
Db 169 VDKMLRDV----- 177
QY 176 AQAALLAARVPSEVYRLFLGPLDLGKFLRKQEPWHLGNSPLFQMEELLAPALLE 235
Db 176 AQAALLAARVPSEVYRLFLGPLDLGKFLRKQEPWHLGNSPLFQMEELLAPALLE 235
QY 178 -----IL-----HKVFLQYOLHITSICNGSKSEEMIQDQVESELGLPK 219
Db 178 -----IL-----HKVFLQYOLHITSICNGSKSEEMIQDQVESELGLPK 219
QY 236 QLTCAPOSGELGRLLTPEGHQVDLQGR--DVCSGQATARA-----OHFSDL----- 282
Db 236 QLTCAPOSGELGRLLTPEGHQVDLQGR--DVCSGQATARA-----OHFSDL----- 282
QY 220 EKIAAARVLRNSMDILKPLIRTL-----NSTSPFSEKLEAETKLLHSLGTLAOLFS 274
Db 220 EKIAAARVLRNSMDILKPLIRTL-----NSTSPFSEKLEAETKLLHSLGTLAOLFS 274
QY 283 -----ATE--LRNOLDIAK--IAQQLGFNVPGSDPOAPSPQSLALGLDLDVQVLIQD 335
Db 283 -----ATE--LRNOLDIAK--IAQQLGFNVPGSDPOAPSPQSLALGLDLDVQVLIQD 335
QY 275 MRSMSDKRQEMFLTNSSSSSTQIQAVSRVYCGHPBGGLKIKLSLNNYEDNNYKALF 334
Db 275 MRSMSDKRQEMFLTNSSSSSTQIQAVSRVYCGHPBGGLKIKLSLNNYEDNNYKALF 334
QY 336 V-----DVLALALLLPQACAGRAPAQ-----GSPSGPA-----NSTGAG 373
Db 336 V-----DVLALALLLPQACAGRAPAQ-----GSPSGPA-----NSTGAG 373
QY 335 GGNTEEDATFYDNTPTPCNDLMKNLSESPLSRIITKAKLKPLVG----- 381
Db 335 GGNTEEDATFYDNTPTPCNDLMKNLSESPLSRIITKAKLKPLVG----- 381
QY 374 ANTGPNTVEEGTOSPTVTPASPTLQGGCSAFVO--LWAGLOPILCGNNETTEPALRGG 431
Db 374 ANTGPNTVEEGTOSPTVTPASPTLQGGCSAFVO--LWAGLOPILCGNNETTEPALRGG 431

```

```

QY 382 -----KILYTPDTPATROVAENKVTQELAVFHDEGM 415
Db 382 -----KILYTPDTPATROVAENKVTQELAVFHDEGM 415
QY 432 NMSLSFTSKEQRNLGLLVHMTSNKLLIYAPAGSADHVIILKANETFAVGNTHYAKOV 491
Db 432 NMSLSFTSKEQRNLGLLVHMTSNKLLIYAPAGSADHVIILKANETFAVGNTHYAKOV 491
QY 416 WEELSPKTIWTEWNSOEMDLVRLDSDRNDFHFEQQLDGLDWTQADIVAFIAKPEVQ 475
Db 416 WEELSPKTIWTEWNSOEMDLVRLDSDRNDFHFEQQLDGLDWTQADIVAFIAKPEVQ 475
QY 492 WNTISAIRSFLE-----OGRLOQH-----LHM-LQYVYADRLRHEAMN 530
Db 492 WNTISAIRSFLE-----OGRLOQH-----LHM-LQYVYADRLRHEAMN 530
QY 476 SS-----NGSVYTWREAFNETNOAIRTS-----PFMECVNKLKEP 512
Db 476 SS-----NGSVYTWREAFNETNOAIRTS-----PFMECVNKLKEP 512
QY 531 LSLDELPAALRLDYPSLPNGTALL-----QOLDITDAACGMIOPMSVSVDIRKG 581
Db 531 LSLDELPAALRLDYPSLPNGTALL-----QOLDITDAACGMIOPMSVSVDIRKG 581
QY 513 IATEVWLINKSME--LDERKFMAGIVETGTPGSELPNHYKTKRMDIDVERTNKK 570
Db 513 IATEVWLINKSME--LDERKFMAGIVETGTPGSELPNHYKTKRMDIDVERTNKK 570
QY 582 FPDSEIVVYTLNQAVQDQVWVFASVIFQTRDGS--LPHVHYKTIKRONSSPTEKTEIR 639
Db 582 FPDSEIVVYTLNQAVQDQVWVFASVIFQTRDGS--LPHVHYKTIKRONSSPTEKTEIR 639
QY 571 DGWDDGRPADDFEDMRVYWGFAIYQDVBOAIIIRVLGTE--KTYGYVMQMPPCYVD 629
Db 571 DGWDDGRPADDFEDMRVYWGFAIYQDVBOAIIIRVLGTE--KTYGYVMQMPPCYVD 629
QY 640 RAYWRPQNTG---GRFYLYGFVWIDMIERAILITFVGHDVPEPQVDFPYPCYTR 696
Db 640 RAYWRPQNTG---GRFYLYGFVWIDMIERAILITFVGHDVPEPQVDFPYPCYTR 696
QY 630 DIFLRVMSRSMPLFMTLAWISAVIIGIYKEBARLKETMRIGLDSILMFSEFTSS 689
Db 630 DIFLRVMSRSMPLFMTLAWISAVIIGIYKEBARLKETMRIGLDSILMFSEFTSS 689
QY 697 DDFLFVIEHMDPLCWLIVSVSVAMTQIIVAKKEHRLKEVKKTMGLNNAYHWAMFITG 756
Db 697 DDFLFVIEHMDPLCWLIVSVSVAMTQIIVAKKEHRLKEVKKTMGLNNAYHWAMFITG 756
QY 690 LIPPLVSAQLVYIILKGLNLEPDSVYFVFLSVFVAVTTIQCPLISTLSRANLAAC 749
Db 690 LIPPLVSAQLVYIILKGLNLEPDSVYFVFLSVFVAVTTIQCPLISTLSRANLAAC 749
QY 757 FQLSISVATLAILIKYGGVLMHSHVLIIMFLAYAAVATIFCPLSVLSKATLASAC 816
Db 757 FQLSISVATLAILIKYGGVLMHSHVLIIMFLAYAAVATIFCPLSVLSKATLASAC 816
QY 750 GGIIFYTYLIPVYLQ-----VAMQDYVGFYTKIFSLSPVAFGFGCYFALFEEOGCV 804
Db 750 GGIIFYTYLIPVYLQ-----VAMQDYVGFYTKIFSLSPVAFGFGCYFALFEEOGCV 804
QY 817 GGIIFYLVYPIIMYAIAREVAHDKITAE--KCIASLSTAFGLSGKYPALYEVAGGI 875
Db 817 GGIIFYLVYPIIMYAIAREVAHDKITAE--KCIASLSTAFGLSGKYPALYEVAGGI 875
QY 805 QWDNLFESEVDEEDENLTTSISMMLPDTFLVGMVWYIEAVFPQGYIIPRWYPCYKSY 864
Db 805 QWDNLFESEVDEEDENLTTSISMMLPDTFLVGMVWYIEAVFPQGYIIPRWYPCYKSY 864
QY 876 QWHTESQSPVEDDNLILAVTLMVDVYVGVLTWYIEAVHPGKYGIPRWYFPLQKSY 935
Db 876 QWHTESQSPVEDDNLILAVTLMVDVYVGVLTWYIEAVHPGKYGIPRWYFPLQKSY 935
QY 865 WPEGE---ESDEKSHPGSNOKRMS-----ETC-----MEEPYHLKIGSIONL 904
Db 865 WPEGE---ESDEKSHPGSNOKRMS-----ETC-----MEEPYHLKIGSIONL 904
QY 936 WLGSGRTTEWMSWPAHAAPRLSWBEDOACAMESRHEETRGMEETPHLPVYCVKL 995
Db 936 WLGSGRTTEWMSWPAHAAPRLSWBEDOACAMESRHEETRGMEETPHLPVYCVKL 995
QY 905 VVYVYDGMKVAVDGLALNFYEGQITSPFLHNGAGKTTMSITLGLPPTSGTAVIIGNDI 964
Db 905 VVYVYDGMKVAVDGLALNFYEGQITSPFLHNGAGKTTMSITLGLPPTSGTAVIIGNDI 964
QY 996 TKYKKDKKTLANKLSLXNYENQVVSFLCHNGAGKTTMSITLGLPPTSGSATIYHDI 1055
Db 996 TKYKKDKKTLANKLSLXNYENQVVSFLCHNGAGKTTMSITLGLPPTSGSATIYHDI 1055
QY 965 RSEMTIRONLQVCPQHNVLPMLLVEEHIWYIAYLKLSEKHVYABEMQALVDGLPSS 1024
Db 965 RSEMTIRONLQVCPQHNVLPMLLVEEHIWYIAYLKLSEKHVYABEMQALVDGLPSS 1024
QY 1056 KTEMEIRKRLGMCQDHNVLFDQTLVEEHLWFYSRLKSMQAEIRKEMDKMIEDLEL--SN 1114
Db 1056 KTEMEIRKRLGMCQDHNVLFDQTLVEEHLWFYSRLKSMQAEIRKEMDKMIEDLEL--SN 1114
QY 1025 KLSKTSQLSGGMQRRLSYALAFVGSKRVILDEPTAGVDPYSRGIVELLKTYROGRTI 1084
Db 1025 KLSKTSQLSGGMQRRLSYALAFVGSKRVILDEPTAGVDPYSRGIVELLKTYROGRTI 1084
QY 1115 KRHSIVQTLISGGMKRLSVALAFVGSRAIILDEPTAGVDYARAIYDILKTKPKRTI 1174
Db 1115 KRHSIVQTLISGGMKRLSVALAFVGSRAIILDEPTAGVDYARAIYDILKTKPKRTI 1174
QY 1085 ILSITHMDEADVLDRIALISHGKLCYGVSSLEFLKNOLGTGYLYTLVKKDVESSLSGRN 1144
Db 1085 ILSITHMDEADVLDRIALISHGKLCYGVSSLEFLKNOLGTGYLYTLVKKDVESSLSGRN 1144
QY 1175 LLSITHMDEADLLGDRILAIISHGKLCGSGPLFLGAGADGVRLLTVLRPAEPTSOEPG 1234
Db 1175 LLSITHMDEADLLGDRILAIISHGKLCGSGPLFLGAGADGVRLLTVLRPAEPTSOEPG 1234
QY 1145 SSSIVSYLKKEDSEVSSSSDAGISGDHESDPTITDVSANSLIRKHYSEALVDIGHEL 1204
Db 1145 SSSIVSYLKKEDSEVSSSSDAGISGDHESDPTITDVSANSLIRKHYSEALVDIGHEL 1204
QY 1235 MASSPSGRPOLSNCSMO-----VSQPIRHHVASSLLVSDSTSEL 1274
Db 1235 MASSPSGRPOLSNCSMO-----VSQPIRHHVASSLLVSDSTSEL 1274
QY 1205 TYVLYPEAKEGAFVELFHEIDRLSDLGISYSGETTELEIFLKYAE----- 1254
Db 1205 TYVLYPEAKEGAFVELFHEIDRLSDLGISYSGETTELEIFLKYAE----- 1254
QY 1275 SYILPSEAVKKAFFRLPQGLEHSLDALHLSFGLMDPTLLEEVFLKSEEDQJLENSRAD 1334
Db 1275 SYILPSEAVKKAFFRLPQGLEHSLDALHLSFGLMDPTLLEEVFLKSEEDQJLENSRAD 1334
QY 1255 -----SGYDA--ETSDGTL-----PARRNRA--FGDKOS 1280
Db 1255 -----SGYDA--ETSDGTL-----PARRNRA--FGDKOS 1280
QY 1335 VKESRKDALPGAEGILTAVESAGNLARCSLQASQASLSQASVSGASAGDAGAGTYDGYG 1394
Db 1335 VKESRKDALPGAEGILTAVESAGNLARCSLQASQASLSQASVSGASAGDAGAGTYDGYG 1394
QY 1281 CLRPTEDDADPNDSIDDPESRETDLSGMDGSGYGVKWKMLTQOQFALLMKRLILIA 1340
Db 1281 CLRPTEDDADPNDSIDDPESRETDLSGMDGSGYGVKWKMLTQOQFALLMKRLILIA 1340
QY 1395 DYRPLF--DNLQDPD--SVLSDEAMEALARY--GQSGSKLSEBWMKMKQFHLLVKKRHA 1450
Db 1395 DYRPLF--DNLQDPD--SVLSDEAMEALARY--GQSGSKLSEBWMKMKQFHLLVKKRHA 1450
QY 1341 RSRKGFPAQIYLPVAFVCIALVFSLIYVPGKYSLELQWMTYNEQT-----FVS 1392
Db 1341 RSRKGFPAQIYLPVAFVCIALVFSLIYVPGKYSLELQWMTYNEQT-----FVS 1392

```

```

DB 1451 RNSALCSQILLPAFPCVATVALSVPEIGDLPPLVLSQYH-NTTQGRGNFTIPAN 1509
QY 1393 NDAPE-----DTGLLELNLATKDPGFGTCM----- 1419
DB 1510 EERREYRLRLSPADAPQOLVSTRLPSCVAGACVLSKSPANGSLGPMNLSSGESRLAAR 1569
QY 1420 -----EGNPT-----PD-----TTCQAGEEWITAP 1440
DB 1570 FPDSCMESFTQGLPLSNFPPPPSPAPSDSPSLSPDESLAMNTSLPPTAGPBTWAP 1629
QY 1441 -VPOTIMOLFONGNMTPQNPSPACCCSDKIKMLPVCPPGAGLPPPOKONTADIOD 1499
DB 1630 SLPRLYHEVR-----CTCSAGCTFS---CPSSAGG-HPPQOMKRVTDILTD 1673
QY 1500 LTRGNISDYLVTYVOIILAKSLKNKIMWNEFRYGGFSLGVSNTQALPPSOEVNDAIKOMK 1559
DB 1674 TIGHNVSEVLTFTSDRF-----RLHRYGATITG-NIQKSTIPADIGTRPLMYR 1720
QY 1560 KHLKAKDSSADRLPLSLGRTMTGLDTRNNVYVFNKNGMAHISFLVYINNALLRANIQ 1619
DB 1721 K-----IAVRVACVLYNNKGYHSMPTLYNSLNAAILRANLP 1757
QY 1620 KGE-NSHYGITAPNHPNLTKOOLSEVALMTSVDLVLSICVIFAMSPVPASVFLIQ 1678
DB 1758 KSKGNPAAYGITVTHNPKMTSASLS-LDYLOQGDVYATITVYAMSPVPASVFLIYA 1816
QY 1679 ERYSKAKHLOFTSGVPVITYLWLSNFWDMCNVVPATVLIIFIGFOOKSVYSSNLPVL 1738
DB 1817 EKSTAKKHLOFVSGCNPVITYLWLVMDLNLVATCCIIILFVDDLPATYSPINFPAY 1876
QY 1739 ALLLLYKSTIPPLMPASPVKISTAVVLTNVNLFINGSVATFLELT-DNKLN 1797
DB 1877 LSLFLYKWSITPIMYPASFWFVPSAVVFLIVLNLFGITATYATFLLQEHDKDK 1936
QY 1798 NINDILKSWELFPHFCRLGLIDMYKNOAMDALEPGE-NRFVPSLMDLVGRNLFAM 1856
DB 1937 VVNSYKSCFLFPNINLGHMEIAYNEYINETYAKIQOPDKMSPFEMDLYTKGLVAM 1996
QY 1857 AVESGVFLITVLIQYRFFIRPPVNAKLSPLNDEDEDVREORILLDGGQNDILEIKE 1916
DB 1997 TVEGFVGFELTICQYNFLRQPLPVSTKPVED-DVDAVASEKQRYLRGDADNDWKIEN 2055
QY 1917 LTKIYRKK---KRPVADRICVGPPECEGGLGVNGAGSSPFKMLTGTJYTRGDAFEN 1973
DB 2056 LTKVYRSRKIGRIALVADRCLGVRPECGGLGVNGAGKSTFKMLTGDSESTTGGEAFVN 2115
QY 1974 KNSILNIEHVHONMGVYCPQDAITELLGHEHEFFALLRGVEKEVKGVMALIRKLQ 2033
DB 2116 GHSVLADLQVQOSLGCTQDFALFDELTAAREHLOLYTRLRGIPMKDEAQVYRWMALEKLE 2175
QY 2034 LVYKGEYAGNVSGNKKRLSTAMALIGRPVYVLEDEPTGMDPKARPLMNCALSVKE 2093
DB 2176 LTRCACKRPAISYSGNKKRKSTALIGYPAFLFDEPTGMDPKARPLMNLIDLTKT 2235
QY 2094 GRGVNLTSHSEMECEALCTFMAITMNGRPGCISVQHLNRRGEGDTIVVRLAGSPDK 2153
DB 2236 GRGVNLTSHSEMECEAVCTRLATMNGRLCGLSIOHLNRRFGDGMITVR-TKSSQNK 2294
QY 2154 PYVDFGLPFGSVLKEKHNMLQYOLPSSLSIARIFSLISOKRHLIEDYSVSOTLL 2213
DB 2295 DVYRFRNRPRPALMKERHHTKYQYOLKSEHISLAQVFSMEHVGVGLIEDYSVSOTLL 2354
QY 2214 DOYFVNFPAKQSDP 2227
DB 2355 DNVFVNFPAKQSDN 2368

```

```

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ATP-BINDING CASSETTE SUB-FAMILY A MEMBER 2 (ABC TRANSPORTER
DB ABCA2).
GN ABCA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN.
RA Vulevic B., Chen Z., Davis W. Jr., Walsh E.S., Tew K.D.;
RT "Cloning and characterization of human ABCA2."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=11178988;
RA Kaminski W.E., Piehler A., Pullmann K., Poroch-Ozcurumez M., Duong C.,
RA Bared G.M., Buchler C., Schmitz G.;
RT "Complete Coding Sequence, Promoter Region, and Genomic Structure of
RT the Human ABCA2 Gene and Evidence for Sterol-Dependent Regulation in
RT Macrophages."
RL Biochem. Biophys. Res. Commun. 281:249-258(2001).
DR EMBL; AF178941; AACG9372.1; -.
DR EMBL; AF327657; AKR14334.1; -.
DR InterPro; IPR003593; AAA.
DR InterPro; IPR003439; ABC_Transport.
DR InterPro; IPR001687; ATP_GTP_A.
DR Pfam; PF00005; ABC_tran; 2.
DR SMART; SM00382; AAA; 2.
KW ATP-binding
SO SEQUENCE 2436 AA; 269955 MW; E044A3AF14EA25D1 CMC64;

```

Query Match 35.9%; Score 4240.5; DB 4; Length 2436;
 Best Local Similarity 39.8%; Pred. No. 3,7e-271;
 Matches 999; Conservative 347; Mismatches 729; Indels 435; Gaps 61;

```

QY 6 QRLILKRNLFRRRQTOQLLEAVMPLEFILLISVLSVPPYEQHCHPKNKA-MPSA 64
DB 6 QRLILKRNLFRRRQTOQLLEAVMPLEFILLISVLSVPPYEQHCHPKNKA-MPSA 65
QY 65 GLTPWVQGLICANNPCRRYPTPGEPVYVGNFNKSIYARLFSBARLL-----LYSQKD 120
DB 66 GLTPWVQGLICANNPCRRYPTPGEPVYVGNFNKSIYARLFSBARLL-----LYSQKD 115
QY 121 SMKDKRKYRLTLQOIKKSSNLIKLODFLVNMFPSG-----FLYHNLSLP 165
DB 116 SLGSELEALR-QHLEALSACGTSGLHDSSTVSSFSLSVARNPOELMRFLLTQNLSTLP 173
QY 166 KTVKMKLRADY-----ILHKVFLQGYOYLHLS-LCNSS-----KSEPMI----- 204
DB 174 NSTAQAALLAARVDPPEVYHLLGPSSALDSQSGLHKGOEPMSRLGGLNPLFRMEELLAPA 233
QY 205 ---QL-----GDQEVSELGLPKFKLAAB-----RVLRNMDI 235
DB 234 LLEQLTCTPGSELRIILTVPESSQKALQYRDVYCSGQAARARFSGLSAELRNQDYL 293
QY 236 LKPIRLTUNSTSPPSKELAE--TKTLHLSLGLTQDELFSKRSMDRQVEMFLTYNVS 293
DB 294 AK-VSQQLGLIDAPNCSDSQAPAPRRRLQALIGLDD-----AKQYLDDVDYLS 341
QY 294 SSSSTQIYQAVYRIYCGHEGGGLIKSLNMVEDNNYKALFGNGTERDAETFDYDNSTTP 353
DB 342 ALALLLPQACTGRTPGPPASGAGGAN-----GTGAGAVWMPNATABEGAPSAALATP 396
QY 354 YCNDLKKNLSSPLSRIITWALKPLLVG----- 381
DB 397 ---DTLQGGCSAFVQ--LWAGLPILCGNNRTIEPEALRGNMSSLGFTSKQORNLGLLV 451
QY 382 -----KLTYPDPDPATROVAAEVNKTFOELAVHDEGAKMEELSPRIWTFMNSQSDMD 434

```

```

Db 452 HLMTSPNKILYAPAGSEVDVILKANETFAFVGNVTHYAQVWLINISABELRSFLQCRLOQ 511
OY 435 LVMMLDSRDNHFWECOLDGLDWTQODIYAFIAKHPEDVOSSNGSVYTWREAFNETN-- 492
Db 512 HLKWL-----QOYVAELRLHPE--ALNLSIDELPALRBDNPS 547
OY 493 -----QAIRTIS-----REMEOVNLNKLEPIATEVWMLNKSMELDERKFMAG 535
Db 548 LPSGMALLOQDLTDINAAGMIOFMSKVSVDIFKPFDEESTVNTLNOAYQDNVTFAS 607
OY 536 IVEFTGTGSGIELPHHHKKIRMDIDNVERTNKIKDGYWDPGRADPFEDMRVWNGFAY 595
Db 608 VIFQTRKDSG--LPHVHYKIRONSSEFTEKTNEIRAYWRPNTG--GRFYELGFW 662
OY 596 LQDVBOAIIRVLGTE-KKTGYWQMPYPCVVDIPLRWSRSPRLMTLMTISVAV 654
Db 663 IQDMERAILDTFVGHDVYVPGSYVOMFPFCTRDPLFVLEHMPLOLMTISWYSVAM 722
OY 655 IKGIVYEKARLEKTRMIRGLDNLIMFSEFISLIPPLVSAGLLVILKIGNLPYS 714
Db 723 TIQIYAEKEHRLKEVYKTMGLNNVHVMFETGVOGISVITALTALKXGYLMSH 782
OY 715 PSVFEFLSEFAVNTLOGLFISTESRANLAACGGIIFPLIPLPYLC-----VAMOD 769
Db 783 VVITMLFLAYAVATIMFQFLVSILSKALASACGGIIFLSYVYVVAIREEVAHDK 842
OY 770 YVGFLLKIFASLSPVAFEGCEYFALFEQIGVQMDNLFESPYEDEFNTTISML 829
Db 843 ITAFEL-KCIASLMTSTAFGSGKRYFALYEVAGVLOMHFSSPYBGDFNILLATM 901
OY 830 FDFLLYCVMTWYIEAVFPGQYGIPIRPWYPCPKSWFGE--ESDEKSHPGSNOKRMS-- 884
Db 902 VDAVYVGIITWYIEAVHPQMYGLPRFMYFPLOKSYWLGSGRTFAWMSWPMARTRLSYM 961
OY 885 -----MEEPHTHLKGVSTONLYKYVRDGMKAVAVDSLANFEGQTT 929
Db 962 EELQACAMSRREERTGMEEBEFTLPLVAVCYDKLTKYKDKKALANKLSHNLVENDV 1021
OY 930 SFLGNAGAKTTTMSILTLGFPPTSGTAYILGKDIRSEKSTIRONLGVCPQHNVLFDMLT 989
Db 1022 SFLGNAGAKTTTMSILTLGFPPTSGSATLYGHDIRTEDELRKMLGKMPQHNVLFDRLT 1081
OY 990 VEHIMFYARLKGSLKHYKAEQMDALDVGIPSSKLSKTSOLSGGMOKRISVALAEVG 1049
Db 1082 VEHIMFYARLKSMAOELIRREMDKMIEDLEL-SNKRHSLVOTLSGMRKRLSVAIAFVG 1140
OY 1050 GSKVVLIDEPFAGVDPYSRGIWELLKRYOGRTIILSTHMDADVDLGRITAIISHGL 1109
Db 1141 GSRAILIDEPFAGVDPYARARAILMDLITKPKRPTIILSHMDADVDLGRITAIISHGL 1200
OY 1110 CCVGSSFLKNOLGTYVYLTVLKKDVESLSSCRNSSSTVSYLKKRDESVSSSDAGLGS 1169
Db 1201 KCCGSSFLTKGTGTYGDRYRLTLVKKRAPEPG-----GQOPRGAS 1238
OY 1170 DHESDFTLIDVS--AISNLIRKHVEARLYVEDIGHETVYLVEAKAGSAFVLPFHEID 1227
Db 1239 SPPGRAPLSSGSELOVQPIRKHVASCLVSTSTELSTILPSEAKKAGAEFRLQHLER 1298
OY 1228 RUSDGLSSYIGSETTIEELFKVAEE-----SGVDA-ETSDGULP----- 1267
Db 1299 SIDAHLHSFGLMDITLLEVFLKVEDEQSLNSHADVKESKVDLPAGEGASGEHAG 1358
OY 1268 -----ARRNRA-FGDKOSCLRPTEDDAADPNDSDIDPESR 1303
Db 1359 NLARSELTOQASLOSASSVSGARGDEAGYTDVYGYRPLF-DNPDPP--NVSIGEV 1415
OY 1304 ETDLLSGMDGSGYOVKGWKLQOQFVALLMKRLLIARSRKGFPAQIVYLAFFICIALV 1363
Db 1416 EDEALSRV-GQSGRKLDGWLKVRQFHLVKKRPHCARNSALFSQILLPAFFVCVAMT 1474
OY 1364 FSLIYVPPFGKYSLELQPMWYNEQY-----FVSDNABE-----DTGTELELAL 1408
Db 1475 VALSVPEIGDPLPVLPSPSOYH-NTYQPRGNFIYANERREBYRLRLSPDASPOQVSTF 1533

```

```

OY 1409 TKDPEGTROM-----EGNPI----- 1424
Db 1534 RLPSGVATCVLKLKSPANGSLGPTLNLSSGESRLAARFDSMCLESTFGILPSNFVPP 1593
OY 1425 -----PD-----TPQAGEEEMTAP-VPOIIMLPONGMWTQONPSPAC 1463
Db 1594 PSPAPSDSPASPDIEDLQAMNVSILPPTAGPEMTSAPSLPLVREPPV-----C 1641
OY 1464 QCSSDKIKMLPVCPPGAGGLPPQQRKONTADIIQDLTGRNISDYLVKTYVOIIAKSLKN 1523
Db 1642 TCSAGCTGS--CPSSVGG-HPPQMRVYTDILITDIGHVSYLLFTSDRF----- 1690
OY 1524 KIWNEFRYGGFSGISVSTQALPSPQEVNDAIKQMKHKLAKDSSADRLNLSGRMTG 1583
Db 1691 -----RLHRYGATIG--NVLKSLPASFGTRAPVYRK----- 1721
OY 1584 LDFRNVYVWENNGGWAHSSFLVNNAILRAMLOGE-NPSHYGTAFANHPNLTKQ 1642
Db 1722 IAVRAAQVFNNGGYSHPMYLNSLNNAILRANLPKSKGPAAYGITYVNHHPNKTSA 1781
OY 1643 LSEVALMTTSVDVLSICVTRFAMSFVPASVYVELIQBRVSKAKHLOPISGVKPYIWSN 1702
Db 1782 LS-LDYLLQGDVYIYALFIYAMSFPVASFVFLVAKRSTKAKHLOPISGCPNITYWLAN 1840
OY 1703 FVMDICNVVPATLVIIIFICEQOKSYVSPNLPVALLLLILGMSITPLMYPASFVKI 1762
Db 1841 YVMDLNTLVATGCVIILFVFDLPATTSPINFAVLSLEFLIGWSTIPIYMPASTFV 1900
OY 1763 PSTAVVLTYSNLFTINGSVATFVLELT-DNKLNNINDLSVFLPFPHFCIGRLID 1821
Db 1901 PSSAVVFLVNLFTIGITATVATFLLQFHEHDKDLKVNSLSCFLPFNMYHGLME 1960
OY 1822 MVKQAMADALERGE-NRFVSPLSMDLVGRNLFAMAVEGVFFLTIVLQYFFIRPP 1880
Db 1961 MAYNEYNEYAKIGQPKMKSPPEMDIVTRGIVAMAVEGVGFLTIMQYNFLRRP 2020
OY 1881 VNARSLPDEDEDVRRERKRIIDGGGONDLIELKELTKTYRRK--RKPAVRIQVGP 1937
Db 2021 MPVSTKPEVD-DVDVABERQVRLGADNDNMVKENTLTKYKSKIGRIILAVRCLGVR 2079
OY 1938 PGECFGLGVNAGKSSTFMKLTGDTTVTRQDAFLNKSLSLINSIHVHOMNGYPCOPDAI 1997
Db 2080 PGECFGLGVNAGKSTTFMKLTGDESTGGEAFVNGSHVLEKHELQVOOSLGCPCODAL 2139
OY 1998 TELTGREHVEFFALLGVEKEKYGKVAIRLGLYKGEYAGYSGGNKRXISTAM 2057
Db 2140 FDELTAHEHLDLYRLNGISMKDEARVAKALELLELTKYADKPRAGTYSGNKRLSTAI 2199
OY 2058 ALIGPPVFLDEPTTGMKPRARFLMNCALSVKKEGSRVVLTSHMECEALCTFMATM 2117
Db 2200 ALIGYPAFIFLDEPTTGMKPRARFLMNLILDLIKTRSVVVLNHSMECEALCTFLATM 2259
OY 2118 VNGFRLGVSQHLKKNFGGTYTVIRIAGSNPDLEKVDQFGLAPRGSLAKKHHNMIO 2177
Db 2260 VNGRLRLGISTQHLKKNFGGTYMTR--TKSSQSVKXVYVFFRNRPDEALKRHHNTKO 2318
OY 2178 YOLPSSLSLARIPSLISQSKKRRLHIEDYVSQOTLDQVNVNFKPOSD 2227
Db 2319 YOLKSEHISLAQVSKMEQVSGVLGIDYVSQOTLDQVNVNFKAKKOSDN 2368

```

```

RESULT 11
Q9UPUO
ID Q9UPUO PRELIMINARY: PRT: 1529 AA.
AC Q9UPUO:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE K1AA1062 PROTEIN (FRAGMENT).
GN K1AA1062.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RX MEDLINE=9397452; PubMed=10470851;
 RA Kikuno R., Nagase T., Ishikawa K., Hirose M., Miyajima N.,
 Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 6:197-205(1999).
 DR EMBL: AB028985; BAA83014.1;
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR001687; ATP_GTP_A.
 DR InterPro: IPR000561; EGF-like.
 DR Pfam: PF00005; ABC_tran; 2. Lipocalin_cyflab.
 DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
 DR NON_TER 1
 FT SEQUENCE 1529 AA; 170059 MW; BCD65F5E4AACA1A CRC64;

Query Match 28.4%; Score 3345.5; DB 4; Length 1529;
 Best Local Similarity 46.7%; Pred. No. 3.3e-212;
 Matches 721; Conservative 207; Mismatches 381; Indels 235; Gaps 33;

OY 836 GVMVYIEAVFPGQYIPRMVYFPCSTYFGE---ESDEKSHGSGNOKRMS-----ETC 887
 DB 1 GILWYIEAVHPGMYGLPRMYPFLQKSYLMSGRTAEWMSWATPPLSYWEEQAC 60
 OY 888 -----MEEPYHLKLVGSIONLVYVYRDGKAVAVDGLALNFYGCQTSTPLGN 935
 DB 61 AMESRREETRGMEEPETHPLVYVCYDKLTKYVCKDKLKLNTSLMLYENQVVSFEGHN 120
 OY 936 GAGKTTMTSLTGLPPTSGATYLGKDIRSEMSTIRONIGVCPQHVLDTMLTVEEHM 995
 DB 121 GAGTTMTSLTGLPPTSGATYLGKDIRSEMSTIRONIGVCPQHVLDTMLTVEEHM 180
 OY 996 FYARLKLSEKHKVAKEMOALDVLSPSSKLKSTQSLSGGMOKLSVALAFVSGSKVYI 1055
 DB 181 FYSLKSKMAQBEIRREMDKIEDLEL-SNKRHSLVQTLISGMRKLSVALAFVSGSKVYI 239
 OY 1056 LDEPTAGVDPYRSGIEMELLKTYROGRTIISTHMDADVIGRIATISHGKLCYGGSS 1115
 DB 240 LDEPTAGVDPYRSGIEMELLKTYROGRTIISTHMDADVIGRIATISHGKLCYGGSS 299
 OY 1116 LELNKGATGYTLVTKKDVESLSGCRNSSSTVSYLKKEDVSQSSSDAGLSGDSHSDT 1175
 DB 300 LFLKGYGDDGYRLTLVKRPAERG-----GPOEGLASSPPGKA 337
 OY 1176 LTIDVS--AISNLIRKHVSEARLVEDIGHETVYLPYEAKEGAFVELFHEIDRLSLDG 1233
 DB 338 PLSSCELSQVSOFRKHVASCILVSDTSTELSYLLPSEAAKGAERLFGRLERSLDALH 397
 OY 1234 ISSYGISSTLEELFLKVAEE-----SGYDA-ETSDGTLR----- 1267
 DB 398 LSSFGMDTTLLEVFLKVSSEDOLENSSEADYKESRKDYLPAGAPASGECHACNLARCS 457
 OY 1268 -----ARRRRA-FGDKQCLRPFTEDDADNDNDIPESRETDLS 1309
 DB 458 ELTOSQASLSQASSVSGARDEGAGYDYDYRPLF-DNQDPPD--NVSLEVEALALS 514
 OY 1310 GMDGKGYQVGMKLTQOQVYALLMKRLIARSRKGFPAQIVLPAYVCTALVSLVLP 1369
 DB 515 RV-GGGSRRKLDGMLKVKQFGLLVKRFHRCARNSKALFSQILLPAFVVCYAMTVALSV 573
 OY 1370 PFGKPSLEIQPMYNEQYT-----FVSNDAPE-----DTGTELLNALTIXPGF 1414
 DB 574 EIGDLPPLVLTSPQTH-NYTOPKGNFIPYANEEERETRLRLSPASPOQLVSTRLPSGV 632

OY 1415 GTRCM-----EGNDI----- 1424
 DB 633 GATCYLAKSPANGSLGPTLNLSSGESRLAARFDSMCLESTFGULPLSNFVPPSPAPS 692
 OY 1425 -----PD-----TPQAGEEEMTAP-VQTIMDLFONGNWTMONPSPACOSSDK 1469
 DB 693 DSPASDEDLQAMNVSPLPTAGPEMTWTSAPSLRLVREPR-----CYCSAQG 740
 OY 1470 IKKMLVCPGAGGLPPPRKONTADILLODLTGRNISDYLVYVOITAKSLAKNIWNE 1529
 DB 741 TGRS---CPSSVGG--HPPMRVATGDLIDTIGHVSEVLLFTSDRF-----RL 785
 OY 1530 FRYGFSLSVNTQALPPOEVNDAIKQMKHLKADSSADRFNLSIGREMTGIDTRNN 1589
 DB 786 HRYGATTFG--NVLKSTPASFGRAPPMWR-----IAVRA 820
 OY 1590 VYVFNKGMHAISFLVANNALIRANLQGE-NFSHYGTAFNHPLNLTKQOLEVAL 1648
 DB 821 AQVFNKGYHSMPTVNLNNAIRANLPKSGNDPAAGITVTNHPMKTASLS-LDY 879
 OY 1649 MTSVYLVLSICVIFAMSVSPASVYVFLIOERYSKAKHLQFISGYKPYIYMLSNFVMDG 1708
 DB 880 LLOGTVDVTAIFIVAMSEVPASFEVFLVAKSTAKHLQFVSGCNPIIYMLANVMDL 939
 OY 1709 NYVPATVILIFICFOOKSYSTNLPLYALLLLLYGMSITPLMYPASFEVKIPSTAY 1768
 DB 940 NYLVPATCCVILLFVVDLPATSPNFPVAVLSFLITGMSITPLMYPASFEVSSAY 999
 OY 1769 VLTSVNLFIGINSVATFVLELT-DNKLNNINDILKSVELLFPHRCGLIDVKNKA 1827
 DB 1000 FLIVNMLFIGNATVATFLLQLEHDKDLVNVSYLKSCLFIPVNYNLGHGEMAYNEY 1059
 OY 1828 MADALRRGE-NRFSVSLMDLVGRNLFAMAVEGVFELITLIOYRFPTRPNNAKLS 1886
 DB 1060 INEYVAKIQFDMKSPFEMDVTTRGLVAVAGVGVLITLMQGNFLRRPQMPVSTK 1119
 OY 1887 PLNDEDEDVREKORILDDGGGNDILEIKELTKIYRRK---RKPAVDRIQVGIPEGCG 1943
 DB 1120 PYED-DVDAASEQRYLRDADNDVYKLEMLTKYVRSKRIIGHLAVDRLCLGVRCGCG 1178
 OY 1944 LIGVNGAGSSFTKMLTGDTTYTRGDAFLANKSILSNIEVQNNQGYCQFPAITBELTG 2003
 DB 1179 LIGVNGAGTSTFKMLTGDESTGGEAFVNGHSVYKLELLQVOOSLGYCQCDALDELTA 1238
 OY 2004 REHVEFFALLRGVPEKEVCGEMAIKLGIVYKGYKAGVSGNKRKLTAMALIGSP 2063
 DB 1239 REHLQTLRLRGISWDEARVYKMALEKLELTKYADKPGYISGKNRKLTALALIGP 1298
 OY 2064 PYYFIDEPTGMDPKARFLMNCALSVYEGRSVLTLSHMECEALCTRMAIMVNGRPR 2123
 DB 1299 AFIIDEPTGMDPKARFLMNLILDITKGRSVVLTLSHMECEALCTRLAIMVNGRLR 1358
 OY 2124 CLGSVOHLKRRFGDGYTYVRIAGSNPDLKPYODFGLAFPGSVLKEKIRNMLQVOPSS 2183
 DB 1359 CLGSIOHLKRRFGDGYTYVRI-TRKSQSVKADVVRFFNRNPEAMLEKIRHTTVQYOLKSE 1417
 OY 2184 LSSLARFSTLSQSKRRLHIEDYSQTTLDQVFNFAKDQSD 2227
 DB 1418 HISLAQVFSKMEQVSGYLGIEDIYSQTTILDVFNFAKQSDN 1461

RESULT 12
 096CT3
 ID 096UT3 PRELIMINARY; PRT: 2277 AA.
 AC 096UT3;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
 DE ATP-BINDING CASSETTE TRANSPORTER FAMILY A MEMBER 12.
 GN ABCA12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

Query Match	27.4%	Score 3229.5	DB 4	Length 2277
Best Local Similarity	33.4%	Pred. No. 3.1e-204		
Matches 767	Conservative 426	Mismatches 726	Indels 377	Gaps 59
OX NCBI_TaxID=9606;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC TISSUE=RETINA.				
RA Bonner T.I., Moses T., Deterna-Wadleigh S.;				
RT "A retinal cDNA for the ATP-binding cassette transporter ABCA12.";				
RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.				
DR EMBL; AY034486; AAK54355.1; -				
KW ATP-binding.				
SO SEQUENCE 2277 AA; 256970 MW; EDA2FE00280361E2D CRC64;				
QY 103	ARLFSDARLLLYSOKDTSMKDKRVLRLLQOLIKSSSLMKLQDEL-----VDNET-	153		
DB 159	ALGGEIETIASLLYHDNVISRK-----VRDLTGDPCKILANDMOFLEGALONNYLENIQTQ	213		
QY 154	-----FSGFLYHMLSLPKS-----	173		
DB 214	LRLPIIEAMLHVNNNSADASKRGQOLLEMPKRVBEKEDLRRITGMSKRTIDKLALIPDN	273		
QY 174	RADVYLHKVEFLOGYOLHTLS-----LCNGSKSEEMIQLDGEVSEELG-----	217		
DB 274	RAEILISQVFWLHSCDTNITTPKLEDAKMEFCMILSEERSQ-----SYLIGLTLHYLN	327		
QY 218	-----PKKILAAARVLRSMNDILKPLRLRLNSTSPPKSELEAETTLHLSIGT	267		
DB 328	INFTYKVFPPKDKQPVKKM-----MELFIRLKEILN-----QMSGTHPLD----	371		
QY 268	LAQELLESMSKSDMR-----QEVAFITLN-VNSSSSSTQIYQAVSRVCGHPREGGKI	319		
DB 372	-----KMRSLKQMHLPKRSVPLTQAMYSRNRNTPQGS---FSTISQALCSQ-----GITT	418		
QY 320	KSLNMY-----EDNNYKALFGGNGTEDEATFP--DNSTTPYCNQIMKNISSPLSRI	370		
DB 419	EYLTLMDPSSQRPKKNHTKDTLTYKLTKEQJASKGIGDIPNTIPFCFSYKDIINMPAGV	478		
QY 371	IKKALKPLVGLKILTPDIPATROYMAEKNKFCQELAVFHDLGSMEEELSPK-----	422		
DB 479	IMAFILKPMILGRILVAPVNPVTKALMEKSDVTLRLQDLAELREKSSQGMMDKSLPLFNMSFLL	538		
QY 423	-----IWFPMNSQMDLYRMLLDSRDDHMEQQLDGLMDTAQDIAPFL	467		
DB 539	NCALPMLQNTLRNPFQVQYFKFSVGLDAVELL-----KQIDEL-----DILRLK	582		
QY 468	AKHPEDVOSSNGSVYTWREAEFNETMQAIRTISRFMECVNLKLEPIAEVWMLINKSMEL	527		
DB 583	LENNIDI-----IDQLNTLSSLIYVNISSCVLRIQAKTIIDEMEKARAKLY	629		
QY 528	DERKRWAGIVF-----TGITPGSIELDHHVAKYKIRMDIENVERTNKIKDGYWDPG	578		
DB 630	KSNELFGSVIKFLPNSRSMWHRQYDSGANFLPVLVIYTRIMSLKTPAQITRSILRTKIMAGP	689		
QY 579	RADPFEDMRYYWGGVGLQDYVEQAIIHVLVG--TEKKTGYVMQOQPRVCYVDILFLRMS	637		
DB 690	HNSPQHNIY--GRAFTIYIQDSIERAIIIELOIGRNSQELAVYOQAIPYPCFKMDFLISVS	748		
QY 638	RSMPLFMTLMTYSVAVIITKIIVYEKARLEKTRMIMGLDNLIMFSWFISSLPLPLVSA	697		
DB 749	YSLPIPLVAVWAVFIAAEVKKIYVEKDRILHEYMKMGVNCSCSHFPAWLISVGLVITI	808		
QY 698	GLAVYIILKGLMLRPSDSVVEFLSVAVVYTIIOCLPISTLFSRANIAAACGGLIFTL	757		
DB 809	VILIITLKFGLNLRKTNGLFLFLFSDISSESVIAMSYSITISVFNNNTNIAALIGSLITYIA	868		
QY 758	YLPFLVLCAMODYVGTFLIKFASLISPAFEGCEYAFEEQIGVOMDLFESSPEED	817		
DB 869	FFPFLVLTAVENELSYVLKVFENSLSPATFASVQDIYARVEQDGIQLOWEMMTYSPVQDD	928		
QY 818	GFNLTLTIS-----MMEDPTLIXGVMTVYIEAVFVGQYGIIRPWTVPCTCKSTW---FG--E	868		

Dd	929	----	TTSGWMLCCLILADSLFTYFLIAMVRNWFPGITGMAMPYFPLLPYKWERGCAE	984
Qy	869	ESDKS-----	-----HGSNOKRNSSEICEEPTTHLKLSIONLTKVVRDMDKVA	915
Dd	985	VKPEKSNGLMFTNIMQNTNPSASDEWFSNIEPEKDLTVGALHGVKTI--	GSXYA	104
Qy	916	VDGLANFYEQITSFGLNAGATTMSILTCGFPPTSGTAVILGKDISEMSTTRONL		975
Dd	1043	VDNLINLFYEGHITSLGPNAGATTIISMLTGJFGASAGTITVYGDKITDHTKRYKM		110
Qy	976	GVCPQHNVLFWMLVFEHIFWYARLK--GJSEKIVKREOMALDVGJPSKLSKSTSOJ		103
Dd	1103	GVCMQHDVLFVLTIKHLLKYSIXKPYHMKQJLHEVAKRTKLDGYSIHRK--RVGL		116
Qy	1034	SGCMOKTISVALAFVYGSKVILDEPTAGDVPYSRRCIWELLKYNQRTIILSTHND		109
Dd	1162	SGCMKRKLTISIALIGGSRVYLIDEPSTGVDPCSRISIMVJISKNXTARTIILSTHND		122
Qy	1094	ADVLDRLAITISHKLTCCVSSLSLKNQJGYYTLTKKDVASSLSJSCSNSSITYSLK		115
Dd	1222	AEVLSRLAFLEOGGLRCCSPFLKAFGJGHLHTRK-----		126
Qy	1154	KEDSVSOSSDAGLGDHESDTLIDVSAISNLIRKVSARLVEDIGHETLYVL--PYEA		121
Dd	1262	-----KSPNLNANAVCDT-----AVTAMIOSHLPAYLKEDIGGELVYLPPEST		130
Qy	1213	AKEGAFVLFHEIDRLSDIGISYGETTELEIFLKAEEGVAFESDGLPARR--		127
Dd	1308	KVSGAYTSLRLALDNGMDLNGCYGISDPTVEEVLNTRKESQKMSAMSLHTQKKFG		136
Qy	1271	NRRAFQDQKOCRLPFTEDDADPADPDSIDIDESPRTDLSGMDKSGSYQVKNMLTQOCV		133
Dd	1368	NSNANGIS-----TDDLSVSSSNTD--RDKILT--RGE-RIDGGLLKKTM		141
Qy	1331	ALMKRLLIARSRKGFPAQIVLPAFVCLALVPSLIVPEGYPSLELQPMY--NEOY		138
Dd	1413	ALIKRPHHTRNNKGLIAOVITLPIVATMCLGTLRNSNSYSPETIOISPLYSGETQ		147
Qy	1389	TFVSNDADEDTGTELLNALTKDGFCTRCMEGNPIPDTRC--QACEEEMTAPADQITM		144
Dd	1443	AFYANYH--STALYASAMDFPDGIDNKLNTS---DLOCLKDSLEKMNSTGERTYF		152
Qy	1447	DLFONGNMTWONPSPACQSSDKIKKMLPVCPGAGGLPPQKONTADILDTGRNIS		150
Dd	1527	GV-----CSCSEN-----VOECB--KFNYSPPHRTYSSOVILNIGORVE		156
Qy	1507	DYLVKTYQIILAKSLKMIWNEF--RYGSESLGYSNQAOLPPQSEVADAIKOKKHKLK		156
Dd	1566	NYLIST-----ANEFVOKRIGGMSFG-----LP		158
Qy	1564	LAKDSSADRFNLISGRPMTGID--TRNNVYKWFNNKGMHAISSEFLVYNNALIRANLORGE		162
Dd	1589	LTKDLRFD-----ITGVANRRTLAKWYMPDEGYSHPALVNLINLFLIRVNMSSKYD		163
Qy	1623	NPSHYGTAEHNLNLKQOLSEVALMTSVDVLSICVIFAMSPVPAASFVFLLOERTS		168
Dd	1640	AARH-GIIMTSHRPGVOD--BOATISLIDLIVALSILMGSYTTAASFVYVREHOT		169
Qy	1683	KAKHJQETISGVKPIYVLSNFVMDCKMYVPAVLVIIFICEQOKSYVSTMLPYALAIL		174
Dd	1697	KAKQJHISGVGYCVMWNTFYIDMVFYLPVPAFSGIIAIFKRLAPAFSENNLGAVSILL		176
Qy	1743	LLYKMSITPLMTPASVEFKLPSTAIYVVLISVNLFGINGSVATEVLELFTDNKLN---		179
Dd	1757	LLFEPYAFESWMLYLAGLFHETGMAFTTYVVCNLFEGINSYLSVVPYLSKEKPNDPLYE		181
Qy	1799	-INDILKSVFLIPFPHCLGSLIDWKNQAMADALERFENRFVSPLSMDLVRNLFPMA		185
Dd	1817	LISITLKRILFIPQCFGIGIELSQOOSVLDPLKAYEVEPNTEFEMKTLGAMFALV		187
Qy	1858	VEGVFELITVLI-----QYREFLRPNVAKLSFLUNDEIVRERORITLDGGGONDI		191

Db 1877 SGTMPFSLRLINELIKLRLFFR-KENSSHRETIDEDVBARLRVESGAEEFL 1935
 Qy 1912 LEIETLKIYR-RKKPAVDRICVGIIPGCEPGLLVGNAGKSTFKMLTGDTTVRGD 1969
 Db 1936 VOLCLTKTYOLIKKILIAVNNISIGIPAGCEFGLLVGNAGKTIKMLTGDTIPSSGN 1995
 Qy 1970 AFL-NKSIISINIEHVONMGYCPQPAITETLTLGRRHEVEFALLRGVPEKEVKGCEMA 2028
 Db 1996 ILINKKSGSLGHVDSHSIYCYCPQEDALDVLVEEHLIFYAARVHPIPERKDIETVHKL 2055
 Qy 2029 IRLKGLVYGEKYVAGNSGKRRKLSTPAMALIGSPVFLDEPTTGMKPRARPLMNCAL 2088
 Db 2056 LRLHLMPFKDRATSMCSYCFKRRKLSTPAMALIGKPSILLIDEPSSGMDPKSRHLMKIIS 2115
 Qy 2089 SYVEGSGSVLTSHMECEALCTRMALIMVNGRRCGSHVONHKNRGDCGTYIVYRAGS 2148
 Db 2116 EEVONKCSVLTSHMECEALCTRLIMVNGKFCQIGSLQHIKSRGGRGTVAVHLKNN 2175
 Qy 2149 NPDLKPVODFGLAFPSVLKEKRRNMLOLQOLPSSLSLARIFSLISQSKRLHIEDYSV 2208
 Db 2176 KVTMETLTKFMQGLHFKPTLYLKQDLMSLEHYHVPYTAGVANIPDLLETNTALNTINFLV 2235
 Qy 2209 SQTLLDQYVFNFAKQ 2224
 Db 2236 SQTLLLEVFINFADQ 2251
 RESULT 13
 QYVRS4 PRELIMINARY: PRT: 1713 AA.
 AC QYVRS4;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE CG1718 PROTEIN.
 GN CG1718.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; Pubmed=10731132;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 Georjon R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Burton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Niklos G.L.G.,
 Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 Balcer R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman W.,
 Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 Glodet A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
 Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Liao X., Liao Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mpherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paigled J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 SC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL: AE003568; AAF50837.1; -
 DR Flybase: FBgn0031170; CG1718.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR001687; ATP_GTP_A.
 DR Pfam: PF00005; ABC_tran; 2.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Transport.
 SQ SEQUENCE 1713 AA; 192888 MW; 9DE20DB3BF9DC1CA CRC64;

Query Match 21.1%; Score 2485.5; DB: 5; Length 1713;
 Best Local Similarity 32.3%; Pred. No. 3,6e-135;
 Matches 622; Conservative 354; Mismatches 603; Indels 345; Gaps 49;

Qy 410 HDLEGWMEELSPKRTFMENSEQMDLVRLMLDSRND--HFMEQOLUDMTAODIAPFL 467
 Db 24 HKQWVIELVLPALPISL-----LVLRVLVDEQKGVRYNEQNLTDNL----- 69
 Qy 468 AKHPEDVQSSNG-SVYTWREAFNETNOAIRTT-----SRMECVNLKLEPIATE 516
 Db 70 -----LQKNGFSKFEELICYSPVNPVLKKILVEEAMQSLGKNNKICSEENATOLE----- 118
 Qy 517 VMLINKSMELIDRRKWAGIVFGITRPGSE--LPHNKKYKR-----MDIDNVE 564
 Db 119 -----LDTVSKNAF-AGVQFDAMANLTENDPLRDNDFALRPALERTATATANW 170
 Qy 565 RTNKIKDGYNDPPRADPDED---MRYWGFAYLQDVQEAOLIRVLVLTGTEKKTGYVMO 620
 Db 171 LTRRLPFTIDLRPRNEDGDDGIPPGYLRGFLPLQHSLSMAVYLRKGGEDLPVYVAK 230
 Qy 621 QMPYPCYVDIDFLVMSRSPLEFMTLAWIYSAVVIKGIYVERKARLKTMRIMGLDINSI 680
 Db 231 RYFPFAVIFDPLLEGSSIMSILILSFYPCYTYIKTYTAKEKOLKEVMKIMGISNML 290
 Qy 681 LMSWFISSILPLVSNAGLIVLILKIG-----NLRLYSDPSVVFVLSFAVAVTILQCL 735
 Db 291 HWTAMVPKSFIMLTISAILLAILIKINSEDAVALTHANFTALVFPLIIVSSICECFM 350
 Qy 736 ISLTFRANLAACGIIYFTLVPLVCVAMQDYGFILKIFASLSPVAFGCEYPA 795
 Db 351 MATFFSASATAAVTGLIWTIAIPIYSFTINSYDDLSLSKLSMSLSTNMGFGIKLL 410
 Qy 796 LPEEOGIGVQWMDLFPVSEEDGFNLTTISMLFDTFLGYWTWYIEAVFPQGIPIRP 855
 Db 411 GFEGTGGGLQWSNFFPVSVDDTLTGAIVIMLVCAVIMILCLIVEQVMSFSEVPRP 470
 Qy 856 WYRPPCKSYAFGE--SDEKSHPGSNOKRNSLCMEEPETHLKLGSIONLVKVRGDK 913
 Db 471 WNPFPREFPCGREGYTGVEDIPNGVEQDPAFTEPEGKHIGLOMHLK--RFGNK 528
 Qy 914 VAVDGLALNFEEOITSPFISNGAGKTTMSILTGLFPTSGTAVYILGDIRSENGSTIO 973
 Db 529 MVTGKLSMNFEDIELVILGHNGAGKTTISMLTGFPPTSGAIINGSDIRNTIEGARM 588
 Qy 974 NLGVCPOHNVLFMLTVEEHIWYARLKLSEKHVAEOMALDGLPSSKLKSTSQL 1033
 Db 589 SLGICPOHNVLFDEMGSVNHIRFSSRMKGRGAKVAEQEVAKYLMTEL--EDKANVAASXL 647
 Qy 1034 SGMOKRLSVALAFVGGSKVYIIDEPTAGVDPISRGKIVIELLKYOGSTIILSHHME 1093
 Db 648 SGMOKRLSVALCGDTRKVLVLCDEPSSGMDPBARQIWDLLQOEKVGRTLLTTHFME 707

Db 190 DN-----PLT-----AGIVFDDSIADKLNKDPKRDFTYIRLSNTH 225
 QY 565 RTNKIKIDGWDPGRADPFEDMRYWG-----GFAV 595
 Db 226 RRRR-----NACFDNSYPWDTSVSAVOYVSGPINDDDGSGPGYMOGEMT 273
 QY 596 LQDVEQAIIRVLTEK-----TGVMQOMPYPYVDIFLRASRSMPLMTLAWY 650
 Db 274 VQRAVVAITEITIGDAOLTPLLDSYVSRFPFGYSTKI-TEICAFMPYVIFSMT 332
 QY 651 SVAVIIGIYERKARLKTETRMIGDINSIMFSSISLIPPLVAGLLVILKGNL 710
 Db 333 SVIYIRAVVVEKEDRLKEKMRVMSLOFINVAFHILYNAKLFYAVILTIMHFVAL- 391
 QY 711 PYSDPSVPELSEFAVNTILOCELSTESRANLAACGIIYTFLLY----- 759
 Db 392 -KSDMTLMEFLMIVAFDVYFAFMISFPMNSATSLISVFMALLYFVAFSSIDOT 450
 QY 760 -PYVLCAWADYVFTLKIIFASILSP-VAFGCEYFALFEEOGIGVOMDLFESEVED 817
 Db 451 NPYPL-----GYRL-----INCINDIALNYGLLOLAIVETQADLKNGLFTPSPDN 499
 QY 818 GFLUTISIMMLFDTFLYGMVYIAVPPGYGIP-REMYFPCTSYWF--GEPSDEK 873
 Db 500 NLTFGHALIALIYDGIIMILTYIAVPIPGEGVPOKPMWF-VLPSYFPMNGSKTVDS 558
 QY 874 SHFGSNOKRMSSEIOMEPEPHTLKGVSIOQLVYV-----RDGKKVAVDGL 919
 Db 559 SDOPFOIYADHVLEKEPDLIPTINVVALTYGTSPFKKLEDCFGSGKRAVSNL 618
 QY 920 ALNFYEQSITPLGHNAGAKTTMTSLTGLPPTSGTAVILKIDISEKSTIQNLGVC 979
 Db 619 NLKMYPGQCTVLLGHNGAGSTTFMSLTGASPSGSAVYNDPITSLPKIRREGCLP 678
 QY 980 QHNVLEDMLTVEEHIMFYARLKLGS--EKHVKAMEOMALDVLGPPSKLKSITSGM 1037
 Db 679 QYMTLFGFTVMEHLEFFAKLERTMDPEAREILARLIDF-----KADFMAGALSQ 733
 QY 1038 QRLSVALAVGSGSKYVILDEPTAGVDPYSRKRITWELLKRYGRTIILSTHMDADVL 1097
 Db 734 KRLSLAIALIGSEYVWMDPEPSGMDPGARHETWLLIOREKERRITLTHMEADVL 793
 QY 1098 GDRITAIISHKLCVGSLEFLKNOGLGYLLTVKKDVESLSSCNSSSTVSLKEDS 1157
 Db 794 GDRITAIHAHQLECCSGPMLKQOYGDYHLYV----- 827
 QY 1158 VSGSSSDAGLSDHESDITLIDVSAISNLIRKHVSEARLYEDIGHLLTYVPEAKEGA 1217
 Db 828 -----YDTPSPVSKTTDILREYIPEAHVSYIGQATYLL--SATHRPI 871
 QY 1218 FVELFHEIDRLSLDGLSSIGISSETILELFLVAF-----ESGVDAETSDGTLPAR 1269
 Db 872 FPLFLFELEHOGTCGTSGVSIITMEEFVLKVTADERYNYEKGIEENDISE----- 925
 QY 1270 RNRRAFQDKQSCRLPTEADAPNDSDIDPESRETDLLSGMGKSGYOKGKLTQOOF 1329
 Db 926 -----MEKR--DPILOD-----KQVRYTGTLOMQRA 953
 QY 1330 VALLMKRLIARSRKGFQAIVLPAVFCIALVFSLIYPPFGKYPSELQPMWNEYOT 1389
 Db 954 KAMEYKRAIFFFRKMTQFLPOLVPAVYLVAMVTSQVLPSVKE----- 997
 QY 1390 FVSNDAPEDTGTELELNALTKDQFGTRCMGNPIPDTPQAGEEEMTAPVQTIMDLF 1449
 Db 998 -----QDPOTISLA-----PFSDTK-KAG-----HLVSD- 1020
 QY 1450 QNGWMTQNSPACQCSSDKIKKMLPVCPPGAGGLPPQKOKMTADILDLGRNSDYL 1509
 Db 1021 -SGNYVTL-----LOG-----SONLSSWY 1038
 QY 1510 VKTYOIIANSLKNIWNEFRYRGFSLGVSNTQALPPSGEVDAIKOMKHLKLAKDS 1569

Db 1039 QCTVQ-----LGVTQI-----VVDITSNVEKFINQDNAM 1069
 QY 1570 ADR-----FLNSLGRFMTGLDTRNNVYVFNKNGMAISSFLYINNAIIRANLOK 1620
 Db 1070 GSRITGLHYALGFVPSMNFST--VSPSLKTFENNFELYPALAITTDSMIILSOKOK 1127
 QY 1621 GENPSYGITAFNHPDLNLKQOLSEVALMTTSVDVLSICVIFAMSEFVAFVFLIOER 1680
 Db 1128 -----QYSEFVANNHPLPSTQDTLKNRSGGAFLIAGLIVSAVAVAGYSQFLITER 1182
 QY 1681 VSKAHLOFISGVKRYVYIWSNFVMDKCNVYPATLVIIITFCQOKSYSTN-LPYLA 1739
 Db 1183 KKSXKHMOILSGIRPMFMWMLFAFIDAMFYIRILCFDAIFYINITAYTDFGMLLT 1242
 QY 1740 LLLILGMSITPLMYPASVFEKIPSTAVVLTYSVLFINGSVATFVLELFTONKLN 1799
 Db 1243 LSFILKGTALPFTYWFQFFESAPKGMWMTWHIILGMIGIAVPIISOTSISDAGYL 1302
 QY 1800 NDILKSVLIFPFLCGLRLIDMYKNQAMADALERE-----GENRFVS 1842
 Db 1303 WSLTFA--WLFPTYNISQIATVTFQENYRIACKRLDCTIPMKFVATACGTSABRLYD 1360
 QY 1843 PLSMVLGN-----LRMAVEGVFFLIYLIQREF-----IRPPYNAKLSPLND 1890
 Db 1361 NVLF--VGNRKGIYVYFLAVQGFYIWMFMRENDOFTLALIRCKADNPIMDITD 1418
 QY 1891 -----EDEDVRRER--ORLIDGGQNDILEIKELTIRYRKRKPAYDRICVGI 1938
 Db 1419 TKVDREYEDSDVIAESVORL--ANNKKTALVSNLNYKMGFN--AKGVNHFNS 1474
 QY 1939 GECFGLGVNAGKSGSTFKMLTGTDTYTGDAFLNKSILSIHIEHOMGYCPOFDAIT 1998
 Db 1475 KCFGLGVNAGKSTFQMLTGEMSISSGDAYVNGSVKNMWRGANGYCPQYDALI 1534
 QY 1999 ELLTGREHVEFPALLRGVPEKGVGEMARLKLGLVYGEKYAGNIGCKKRLSTMA 2058
 Db 1535 KEMSGEETLYMFAIRJPEKIDPKVNAVIAHIGIYASROIKTYGKKRRSLGIA 1594
 QY 2059 LIGGPYVFLDEPTGMPKARFLMNCALSVYKGRSVLTSHECEALCTRMATV 2118
 Db 1595 IYGLPVLILDEPTSGVDKARITLWNLINLRDGLTALVLSHMDCEALCTELATV 1654
 QY 2119 NGRFCLGSVQHLKRNFGGYTIVRIAGSNPDLKPVDFGLAFPGSVLKEKRNMLQY 2178
 Db 1655 YKFRFCYSGCHIKRSGYTYLLIRLKNRN-DARKTSTIKQFRGSVINEHLOLNF 1713
 QY 2179 QLPSSLARIFSLISQSKRLHIEDYSVSQTTIDQYFVNPAKD--QSDDD 2228
 Db 1714 DIPRQDSWSRLEFKLETYSTLSLMDDDYLSQTTLEQVFIERSRDAGVSDSE 1766
 RESULT 15
 Q9VVJ9 PRELIMINARY; PRT; 1660 AA.
 AC Q9VVJ9;
 DT 01-MAY-2000 (Tremblrel. 13, created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CG6052 PROTEIN.
 GN CG6052.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Gelinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Adamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 George R.A., Lewis S.E., Ashburner M., Henderson S.N.,
 Sulton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mlikos G.L.G.,
 Abrell J.F., Abdayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 Bailey R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegwan C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradlin A.C., Stapleton M., Strong R., Sun E.,
 Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE005523; AAF49312.2;
 DR Flybase: Fgn0036747; CG6052.
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR001687; ATP_GTP_A.
 DR Pfam: PF00005; ABC_tran; 2.
 DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN 1.
 SO SEQUENCE 1660 AA; 187552 MW; 76622965ECEF7814B CRC64;

Query Match 17.3%; Score 2041.5; DB 5; Length 1660;
 Best Local Similarity 28.9%; Pred. No. 8.8e-126;
 Matches 527; Conservative 332; Mismatches 575; Indels 389; Gaps 48;
 QY 532 FMAGIYF---TGITPSEILPHHVKKIIM-----DINVERIKKIKGYNDPPR 579
 DB 84 FLAAGVGFENENNTNDAGYPLNLTSLRPSRLRTMOGPIITDWTSLFSLSTYTSGR 143
 QY 580 ----ADPFEDMRVWGFAVLQDVVEQALIRVLGTETKTG---VYMOQMPYCVVDIF 632
 DB 144 NRLNDGCVPGVYIRGELPIQHALTMSWALASGV-IDTGIPALHIDRFPYRATYIOL 202
 QY 633 LKVMKSMPLFMTLMTIYVAVIYKGYEKARLKTMRKINGLONSILMSWFTSLIP 692
 DB 203 LSGRLQLFVILITFIPASTVTKYVSEKELQKEIMKLIGVHNHLMWAMFAFKSYIM 262
 QY 693 LTVSAGLVVILKLG-----NLTPYSDPSVYVFLSVAVVYIIOCLFISTLFSANLAA 747
 DB 263 LMLVFLIMSLMKFYASVAVLTSSWVPLFLHTYVYVSVCLCPMLAVLESASTAS 322
 QY 748 AGCGIITFLYLVLYLCVAMQDYVGTFLTKIFASL-SPVAFGFCGEYALFEEOGIGVQ 806
 DB 323 AVAAIFMFLTYIPYSGFYVYERLSLMSKLLISLFSNSALGFGIHVYVMWEGEGITW 382
 QY 807 DNLFSPEVEDFNLTSTSMALPFTFLXGYMTWIEAVFPGQIGIPRPWTPTCTKSYW 866
 DB 383 RMMFHPVSTDSLFLFYIIMTMSFSGIMFISICLVYEQVFPGEVGRPRWFMCHKNYW- 441
 QY 867 GESEDEKSHPSGN-----QKRMSEICMEEPFHLKLGVSIONLVKYYROSKMAYV 916

DB 442 ----ROYVPSLNTVPSFOTILHGSAAKASCRRAR-----EVGIQLEFNIQKNY--GKLKAV 490
 QY 917 DGLALNFEQGITFLPFGNNGAGKTTTMSILTGPPSTGATVILGNIRSEMSI IRONL 976
 DB 491 KGISLKHARNETTYLGHNGAGKTTTMMITGYIKPSTGATVIGYITRHLKAKRESLG 550
 QY 977 VCPQHNVLFDMLTVEEHIWIFYARLGL-SEKHVKAEMQALDVGILPSSKLSKT-----S 1031
 DB 551 ICPNNILFKEMSVRDIHIFESKLKIGTKRAVENEGKY-----MTMLKIDKQSVYAAK 605
 QY 1032 QLSGMOBKLSVALAFVGSKVYVLDDEPTAGVDPYSRGIWELLLKROGRTIILSTHHM 1091
 DB 606 NLSGMKRKLSLCCALCGNAKAVYLCDEPSSGIDAGRSIMLDLQSEKDRITLLTHYM 665
 QY 1092 DEAVLDRLAIIISHGKLCVGSLSFLKNQDGTGYTLTVKKDVESLSLSCRSSTVSY 1151
 DB 666 DEADVLGRIALISEGKLCOGSTFYLLKRRGTYLLVCIMQ-----SSC----- 710
 QY 1152 LKKEDSVSSQSSDGLSDHESDITLDVGAISLTKKHVSEARLVDDIGHETLYLPTE 1211
 DB 711 -----DGAIVTQILKKYVPIKPERVLTETLYRLPE 743
 QY 1212 AAKGAEVLEFHEIDRLSDLGISYVIGSETTELEIFLK-----AESGVDAETSDGTL 1267
 DB 744 YSKR--FAELLQDDEKCAQQLVGYGLSGATLEDVAVNTDKRYVGGAGEPPVDSI- 800
 QY 1268 ARKRRAFGDKQSLRPFEDDAADPNDSDIDPESRRTDLISGMDKGSYQVKGWLTQO 1327
 DB 801 -----DFKELVDSKTRER-----RRIR 819
 QY 1328 QEV---ALIMRLILARRSRKGFPAQIVLPAVFCIALVSLVPPGKPSLELOPMWY 1384
 DB 820 CFMWQALFLKFTYTRNNWLLQIOLVLPILAVKALITLMSRGRITYELPAPISINQY 879
 QY 1385 NEQTEVSNDAPEDTGTELLMALNKD-PGGTRCMEGNPIPTPCQAGEEWTPAVPO 1443
 DB 880 SSAYVLEDDNTDTKTSS--LADAVSKHLEHYARC----- 912
 QY 1444 TINDLFGNMTWQNPSPACQSSDKIKMLPVCPPAGGLPPQKQONTADILQDUTGR 1503
 DB 913 TLL-----KRGDL----- 920
 QY 1504 NISDYLVKTYVQIIAKSLKKIWNVEFYGGFSLGVSNTQALPPSOEVDNAIKQMKHLK 1563
 DB 921 KFEEDYIL-----SHDVNHS-BRIDFH-- 940
 QY 1564 LAKSSADRFLNSIGRMTGLD--TRNNVYKVPNNKGNHAISSPLVYNNALILANLQKBE 1622
 DB 941 -----FLAGLVSENNFIWLNKRPLHTAPLTNLNLHNLAIKL--GQ 982
 QY 1623 NPSHYGITAFNHP-----INLTFKQOLSSEVALMTTSVDVLVSLCVIFAMSFVPSAPV 1673
 DB 983 DASLY---VINEPLPYSDDRTLRLNKGYV-----LGAEISINLSITWCFITAFPA 1030
 QY 1674 VFLIQEVNSAKHLQITISGVKPVYIYLSNFWDMCNVVPATLVITITFCQOKSVYST 1733
 DB 1031 IPIIRETRFAKLQIFSGVQVCAVYWSHIMVYLVFVLSALSIITIAAFKEIGYITPD 1090
 QY 1734 NLPLYALLLLLYGMSITPLWYSPAFVKIPSTPVYVLTSLVNTLGTINGSAATPVLELFD 1793
 DB 1091 DLSRTFYMLLIFGPGIMLSYLAASGCSDAATGFTYRISITNTLMG--TGLFLMFTINTFER 1149
 QY 1794 NKLNNINDILKSVLFLPHFCLGRGLDM-----VKNQAMADALEFFGEN---RFVSPLS 1845
 DB 1150 FQKLDAVEKILAMFRLSPSLASSHSIHIGNIRGCSIGIRKLRLPQOLRCRNV-PLC 1208
 QY 1846 WDLVGR-----NLPMAVEGVVFLITVLYLQYRF-----FIRPPRYNAK 1884
 DB 1209 CDIPGYGWMKPGVLYEITYIMIGSTLFLIYMHAKACONLAEKLGNCFSKRRKVEEG 1268
 QY 1885 LSPINDEDEDVREBORILDGGONDILKEIKLTKLYRRKRAVAVDRICVGPCCFGL 1944
 DB 1269 TSIENDSVAAEORVVRKEMINSGRKVDPLVYKISKIRSKL--AVAKISFHVPHACEFGL 1326

